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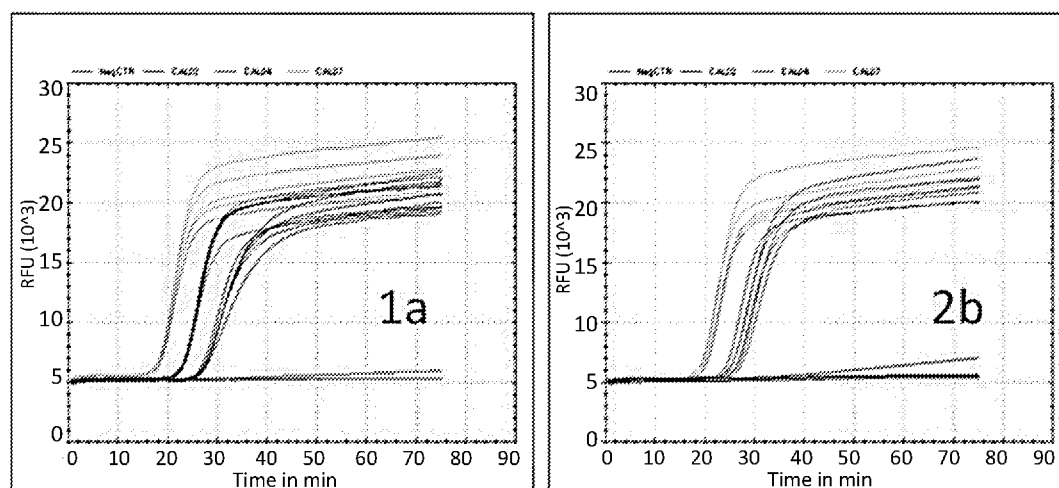


Fig. 2-1

(57) Abstract: This disclosure provides oligomers, compositions, and kits for detecting and quantifying Hepatitis C virus (HCV), including different genotypes and variants thereof, and related methods and uses. In some embodiments, oligomers target the 5' untranslated region of HCV and are configured to provide substantially equivalent quantification of different genotypes and variants of HCV.

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COMPOSITIONS AND METHODS FOR DETECTING OR QUANTIFYING HEPATITIS C VIRUS

CROSS-REFERENCE TO RELATED APPLICATIONS

[001] This application claims the benefit of U.S. Provisional Application No. 62/410,188, filed October 19, 2016, the contents of which are hereby incorporated by reference herein.

INTRODUCTION

[002] This disclosure relates to compositions, kits, and methods useful for the detection and quantification of Hepatitis C Virus nucleic acid.

SUMMARY

[003] Hepatitis C Virus (HCV) can cause acute and chronic disease, with infected individuals being at risk of liver cirrhosis and cancer. Approximately 130-150 million individuals worldwide are estimated to be infected, with approximately 700 thousand deaths per year attributable to hepatitis C-related liver disease according to the July 2016 WHO Hepatitis C Fact Sheet. Transmission of HCV can occur through typical routes for bloodborne viruses including transfusion and use of contaminated needles or medical equipment. Sexual and mother-to-infant transmission are also known to occur.

[004] HCV is a positive-sense single stranded RNA (ssRNA) virus. Its distribution is worldwide, with seven genotypes and multiple subtypes known. Antiviral therapy can be effective against HCV, but reliable and sensitive nucleic acid-based detection and quantification is complicated by marked genetic heterogeneity among the different genotypes. See, e.g., Ohno O, Mizokami M, Wu RR, Saleh MG, Ohba K, Orito E, Mukaide M, Williams R, Lau JY, et al. (1997), "New hepatitis C virus (HCV) genotyping system that allows for identification of HCV genotypes 1a, 1b, 2a, 2b, 3a, 3b, 4, 5a, and 6a," *J Clin Microbiol.* **35** (1): 201–7, PMID: PMC229539. Quantification can be useful, e.g., in monitoring viral load before, during, or after antiviral therapy, or in assessing severity of infection.

[005] Accordingly, there is a need for sensitive detection and quantification of HCV irrespective of genotype. Compositions, kits, and methods are provided herein to meet this need, provide other benefits, or at least provide the public with a useful choice.

[006] In some embodiments, a composition or kit is provided comprising at least first and second amplification oligomers, wherein: the first amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 2, including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 2; and the second amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 3 including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 3; and the target-hybridizing sequences of the first and

second amplification oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence. In some embodiments, the composition or kit further comprises a third amplification oligomer, wherein the third amplification oligomer comprises at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence and is configured to specifically hybridize downstream of HCV genomic position 78.

[007] In some embodiments, a method is provided of detecting Hepatitis C virus nucleic acid in a sample, comprising: contacting the sample with at least first, second, and third amplification oligomers, thereby forming a composition, performing a nucleic acid amplification reaction in the composition which produces one or more amplicons in the presence of a Hepatitis C virus nucleic acid, and detecting the amplicon, wherein: the first amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 2, including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 2; the second amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 3 including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 3; the third amplification oligomer comprises at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence and is configured to specifically hybridize to downstream of HCV genomic position 78;

the target-hybridizing sequences of the first and second amplification oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence; and

the one or more amplicons are produced through extension of the first and third amplification oligomers or second and third amplification oligomers in the presence of the Hepatitis C virus nucleic acid.

[008] In some embodiments, a composition or kit is provided comprising at least first and second capture oligomers, wherein: the first capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 54; and

the second capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 55; and the target-hybridizing sequences of the first and second capture oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

[009] In some embodiments, a method of isolating Hepatitis C virus nucleic acid from a sample is provided, comprising: contacting the sample with at least first and second capture oligomers under conditions permissive for annealing of the first and second capture oligomers to the Hepatitis C virus nucleic acid, thereby forming at least one complex of Hepatitis C virus nucleic acid and a capture oligomer; and isolating the at least one complex, thereby providing a composition comprising the complex; wherein: the first capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 54; and the second capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 55; and the target-

hybridizing sequences of the first and second capture oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

[0010] In some embodiments, a composition or kit further comprises an initial amplification oligomer comprising at least 10 contiguous nucleotides of SEQ ID NO: 6.

[0011] In some embodiments, a composition or kit further comprises a probe oligomer comprising at least 10 contiguous nucleotides of SEQ ID NO: 13 and at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

[0012] In some embodiments, the initial amplification oligomer and probe oligomer anneal to at least one common position in an HCV nucleic acid.

[0013] In some embodiments, a kit or composition is provided comprising an initial amplification oligomer and a probe oligomer, wherein: the initial amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 6; the probe oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 13;

the initial amplification oligomer and probe oligomer each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence; and the initial amplification oligomer and probe oligomer anneal to at least one common position in an HCV nucleic acid.

[0014] In some embodiments, a kit or composition further comprises at least 1, 2, or 3 of: a first amplification oligomer comprising a target-hybridizing sequence comprising at least about 14 contiguous nucleotides of Hepatitis C virus sequence that is configured to specifically hybridize upstream of HCV genomic position 81;

a second amplification oligomer different from the first amplification oligomer comprising at least about 14 contiguous nucleotides of Hepatitis C virus sequence that is configured to specifically hybridize upstream of HCV genomic position 81; and

a third amplification oligomer different from the initial amplification oligomer comprising at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence that is configured to specifically hybridize downstream of HCV genomic position 90.

[0015] In some embodiments, a kit or composition further comprises one or more capture oligomers comprising at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence.

[0016] In some embodiments, a method of detecting Hepatitis C virus nucleic acid in a sample is provided, comprising: contacting the sample with one or more capture oligomers and an initial amplification oligomer, thereby associating at least one capture oligomer and amplification oligomer with HCV nucleic acid if present; removing initial amplification oligomer not associated with the HCV nucleic acid; performing an extension reaction that extends initial amplification oligomer associated with HCV nucleic acid if present; performing an amplification reaction with the extended initial amplification

oligomer as template if present, thereby producing an amplicon; and detecting the presence or absence of the amplicon using a probe oligomer; wherein the initial amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 6; the probe oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 13 and is configured to specifically hybridize to the amplicon if present; the initial amplification oligomer and probe oligomer each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence; and the initial amplification oligomer and probe oligomer anneal to at least one common position in an HCV nucleic acid.

[0017] In some embodiments, performing the amplification reaction comprises: adding (i) at least one of first and second amplification oligomers that anneal to the template or amplicon upstream of the probe oligomer and (ii) a third amplification oligomer that is configured to specifically hybridize to the template or amplicon downstream of the probe oligomer; and if the template is present, extending the first and second amplification oligomers.

[0018] An initial amplification oligomer is provided comprising a promoter and a 3'-terminal target-hybridizing sequence, wherein the target-hybridizing sequence comprises at least 10 contiguous nucleotides of SEQ ID NO: 6 and at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

[0019] In some embodiments, the initial amplification oligomer comprises a T7 promoter. In some embodiments, the initial amplification oligomer comprises the sequence of SEQ ID NO: 8, 9, 10, or 11. In some embodiments, the initial amplification oligomer is configured to specifically hybridize to positions comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 of HCV genomic positions 81-92. In some embodiments, the initial amplification oligomer is configured to specifically hybridize to positions comprising at least 1, 2, 3, 4, 5, 6, 7, 8, or 9 of HCV genomic positions 81-89.

[0020] A probe oligomer is provided comprising at least 10 contiguous nucleotides of SEQ ID NO: 13 and at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

[0021] In some embodiments, the probe oligomer is configured to specifically hybridize to positions comprising at least 6, 7, 8, 9, 10, 11, or 12 of HCV genomic positions 81-92. In some embodiments, the probe oligomer is configured to specifically hybridize to positions comprising at least 11, 12, 13, 14, 15, or 16 of HCV genomic positions 81-96.

[0022] In some embodiments, the first amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 2.

[0023] In some embodiments, the second amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 3.

[0024] In some embodiments, the third amplification oligomer does not anneal downstream of an HCV genomic position selected from position 120, 125, 130, 135, 140, 145, or 150 in at least one HCV type. In

some embodiments, the at least one HCV type includes one or more of HCV types 1a, 1b, 2b, 3b, 4b, 5a, and 6a.

[0025] In some embodiments, the third amplification oligomer is configured to specifically hybridize to a site comprising at least one of HCV genomic positions 80-119. In some embodiments, the third amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 6 or 7. In some embodiments, the third amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, or four of SEQ ID NOs: 33-37. In some embodiments, the third amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 contiguous nucleotides of SEQ ID NO: 7. In some embodiments, the third amplification oligomer comprises the sequence of SEQ ID NO: 7. In some embodiments, the third amplification oligomer comprises the sequence of at least one, two, three, four, or five of SEQ ID NOs: 42-47. In some embodiments, the third amplification oligomer comprises the sequence of SEQ ID NO: 5.

[0026] In some embodiments, the first amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, or four of SEQ ID NOs: 23-27. In some embodiments, the first amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or 26 contiguous nucleotides of SEQ ID NO: 2. In some embodiments, the first amplification oligomer comprises the sequence of SEQ ID NO: 2.

[0027] In some embodiments, the second amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, or four of SEQ ID NOs: 28-32. In some embodiments, the second amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or 26 contiguous nucleotides of SEQ ID NO: 3. In some embodiments, the second amplification oligomer comprises the sequence of SEQ ID NO: 3.

[0028] In some embodiments, the first and second amplification oligomers are present in relative molar amounts (first:second) ranging from about 8.5:1.5 to about 1.5:8.5, about 7.5:2.5 to about 2.5:7.5, about 8:2 to about 7:3, about 7:3 to about 6:4, about 6:4 to about 5:5, about 5:5 to about 4:6, about 4:6 to about 3:7, or about 3:7 to about 2:8. In some embodiments, the first and second amplification oligomers are present in relative molar amounts (first:second) ranging from about 6:4 to about 1.5:8.5, about 4:6 to about 6:4, or about 4.5:5.5 to about 5.5:4.5.

[0029] In some embodiments, the initial amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, four, five, six, or seven of SEQ ID NOs: 33-41. In some embodiments, the initial amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 contiguous nucleotides of SEQ ID NO: 6. In some embodiments, the initial amplification oligomer comprises the

sequence of SEQ ID NO: 6. In some embodiments, the initial amplification oligomer comprises the sequence of at least one, two, three, four, or five of SEQ ID NOs: 42-47. In some embodiments, the initial amplification oligomer comprises the sequence of SEQ ID NO: 4.

[0030] In some embodiments, the probe oligomer comprises a target-hybridizing sequence comprising at least one or two of SEQ ID NOs: 50-52. In some embodiments, the probe oligomer comprises the sequence of SEQ ID NO: 48 or 49. In some embodiments, the probe oligomer comprises at least 11, 12, 13, 14, or 15 contiguous nucleotides of SEQ ID NO: 12. In some embodiments, the probe oligomer comprises a target-hybridizing sequence comprising at least 11, 12, 13, 14, or 15 contiguous nucleotides of SEQ ID NO: 13. In some embodiments, the probe oligomer comprises a first self-complementary region at its 5' end and a second self-complementary region at its 3' end. In some embodiments, the self-complementary regions can hybridize to form about 4 to 7 Watson-Crick or wobble base pairs. In some embodiments, the self-complementary regions can hybridize to form about 5 Watson-Crick or wobble base pairs. In some embodiments, the probe oligomer comprises the sequence of SEQ ID NO: 12. In some embodiments, the probe oligomer comprises a target-hybridizing sequence comprising the sequence of SEQ ID NO: 13. In some embodiments, the probe oligomer comprises a non-nucleotide detectable label. In some embodiments, the non-nucleotide detectable label is a fluorescent label. In some embodiments, the probe oligomer comprises a quencher. In some embodiments, the non-nucleotide detectable label is a fluorescent label and the quencher absorbs fluorescence to a greater extent when the probe is free than when the probe is annealed to a target nucleic acid. In some embodiments, the fluorescent label is FAM, HEX, or acridine. In some embodiments, the quencher is DABCYL or ROX. In some embodiments, the fluorescent label is attached to the 5'-terminus of the probe oligomer and the quencher is attached to the 3'-terminus of the probe oligomer, or the fluorescent label is attached to the 3'-terminus of the probe oligomer and the quencher is attached to the 5'-terminus of the probe oligomer. In some embodiments, at least about half, at least about 90%, or all of the sugars in the probe oligomer are 2'-O-methyl-ribose.

[0031] In some embodiments, a first capture oligomer is present comprising a target-hybridizing sequence comprising at least 10, 11, 12, 13, 14, 15, 16, 17, or 18 contiguous nucleotides of SEQ ID NO: 54. In some embodiments, the target-hybridizing sequence of the first capture oligomer comprises at least one or two of SEQ ID NOs: 57-59. In some embodiments, the first capture oligomer comprises the sequence of SEQ ID NO: 54. In some embodiments, the first capture oligomer comprises the sequence of SEQ ID NO: 16.

[0032] In some embodiments, a second capture oligomer is present comprising a target-hybridizing sequence comprising at least 10, 11, 12, 13, 14, 15, 16, or 17 contiguous nucleotides of SEQ ID NO: 55. In some embodiments, the target-hybridizing sequence of the second capture oligomer comprises at least

one or two of SEQ ID NOs: 60-62. In some embodiments, the second capture oligomer comprises the sequence of SEQ ID NO: 55. In some embodiments, the second capture oligomer comprises the sequence of SEQ ID NO: 17.

[0033] In some embodiments, at least one capture oligomer further comprises a non-nucleotide affinity label. In some embodiments, at least one capture oligomer further comprises a non-HCV sequence. In some embodiments, the first and second capture oligomers further comprise a non-HCV sequence. In some embodiments, at least one or two capture oligomers further comprise a poly-N sequence. In some embodiments, the poly-N sequence is a poly-A or poly-T sequence. In some embodiments, at least one or two capture oligomers comprise the sequence of SEQ ID NO: 21 or SEQ ID NO: 22.

[0034] In some embodiments, a kit or composition comprises at least one amplification oligomer that is a promoter-primer. In some embodiments, the third amplification oligomer is a promoter-primer. In some embodiments, one or more of the promoter-primers comprises a T7 promoter located 5' of the target-hybridizing sequence. In some embodiments, one or more promoter-primers comprises the sequence of SEQ ID NO: 8, 9, 10, or 11.

[0035] In some embodiments, at least one amplification oligomer comprises a non-nucleotide detectable label.

[0036] In some embodiments, the initial amplification and probe oligomers each anneal to at least 1, 2, 3, 4, 5, 6, 7, 8, or 9 of positions 86-95 in an HCV genome or the complement thereof.

[0037] In some embodiments, a composition further comprises HCV nucleic acid.

[0038] In some embodiments, a composition or kit further comprises at least one DNA polymerase. In some embodiments, the DNA polymerase is a reverse transcriptase. In some embodiments, the DNA polymerase is thermophilic. In some embodiments, the DNA polymerase is mesophilic.

[0039] In some embodiments, composition or kit further comprises an RNA polymerase. In some embodiments, the RNA polymerase is T7 RNA polymerase.

[0040] In some embodiments, a composition or kit further comprises at least one, at least two, or each of Mg²⁺, a buffer, and dNTPs.

[0041] In some embodiments, a composition or kit further comprises rNTPs.

[0042] In some embodiments, a composition or kit further comprises a first control amplification oligomer and a second control amplification oligomer that do not hybridize specifically to HCV. In some embodiments, the first control amplification oligomer comprises at least 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 contiguous nucleotides of the sequence of SEQ ID NO: 18. In some embodiments, the second control amplification oligomer comprises at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or 22 contiguous nucleotides of the sequence of SEQ ID NO: 56. In some embodiments, the first control amplification oligomer or the second control amplification oligomer is a promoter-primer.

[0043] In some embodiments, a composition or kit further comprises at least one control probe oligomer capable of hybridizing specifically to an amplicon produced from the first and second control amplification oligomers. In some embodiments, the control probe oligomer comprises at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23 contiguous nucleotides of the sequence of SEQ ID NO: 20.

[0044] In some embodiments, one, two, three, or more target-hybridizing sequences (e.g., of amplification oligomers, capture oligomers, or probe oligomers) comprise at least about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides of Hepatitis C virus sequence.

[0045] In some embodiments, a method further comprises performing a linear amplification wherein at least one amplification oligomer is extended. In some embodiments, prior to the linear amplification, the amplification oligomer is associated with a complex of HCV nucleic acid and a capture oligomer and the complex is associated with a solid support, and the method comprises washing the solid support. In some embodiments, the solid support is a population of microbeads. In some embodiments, the microbeads of the population are magnetic. In some embodiments, following the washing step, the method comprises adding one or more additional amplification oligomers oppositely oriented to an amplification oligomer associated with the complex of HCV nucleic acid and the capture oligomer. In some embodiments, one or more oppositely oriented additional amplification oligomer is a promoter-primer. In some embodiments, one or more oppositely oriented additional amplification oligomer is not a promoter-primer. In some embodiments, one or more oppositely oriented additional amplification oligomer includes a first amplification oligomer as disclosed herein. In some embodiments, the one or more oppositely oriented additional amplification oligomer includes a second amplification oligomer as disclosed herein.

[0046] In some embodiments, a method further comprises performing an exponential amplification following a linear amplification. In some embodiments, the exponential amplification comprises extending a third amplification oligomer as disclosed herein. In some embodiments, the exponential amplification is isothermal amplification. In some embodiments, the isothermal amplification is transcription-mediated amplification.

[0047] In some embodiments, a method further comprises quantifying at least one amplicon produced by the method. In some embodiments, the amplicon is quantified in real time.

[0048] In some embodiments, a composition is aqueous, frozen, or lyophilized.

[0049] In some embodiments, a composition further comprises an extension product of an initial amplification oligomer, the extension product comprising a sequence of an initial amplification oligomer recited in any one of claims 106-111 and at least 1, 2, 3, 4, 5, 10, 15, or 20 additional 3'-terminal nucleotides of Hepatitis C nucleic acid sequence.

[0050] Section headings are provided for the convenience of the reader and do not limit the scope of the disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

[0051] FIG. 1 shows alignment of HCV sequences and indicates regions bound by amplification and probe oligomers. In this and subsequent alignments, dots indicate matches to the reference sequence (here, the HCV 1a transcript), dashes indicate gaps, carets indicate complementary positions, and mismatches are shown as the mismatching base. The ovals highlight certain mismatches relative to genotype 1a. The left box indicates a region where no mismatches were observed in the listed genotypes (1a, 2b, 3a, 3b, 4h, 5a, and 6a). The right box indicates a G+C-rich region.

[0052] FIG. 2 shows amplification kinetics for various HCV genotypes at three concentrations. In these experiments, genotype 1a showed distinct groupings of traces for the three concentrations, but at the lowest concentration (10^2 copies/ml), other genotypes either failed to amplify (2a) or showed heterogeneous emergence times (3b, 4h, 3a, 5a, 6a).

[0053] FIG. 3 shows calibration curves for genotypes 1a and 3a using different NT7 primers.

[0054] FIGs. 4A, 4B, and 4C show genotype quantitation with different NT7 primers (HCV 52-78, matching genotype 1a sequence, in FIG. 4A; HCV 52-78tg, matching genotype 3a sequence, in FIG 4B; or a 50:50 mixture of HCV 52-78 and HCV 52-78tg in FIG 4C). Arrows indicate the curve for genotype 1A in FIGs. 4A and 4B. In FIG. 4C, the curves for genotypes 1a and 3a substantially overlapped.

[0055] FIGs. 5A and 5B show results across multiple HCV genotypes for nonT7 primers 52-78t only (FIG 5A; arrow indicates genotype 3a) and 52-78tg only (FIG 5B).

[0056] FIG. 6 shows log difference from target (LogDiff) for quantitation assays with various genotypes. The genotypes are presented from left to right in the order 1a, 2b, 3a, 3b, 4h, 5a, 6a, with each genotype having two bars reflecting 10^4 (left) and 10^7 (right) copies/ml conditions.

[0057] FIG. 7 shows a side-by-side comparison of HCV torch 68-86 versus HCV torch 80-98 5st a with the indicated genotypes at 10^2 , 10^4 , and 10^7 copies/ml. Arrows indicate traces for the 10^2 copies/ml condition.

[0058] FIG. 8 shows calibration curves with different HCV torches and T7 oligomers. The straight arrow indicates the curve for genotype 3a, T7 95-119, torch 68-86. The curved arrow indicates the curve for genotype 1a, T7 95-119, torch 68-86.

[0059] FIG. 9 shows calibration curves for HCV torches 81-96, 81-97, and 80-98.

[0060] FIG. 10 shows calibration curves with different T7 primers, which are listed in the figure in order from highest to lowest curves.

[0061] FIG. 11 shows an alignment of T7 primers against HCV genotypes.

[0062] FIGs. 12A, 12B, 12C, and 12D show a series of emergence curves for 3 copy levels with genotypes 1a, 2b, 3a, 3b, 4h, 5a, and 6a for 3 T7 93-119 initial amplification oligomers which either matched genotype 1a sequence (top row in 12A-D) or contained inosines (bottom 2 rows in each of 12A-D). Each plot shows traces for 100, 10000, and 1000000 copies/ml. The arrows (FIGs. 12B-12D) indicate the collapse of the traces when inosine bases were used in the T7 oligomers.

[0063] FIGs. 13A, 13B, and 13C show emergence curves using control T7 93-119 (13A), T7 89-119 (13B), and T7 80-119 (13C) primers against genotypes 1a, 2b, and 5a at 10^2 , 10^4 , and 10^6 copies/ml, showing greater consistency across genotypes and separation of curves for different concentrations for T789-119 and T7 80-119.

[0064] FIG. 14 shows log difference (LogDiff) versus HCV1a for different HCV genotypes at 2.3, 4.3, and 6.3 log copies/ml when T7 93-119, T7 89-119, and T7 80-119 initial amplification oligomers were used.

[0065] FIG. 15A, 15B, and 15C show calibration curves for genotypes 1a, 2b, 3a, 3b, 4h, 5a, and 6a when the initial amplification oligomer was T7 93-119 (15A), T7 89-119 (15B), or T7 80-119 (15C). The arrow in FIG. 15A indicates the curve for genotype 5a, which was visibly separated from the curves for other genotypes when T7 93-119 was used but which appeared among the other curves when longer initial amplification oligomers were used.

[0066] FIG. 16 shows difference in quantitation for various genotypes relative to HCV 1a calibrators when different target concentrations and initial amplification oligomers were used. For each genotype, the 9 bars from left to right are arranged as A1 A2 A3 B1 B2 B3 C1 C2 C3 where A is 200 copies/ml (c/ml), B is 20000 c/ml, C is 2M c/ml, 1 is with the 80-119 T7ip, 2 is with the 89-119 T7ip, and 3 is with the 89-119 T7ip (T7ip = T7 initial amplification oligomer).

[0067] FIG. 17 shows an alignment of T7 initial amplification oligomers with selected HCV genotypes.

[0068] FIG. 18 shows characterization of LogDiff data on HCV genotypes using different T7 initial amplification oligomers. The genotypes and concentrations are as follows from left to right: 1a (10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 , 10^8 c/ml); 2b (10^2 , 10^4 , 10^6 c/ml); 3a (10^2 , 10^4 , 10^6 c/ml); 3b (10^2 , 10^4 , 10^6 c/ml); 4h (10^2 , 10^4 , 10^6 c/ml); 5a (10^2 , 10^4 , 10^6 c/ml); 6a (10^2 , 10^4 , 10^6 c/ml). For each genotype and concentration, the seven adjacent bars from left to right represent data with a T7 initial amplification oligomer as follows: 81-119; 83-119; 85-119; 87-119; 89-119; 91-119; 93-119.

[0069] FIG. 19 shows 10K panel results on HCV genotypes for T7 initial amplification oligomers. This is an enlargement of the 10^4 c/ml data only from FIG. 18 subset of the data, with the genotypes and primers in the same order.

[0070] FIG. 20 shows HCV genotype quantification for various genotypes versus HCV 1a with an exemplary oligomer set.

[0071] FIG. 21 shows an alignment of oligomers with HCV genotype sequences HCV 1 through HCV 6.

[0072] FIGs. 22A and 22B show *in vitro* transcript HCV mutant testing with initial assay feasibility oligomer system log difference for all tested mutants (FIG. 23A) and log difference c/ml of mutants with >0.4 log c/ml divergence from expected target (FIG. 23B).

[0073] FIG. 23 shows a sequence alignment with the 13 HCV mutants that under quantified by > 0.4 log c/mL.

[0074] FIG. 24 shows a sequence alignment of an exemplary oligomer set.

[0075] FIGs. 25A and 25B show IVT mutant detection across HCV mutants (target concentration: 10^4 c/ml) (FIG. 26A) and subtype detection (FIG. 26B) for an exemplary oligomer set.

[0076] FIG. 26 shows linearity of assay $30\text{-}1\text{e}9$ c/ml (30c/mL $n=60$, $1\text{e}2\text{-}1\text{e}9\text{c/mL}$ $n=12$).

[0077] FIGs. 27A and 27B show HCV genotype IVT percent positive results for one target capture oligomer (TCO) (0297; dark bars) and two TCO (0297 + 0327b; light bars) conditions.

DETAILED DESCRIPTION

A. Definitions

[0078] Before describing the present teachings in detail, it is to be understood that the disclosure is not limited to specific compositions or process steps, as such may vary. It should be noted that, as used in this specification and the appended claims, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. Thus, for example, reference to "an oligomer" includes a plurality of oligomers and the like.

[0079] It will be appreciated that there is an implied "about" prior to the temperatures, concentrations, times, etc. discussed in the present disclosure, such that slight and insubstantial deviations are within the scope of the present teachings herein. In general, the term "about" indicates insubstantial variation in a quantity of a component of a composition not having any significant effect on the activity or stability of the composition. Also, the use of "comprise", "comprises", "comprising", "contain", "contains", "containing", "include", "includes", and "including" are not intended to be limiting. It is to be understood that both the foregoing general description and detailed description are exemplary and explanatory only and are not restrictive of the teachings. To the extent that any material incorporated by reference is inconsistent with the express content of this disclosure, the express content controls.

[0080] Unless specifically noted, embodiments in the specification that recite "comprising" various components are also contemplated as "consisting of" or "consisting essentially of" the recited

components; embodiments in the specification that recite "consisting of" various components are also contemplated as "comprising" or "consisting essentially of" the recited components; and embodiments in the specification that recite "consisting essentially of" various components are also contemplated as "consisting of" or "comprising" the recited components (this interchangeability does not apply to the use of these terms in the claims).

[0081] "Sample" includes any specimen that may contain hepatitis C virus (HCV) or components thereof, such as nucleic acids or fragments of nucleic acids. Samples include "biological samples" which include any tissue or material derived from a living or dead human that may contain HCV or target nucleic acid derived therefrom, including, e.g., peripheral blood, plasma, serum, lymph node, gastrointestinal tissue (e.g., liver), or other body fluids or materials. The biological sample may be treated to physically or mechanically disrupt tissue or cell structure, thus releasing intracellular components into a solution which may further contain enzymes, buffers, salts, detergents and the like, which are used to prepare, using standard methods, a biological sample for analysis. Also, samples may include processed samples, such as those obtained from passing samples over or through a filtering device, or following centrifugation, or by adherence to a medium, matrix, or support.

[0082] "Nucleic acid" refers to a multimeric compound comprising two or more covalently bonded nucleosides or nucleoside analogs having nitrogenous heterocyclic bases, or base analogs, where the nucleosides are linked together by phosphodiester bonds or other linkages to form a polynucleotide. Nucleic acids include RNA, DNA, or chimeric DNA-RNA polymers or oligonucleotides, and analogs thereof. A nucleic acid "backbone" may be made up of a variety of linkages, including one or more of sugar-phosphodiester linkages, peptide-nucleic acid bonds (in "peptide nucleic acids" or PNAs, see, e.g., International Patent Application Pub. No. WO 95/32305), phosphorothioate linkages, methylphosphonate linkages, or combinations thereof. Sugar moieties of the nucleic acid may be either ribose or deoxyribose, or similar compounds having known substitutions such as, for example, 2'-methoxy substitutions and 2'-halide substitutions (e.g., 2'-F). Nitrogenous bases may be conventional bases (A, G, C, T, U), analogs thereof (e.g., inosine, 5-methylisocytosine, isoguanine; see, e.g., The Biochemistry of the Nucleic Acids 5-36, Adams et al., ed., 11th ed., 1992; Abraham et al., 2007, BioTechniques 43: 617-24), which include derivatives of purine or pyrimidine bases (e.g., N⁴-methyl deoxygaunosine, deaza- or aza-purines, deaza- or aza-pyrimidines, pyrimidine bases having substituent groups at the 5 or 6 position, purine bases having an altered or replacement substituent at the 2, 6 and/or 8 position, such as 2-amino-6-methylaminopurine, O⁶-methylguanine, 4-thio-pyrimidines, 4-amino-pyrimidines, 4-dimethylhydrazine-pyrimidines, and O⁴-alkyl-pyrimidines, and pyrazolo-compounds, such as unsubstituted or 3-substituted pyrazolo[3,4-d]pyrimidine; U.S. Pat. Nos. 5,378,825, 6,949,367 and International Patent Application Pub. No. WO 93/13121, each incorporated by reference herein). Nucleic acids may include "abasic" residues in which

the backbone does not include a nitrogenous base for one or more residues (see, e.g., U.S. Pat. No. 5,585,481, incorporated by reference herein). A nucleic acid may comprise only conventional sugars, bases, and linkages as found in RNA and DNA, or may include conventional components and substitutions (e.g., conventional bases linked by a 2'-methoxy backbone, or a nucleic acid including a mixture of conventional bases and one or more base analogs). Nucleic acids may include "locked nucleic acids" (LNA), in which one or more nucleotide monomers have a bicyclic furanose unit locked in an RNA mimicking sugar conformation, which enhances hybridization affinity toward complementary sequences in single-stranded RNA (ssRNA), single-stranded DNA (ssDNA), or double-stranded DNA (dsDNA) (Vester et al., *Biochemistry* 43:13233-41, 2004, incorporated by reference herein). Nucleic acids may include modified bases to alter the function or behavior of the nucleic acid, e.g., addition of a 3'-terminal dideoxynucleotide to block additional nucleotides from being added to the nucleic acid. Synthetic methods for making nucleic acids in vitro are well-known in the art although nucleic acids may be purified from natural sources using routine techniques.

[0083] A sequence is a "Hepatitis C virus sequence" if it or its complement occurs in, is at least about 90% or at least about 95% identical to, or contains no more than one mismatch relative to any genotype, subtype, or isolate of HCV, thereto, such that, for example, "14 contiguous nucleotides of Hepatitis C virus sequence" refers to a 14-mer that matches at least 13 out of 14 positions of a genotype, subtype, or isolate of HCV, or the complement thereof. The presence of a U is considered equivalent to a T and vice versa for purposes of determining whether a sequence qualifies as a Hepatitis C virus sequence. The target-hybridizing regions of exemplary oligomers disclosed herein, the HCV-derived sequence of in vitro transcripts disclosed herein, and subsequences thereof are also considered Hepatitis C virus sequence. Thus, examples of Hepatitis C virus sequence include SEQ ID NOs: 1-3, 6-7, 13-14, 23-41, 48, 50-52, 54-62, and 76-107; the HCV sequence fragments of SEQ ID NO: 166-214 and 221 and the HCV sequences indicated by the accession numbers in Table 5; the transcript sequences of SEQ ID NOs: 63-74, excluding any non-HCV component (e.g., TOPO or pBlueScript vector sequence that may be present in the transcript); the target-hybridizing regions of T7 amplification oligomers of SEQ ID NOs: 108-147 (excluding non-HCV sequence such as T7 promoter regions, e.g., as in SEQ ID NO: 11); the target-hybridizing regions of capture oligomers of SEQ ID NOs: 161-165 (excluding non-HCV sequence such as artificial regions, e.g., as in SEQ ID NO: 21). In some embodiments, the genotype, subtype, or isolate of HCV referred to above is a known genotype, subtype, or isolate of HCV, e.g., which is present in a sequence database or publication available at the date of this disclosure.

[0084] When an oligomer comprises, e.g., "at least 10 contiguous nucleotides of" a specified SEQ ID NO and "at least about 14 contiguous nucleotides of Hepatitis C virus sequence," the same nucleotides can be counted toward both (i) and (ii), e.g., the at least 14 contiguous nucleotides of Hepatitis C virus

sequence can comprise any or all of the at least 10 contiguous nucleotides of the specified SEQ ID NO, to the extent consistent with the foregoing definition of Hepatitis C virus sequence. Similarly, an "oligomer" comprises a target-hybridizing sequence comprising at least two" (or more) of a plurality of specified SEQ ID NOs if each of the sequence of the SEQ ID NOs is present, regardless of whether they overlap. Thus, as a simplified example, CAT comprises both CA and AT.

[0085] For two molecules to "anneal to at least N common position(s)" means that the molecules have hybridization sites that overlap by N or more nucleotides on the same or opposite strands of a target nucleic acid, e.g., an HCV nucleic acid. For example, a first oligomer that is configured to specifically hybridize to positions 81-96 and a second oligomer that is configured to specifically hybridize to positions 93-119 anneal to four common positions (93, 94, 95, and 96) regardless of whether (i) they both anneal to the same strand or (ii) one is configured to specifically hybridize to the sense or (+) strand and the other is configured to specifically hybridize to the antisense or (-) strand.

[0086] The term "polynucleotide" as used herein denotes a nucleic acid chain. Throughout this application, nucleic acids are designated by the 5'-terminus to the 3'-terminus. Synthetic nucleic acids, e.g., DNA, RNA, DNA/RNA chimerics, (including when non-natural nucleotides or analogues are included therein), are typically synthesized "3'-to-5'," i.e., by the addition of nucleotides to the 5'-terminus of a growing nucleic acid.

[0087] A "nucleotide" as used herein is a subunit of a nucleic acid consisting of a phosphate group, a 5-carbon sugar, and a nitrogenous base (also referred to herein as "nucleobase"). The 5-carbon sugar found in RNA is ribose. In DNA, the 5-carbon sugar is 2'-deoxyribose. The term also includes analogs of such subunits, such as a methoxy group at the 2' position of the ribose (also referred to herein as "2'-O-Me" or "2'-methoxy"). As used herein, methoxy oligonucleotides containing "T" residues have a methoxy group at the 2' position of the ribose moiety, and a uracil at the base position of the nucleotide.

[0088] A "non-nucleotide unit" as used herein is a unit that does not significantly participate in hybridization of a polymer. Such units do not, for example, participate in any significant hydrogen bonding with a nucleotide, and would exclude units having as a component one of the five nucleotide bases or analogs thereof.

[0089] A "target nucleic acid" as used herein is a nucleic acid comprising a target sequence to be amplified. Target nucleic acids may be DNA or RNA as described herein, and may be either single-stranded or double-stranded. The target nucleic acid may include other sequences besides the target sequence, which may not be amplified.

[0090] The term "target sequence" as used herein refers to the particular nucleotide sequence of the target nucleic acid that is to be amplified and/or detected. The "target sequence" includes the complexing sequences to which oligonucleotides (e.g., priming oligonucleotides and/or promoter oligonucleotides)

complex during an amplification processes (e.g., TMA). Where the target nucleic acid is originally single-stranded, the term "target sequence" will also refer to the sequence complementary to the "target sequence" as present in the target nucleic acid. Where the target nucleic acid is originally double-stranded, the term "target sequence" refers to both the sense (+) and antisense (-) strands.

[0091] "Target-hybridizing sequence" is used herein to refer to the portion of an oligomer that is configured to hybridize with a target nucleic acid sequence. In some embodiments, the target-hybridizing sequences are configured to specifically hybridize with a target nucleic acid sequence. Target-hybridizing sequences may be 100% complementary to the portion of the target sequence to which they are configured to hybridize, but not necessarily. Target-hybridizing sequences may also include inserted, deleted and/or substituted nucleotide residues relative to a target sequence. Less than 100% complementarity of a target-hybridizing sequence to a target sequence may arise, for example, when the target nucleic acid is a plurality strains within a species, such as would be the case for an oligomer configured to hybridize to various genotypes of HCV. It is understood that other reasons exist for configuring a target-hybridizing sequence to have less than 100% complementarity to a target nucleic acid.

[0092] The term "targets a sequence" as used herein in reference to a region of HCV nucleic acid refers to a process whereby an oligonucleotide hybridizes to the target sequence in a manner that allows for amplification and detection as described herein. In one preferred embodiment, the oligonucleotide is complementary with the targeted HCV nucleic acid sequence and contains no mismatches. In another preferred embodiment, the oligonucleotide is complementary but contains 1, 2, 3, 4, or 5 mismatches with the targeted HCV nucleic acid sequence. In some embodiments, the oligonucleotide that hybridizes to the HCV nucleic acid sequence includes at least 10 to as many as 50 nucleotides complementary to the target sequence. It is understood that at least 10 and as many as 50 is an inclusive range such that 10, 50 and each whole number there between are included. In some embodiments, the oligomer specifically hybridizes to the target sequence.

[0093] The term "configured to" denotes an actual arrangement of the polynucleotide sequence configuration of a referenced oligonucleotide target-hybridizing sequence. For example, amplification oligomers that are configured to generate a specified amplicon from a target sequence have polynucleotide sequences that hybridize to the target sequence and can be used in an amplification reaction to generate the amplicon. Also as an example, oligonucleotides that are configured to specifically hybridize to a target sequence have a polynucleotide sequence that specifically hybridizes to the referenced sequence under stringent hybridization conditions.

[0094] The term "configured to specifically hybridize to" as used herein means that the target-hybridizing region of an amplification oligonucleotide, detection probe, or other oligonucleotide is

designed to have a polynucleotide sequence that could target a sequence of the referenced HCV target region. Such an oligonucleotide is not limited to targeting that sequence only, but is rather useful as a composition, in a kit, or in a method for targeting a HCV target nucleic acid. The oligonucleotide is designed to function as a component of an assay for amplification and detection of HCV from a sample, and therefore is designed to target HCV in the presence of other nucleic acids commonly found in testing samples. "Specifically hybridize to" does not mean exclusively hybridize to, as some small level of hybridization to non-target nucleic acids may occur, as is understood in the art. Rather, "specifically hybridize to" means that the oligonucleotide is configured to function in an assay to primarily hybridize the target so that an accurate detection of target nucleic acid in a sample can be determined. "Upstream" refers to a location closer to the 5' end of the (+) strand (or the 3' end of the (-) strand) than a given position. "Downstream" refers to a location closer to the 3' end of the (+) strand (or the 5' end of the (-) strand) than a given position.

[0095] The term "fragment," as used herein in reference to the targeted HCV nucleic acid, refers to a piece of contiguous nucleic acid. In certain embodiments, the fragment includes contiguous nucleotides from an HCV RNA corresponding to SEQ ID NO: 1, wherein the number of contiguous nucleotides in the fragment are less than that for the entire sequence corresponding to SEQ ID NO:1.

[0096] The term "region," as used herein, refers to a portion of a nucleic acid wherein said portion is smaller than the entire nucleic acid. For example, when the nucleic acid in reference is an oligonucleotide promoter primer, the term "region" may be used to refer to the smaller promoter portion of the entire oligonucleotide. Similarly, and also as example only, when the nucleic acid is an HCV RNA, the term "region" may be used to refer to a smaller area of the nucleic acid, wherein the smaller area is targeted by one or more oligonucleotides of the disclosure. As another non-limiting example, when the nucleic acid in reference is an amplicon, the term region may be used to refer to the smaller nucleotide sequence identified for hybridization by the target-hybridizing sequence of a probe.

[0097] The interchangeable terms "oligomer," "oligo," and "oligonucleotide" refer to a nucleic acid having generally less than 1,000 nucleotide (nt) residues, including polymers in a range having a lower limit of about 5 nt residues and an upper limit of about 500 to 900 nt residues. In some embodiments, oligonucleotides are in a size range having a lower limit of about 12 to 15 nt and an upper limit of about 50 to 600 nt, and other embodiments are in a range having a lower limit of about 15 to 20 nt and an upper limit of about 22 to 100 nt. Oligonucleotides may be purified from naturally occurring sources or may be synthesized using any of a variety of well-known enzymatic or chemical methods. The term oligonucleotide does not denote any particular function to the reagent; rather, it is used generically to cover all such reagents described herein. An oligonucleotide may serve various different functions. For example, it may function as a primer if it is specific for and capable of hybridizing to a complementary

strand and can further be extended in the presence of a nucleic acid polymerase; it may function as a primer and provide a promoter if it contains a sequence recognized by an RNA polymerase and allows for transcription (e.g., a T7 Primer); and it may function to detect a target nucleic acid if it is capable of hybridizing to the target nucleic acid, or an amplicon thereof, and further provides a detectible moiety (e.g., a fluorophore).

[0098] As used herein, an oligonucleotide "substantially corresponding to" a specified reference nucleic acid sequence means that the oligonucleotide is sufficiently similar to the reference nucleic acid sequence such that the oligonucleotide has similar hybridization properties to the reference nucleic acid sequence in that it would hybridize with the same target nucleic acid sequence under stringent hybridization conditions. One skilled in the art will understand that "substantially corresponding oligonucleotides" can vary from a reference sequence and still hybridize to the same target nucleic acid sequence. It is also understood that a first nucleic acid corresponding to a second nucleic acid includes the RNA or DNA equivalent thereof as well as DNA/RNA chimerics thereof, and includes the complements thereof, unless the context clearly dictates otherwise. This variation from the nucleic acid may be stated in terms of a percentage of identical bases within the sequence or the percentage of perfectly complementary bases between the probe or primer and its target sequence. Thus, in certain embodiments, an oligonucleotide "substantially corresponds" to a reference nucleic acid sequence if these percentages of base identity or complementarity are from 100% to about 80%. In some embodiments, the percentage is from 100% to about 85%. In some embodiments, this percentage is from 100% to about 90%, e.g., from 100% to about 95%. Similarly, a region of a nucleic acid or amplified nucleic acid can be referred to herein as corresponding to a reference nucleic acid sequence. One skilled in the art will understand the various modifications to the hybridization conditions that might be required at various percentages of complementarity to allow hybridization to a specific target sequence without causing an unacceptable level of non-specific hybridization.

[0099] As used herein, the phrase "or its complement, or an RNA equivalent or DNA/RNA chimeric thereof," with reference to a DNA sequence, includes (in addition to the referenced DNA sequence) the complement of the DNA sequence, an RNA equivalent of the referenced DNA sequence, an RNA equivalent of the complement of the referenced DNA sequence, a DNA/RNA chimeric of the referenced DNA sequence, and a DNA/RNA chimeric of the complement of the referenced DNA sequence. Similarly, the phrase "or its complement, or a DNA equivalent or DNA/RNA chimeric thereof," with reference to an RNA sequence, includes (in addition to the referenced RNA sequence) the complement of the RNA sequence, a DNA equivalent of the referenced RNA sequence, a DNA equivalent of the complement of the referenced RNA sequence, a DNA/RNA chimeric of the referenced RNA sequence, and a DNA/RNA chimeric of the complement of the referenced RNA sequence.

[00100] As used herein, a "blocking moiety" is a substance used to "block" the 3'-terminus of an oligonucleotide or other nucleic acid so that it cannot be efficiently extended by a nucleic acid polymerase. Oligomers not intended for extension by a nucleic acid polymerase may include a blocker group that replaces the 3' OH to prevent enzyme-mediated extension of the oligomer in an amplification reaction. For example, blocked amplification oligomers and/or detection probes present during amplification may not have functional 3' OH and instead include one or more blocking groups located at or near the 3' end. In some embodiments a blocking group near the 3' end and may be within five residues of the 3' end and is sufficiently large to limit binding of a polymerase to the oligomer. In other embodiments a blocking group is covalently attached to the 3' terminus. Many different chemical groups may be used to block the 3' end, e.g., alkyl groups, non-nucleotide linkers, alkane-diol dideoxynucleotide residues, and cordycepin.

[00101] An "amplification oligomer" is an oligomer, at least the 3'-end of which is complementary to a target nucleic acid, and which hybridizes to a target nucleic acid, or its complement, and participates in a nucleic acid amplification reaction. An example of an amplification oligomer is a "primer" that hybridizes to a target nucleic acid and contains a 3' OH end that is extended by a polymerase in an amplification process. In some embodiments, the 5' region of an amplification oligonucleotide may include a promoter sequence that is non-complementary to the target nucleic acid (which may be referred to as a "promoter primer"). Another example of an amplification oligomer is an oligomer that is not extended by a polymerase (e.g., because it has a 3' blocked end) but participates in or facilitates amplification. For example, the 5' region of an amplification oligonucleotide may include a promoter sequence that is non-complementary to the target nucleic acid (which may be referred to as a "promoter provider"). Those skilled in the art will understand that an amplification oligomer that functions as a primer may be modified to include a 5' promoter sequence, and thus function as a promoter primer. Incorporating a 3' blocked end further modifies the promoter primer, which is now capable of hybridizing to a target nucleic acid and providing an upstream promoter sequence that serves to initiate transcription, but does not provide a primer for oligo extension. Such a modified oligo is referred to herein as a "promoter provider" oligomer. Size ranges for amplification oligonucleotides include those that are about 10 to about 70 nt long (not including any promoter sequence or poly-A tails) and contain at least about 10 contiguous bases, or even at least 12 contiguous bases that are complementary to a region of the target nucleic acid sequence (or a complementary strand thereof). The contiguous bases are at least 80%, or at least 90%, or completely complementary to the target sequence to which the amplification oligomer binds. An amplification oligomer may optionally include modified nucleotides or analogs, or additional nucleotides that participate in an amplification reaction but are not complementary to or contained in the target nucleic acid, or template sequence. It is understood that when referring to ranges for the length of an

oligonucleotide, amplicon, or other nucleic acid, that the range is inclusive of all whole numbers (e.g., 19-25 contiguous nucleotides in length includes 19, 20, 21, 22, 23, 24 & 25).

[00102] As used herein, a "promoter" is a specific nucleic acid sequence that is recognized by a DNA-dependent RNA polymerase ("transcriptase") as a signal to bind to the nucleic acid and begin the transcription of RNA at a specific site.

[00103] As used herein, a "promoter provider" or "provider" refers to an oligonucleotide comprising first and second regions, and which is modified to prevent the initiation of DNA synthesis from its 3'-terminus. The "first region" of a promoter provider oligonucleotide comprises a base sequence that hybridizes to a DNA template, where the hybridizing sequence is situated 3', but not necessarily adjacent to, a promoter region. The hybridizing portion of a promoter oligonucleotide is typically at least 10 nucleotides in length, and may extend up to 50 or more nucleotides in length. The "second region" comprises a promoter sequence for an RNA polymerase. A promoter oligonucleotide is engineered so that it is incapable of being extended by an RNA- or DNA-dependent DNA polymerase, e.g., reverse transcriptase, in some embodiments comprising a blocking moiety at its 3'-terminus as described above. As referred to herein, a "T7 Provider" is a blocked promoter provider oligonucleotide that provides an oligonucleotide sequence that is recognized by T7 RNA polymerase.

[00104] A "terminating oligonucleotide" is an oligonucleotide comprising a base sequence that is substantially complementary to a sequence within the target nucleic acid in the vicinity of the 5'-end of the target region, so as to "terminate" primer extension of a nascent nucleic acid that includes a priming oligonucleotide, thereby providing a defined 3'-end for the nascent nucleic acid strand. A terminating oligonucleotide is designed to hybridize to the target nucleic acid at a position sufficient to achieve the desired 3'-end for the nascent nucleic acid strand. The positioning of the terminating oligonucleotide is flexible depending upon its design. A terminating oligonucleotide may be modified or unmodified. In certain embodiments, terminating oligonucleotides are synthesized with at least one or more 2'-O-ME ribonucleotides. These modified nucleotides have demonstrated higher thermal stability of complementary duplexes. The 2'-O-ME ribonucleotides also function to increase the resistance of oligonucleotides to exonucleases, thereby increasing the half-life of the modified oligonucleotides. (See, e.g., Majlessi et al., *Nucleic Acids Res.* 26:2224-9, 1988, incorporated by reference herein.) Other modifications as described elsewhere herein may be utilized in addition to or in place of 2'-O-Me ribonucleotides. For example, a terminating oligonucleotide may comprise PNA or an LNA. (See, e.g., Petersen et al., *J. Mol. Recognit.* 13:44-53, 2000, incorporated by reference herein.) A terminating oligonucleotide of the present disclosure typically includes a blocking moiety at its 3'-terminus to prevent extension. A terminating oligonucleotide may also comprise a protein or peptide joined to the oligonucleotide so as to terminate further extension of a nascent nucleic acid chain by a polymerase. A

terminating oligonucleotide of the present disclosure is typically at least 10 bases in length, and may extend up to 15, 20, 25, 30, 35, 40, 50 or more nucleotides in length. While a terminating oligonucleotide typically or necessarily includes a 3'-blocking moiety, "3'-blocked" oligonucleotides are not necessarily terminating oligonucleotides.

[00105] "Amplification" refers to any known procedure for obtaining multiple copies of a target nucleic acid sequence or its complement or fragments thereof. The multiple copies may be referred to as amplicons or amplification products. Amplification of "fragments" refers to production of an amplified nucleic acid that contains less than the complete target nucleic acid or its complement, e.g., produced by using an amplification oligonucleotide that hybridizes to, and initiates polymerization from, an internal position of the target nucleic acid. Known amplification methods include, for example, replicase-mediated amplification, polymerase chain reaction (PCR), ligase chain reaction (LCR), strand-displacement amplification (SDA), and transcription-mediated or transcription-associated amplification. Replicase-mediated amplification uses self-replicating RNA molecules, and a replicase such as QB-replicase (see, e.g., U.S. Pat. No. 4,786,600, incorporated by reference herein). PCR amplification uses a DNA polymerase, pairs of primers, and thermal cycling to synthesize multiple copies of two complementary strands of dsDNA or from a cDNA (see, e.g., U.S. Pat. Nos. 4,683,195; 4,683,202; and 4,800,159; each incorporated by reference herein). LCR amplification uses four or more different oligonucleotides to amplify a target and its complementary strand by using multiple cycles of hybridization, ligation, and denaturation (see, e.g., U.S. Pat. Nos. 5,427,930 and 5,516,663, each incorporated by reference herein). SDA uses a primer that contains a recognition site for a restriction endonuclease and an endonuclease that nicks one strand of a hemimodified DNA duplex that includes the target sequence, whereby amplification occurs in a series of primer extension and strand displacement steps (see, e.g., U.S. Pat. Nos. 5,422,252; 5,547,861; and 5,648,211; each incorporated by reference herein).

[00106] As used herein, the term "linear amplification" refers to an amplification mechanism that is designed to produce an increase in the target nucleic acid linearly proportional to the amount of target nucleic acid in the reaction. For instance, multiple RNA copies can be made from a DNA target using a transcription-associated reaction, where the increase in the number of copies can be described by a linear factor (e.g., starting copies of template $\times$ 100). In some embodiments, a first phase linear amplification in a multiphase amplification procedure increases the starting number of target nucleic acid strands or the complements thereof by at least 10 fold, e.g., by at least 100 fold, or by 10 to 1,000 fold before the second phase amplification reaction is begun. An example of a linear amplification system is "T7-based Linear Amplification of DNA" (TLAD; see Liu et al., BMC Genomics, 4: Art. No. 19, May 9, 2003). Other methods are known, e.g., from U.S. Patent No. 9,139,870, or disclosed herein. Accordingly, the term

"linear amplification" refers to an amplification reaction which does not result in the exponential amplification of a target nucleic acid sequence. The term "linear amplification" does not refer to a method that simply makes a single copy of a nucleic acid strand, such as the transcription of an RNA molecule into a single cDNA molecule as in the case of reverse transcription (RT)-PCR.

[00107] As used herein, the term "exponential amplification" refers to nucleic acid amplification that is designed to produce an increase in the target nucleic acid geometrically proportional to the amount of target nucleic acid in the reaction. For example, PCR produces one DNA strand for every original target strand and for every synthesized strand present. Similarly, transcription-associated amplification produces multiple RNA transcripts for every original target strand and for every subsequently synthesized strand. The amplification is exponential because the synthesized strands are used as templates in subsequent rounds of amplification. An amplification reaction need not actually produce exponentially increasing amounts of nucleic acid to be considered exponential amplification, so long as the amplification reaction is designed to produce such increases.

[00108] "Transcription-associated amplification" or "transcription-mediated amplification" (TMA) refer to nucleic acid amplification that uses an RNA polymerase to produce multiple RNA transcripts from a nucleic acid template. These methods generally employ an RNA polymerase, a DNA polymerase, deoxyribonucleoside triphosphates, ribonucleoside triphosphates, and a template complementary oligonucleotide that includes a promoter sequence, e.g., a T7 promoter, and optionally may include one or more other oligonucleotides. When a T7 promoter-containing oligomer is used, it may be referred to as a "T7 primer" or "T7 oligomer"; other primers/oligomers may be referred to as "non-T7" or "NT7" primers/oligomers. TMA methods and single-primer transcription-associated amplification methods are embodiments of amplification methods used for detection of HCV target sequences as described herein. Variations of transcription-associated amplification are well-known in the art as previously disclosed in detail (see, e.g., U.S. Pat. Nos. 4,868,105; 5,124,246; 5,130,238; 5,399,491; 5,437,990; 5,554,516; and 7,374,885; and International Patent Application Pub. Nos. WO 88/01302; WO 88/10315; and WO 95/03430; each incorporated by reference herein). The person of ordinary skill in the art will appreciate that the disclosed compositions may be used in amplification methods based on extension of oligomer sequences by a polymerase.

[00109] As used herein, the term "real-time TMA" refers to single-primer transcription-mediated amplification ("TMA") of target nucleic acid that is monitored through real-time detection.

[00110] The term "amplicon" or "amplification product" as used herein refers to the nucleic acid molecule generated during an amplification procedure that is complementary or homologous to a sequence contained within the target sequence. The complementary or homologous sequence of an amplicon is sometimes referred to herein as a "target-specific sequence." Amplicons generated using the

amplification oligomers of the current disclosure may comprise non-target specific sequences. Amplicons can be double-stranded or single-stranded and can include DNA, RNA, or both. For example, DNA-dependent RNA polymerase transcribes single-stranded amplicons from double-stranded DNA during transcription-mediated amplification procedures. These single-stranded amplicons are RNA amplicons and can be either strand of a double-stranded complex, depending on how the amplification oligomers are configured. Thus, amplicons can be single-stranded RNA. RNA-dependent DNA polymerases synthesize a DNA strand that is complementary to an RNA template. Thus, amplicons can be double-stranded DNA and RNA hybrids. RNA-dependent DNA polymerases often include RNase activity, or are used in conjunction with an RNase, which degrades the RNA strand. Thus, amplicons can be single stranded DNA. RNA-dependent DNA polymerases and DNA-dependent DNA polymerases synthesize complementary DNA strands from DNA templates. Thus, amplicons can be double-stranded DNA. RNA-dependent RNA polymerases synthesize RNA from an RNA template. Thus, amplicons can be double-stranded RNA. DNA-dependent RNA polymerases synthesize RNA from double-stranded DNA templates, also referred to as transcription. Thus, amplicons can be single stranded RNA. Amplicons and methods for generating amplicons are known to those skilled in the art. For convenience herein, a single strand of RNA or a single strand of DNA may represent an amplicon generated by an amplification oligomer combination of the current disclosure. Such representation is not meant to limit the amplicon to the representation shown. Skilled artisans in possession of the instant disclosure will use amplification oligomers and polymerase enzymes to generate any of the numerous types of amplicons, all within the spirit and scope of the current disclosure.

[00111] A "non-target-specific sequence," as is used herein refers to a region of an oligomer sequence, wherein said region does not stably hybridize with a target sequence under standard hybridization conditions. Oligomers with non-target-specific sequences include, but are not limited to, promoter primers and molecular beacons. An amplification oligomer may contain a sequence that is not complementary to the target or template sequence; for example, the 5' region of a primer may include a promoter sequence that is non-complementary to the target nucleic acid (referred to as a "promoter primer"). Those skilled in the art will understand that an amplification oligomer that functions as a primer may be modified to include a 5' promoter sequence, and thus function as a promoter primer. Similarly, a promoter primer may be modified by removal of, or synthesis without, a promoter sequence and still function as a primer. A 3' blocked amplification oligomer may provide a promoter sequence and serve as a template for polymerization (referred to as a "promoter provider"). Thus, an amplicon that is generated by an amplification oligomer member such as a promoter primer will comprise a target-specific sequence and a non-target-specific sequence.

[00112] "Detection probe," "detection oligonucleotide," "probe oligomer," and "detection probe oligomer" are used interchangeably to refer to a nucleic acid oligomer that hybridizes specifically to a target sequence in a nucleic acid, or in an amplified nucleic acid, under conditions that promote hybridization to allow detection of the target sequence or amplified nucleic acid. Detection may either be direct (e.g., a probe hybridized directly to its target sequence) or indirect (e.g., a probe linked to its target via an intermediate molecular structure). Detection probes may be DNA, RNA, analogs thereof or combinations thereof (e.g., DNA/RNA chimerics) and they may be labeled or unlabeled. Detection probes may further include alternative backbone linkages such as, e.g., 2'-O-methyl linkages. A detection probe's "target sequence" generally refers to a smaller nucleic acid sequence region within a larger nucleic acid sequence that hybridizes specifically to at least a portion of a probe oligomer by standard base pairing. A detection probe may comprise target-specific sequences and other sequences that contribute to the three-dimensional conformation of the probe (see, e.g., U.S. Pat. Nos. 5,118,801; 5,312,728; 6,849,412; 6,835,542; 6,534,274; and 6,361,945; and US Patent Application Pub. No. 20060068417; each incorporated by reference herein).

[00113] By "stable" or "stable for detection" is meant that the temperature of a reaction mixture is at least 2° C below the melting temperature of a nucleic acid duplex.

[00114] As used herein, a "label" refers to a moiety or compound joined directly or indirectly to a probe that is detected or leads to a detectable signal. Direct labeling can occur through bonds or interactions that link the label to the probe, including covalent bonds or non-covalent interactions, e.g., hydrogen bonds, hydrophobic and ionic interactions, or formation of chelates or coordination complexes. Indirect labeling can occur through use of a bridging moiety or "linker" such as a binding pair member, an antibody or additional oligomer, which is either directly or indirectly labeled, and which may amplify the detectable signal. Labels include any detectable moiety, such as a radionuclide, ligand (e.g., biotin, avidin), enzyme or enzyme substrate, reactive group, or chromophore (e.g., dye, particle, or bead that imparts detectable color), luminescent compound (e.g., bioluminescent, phosphorescent, or chemiluminescent labels), or fluorophore. Labels may be detectable in a homogeneous assay in which bound labeled probe in a mixture exhibits a detectable change different from that of an unbound labeled probe, e.g., instability or differential degradation properties. A "homogeneous detectable label" can be detected without physically removing bound from unbound forms of the label or labeled probe (see, e.g., U.S. Pat. Nos. 5,283,174; 5,656,207; and 5,658,737; each incorporated by reference herein). Labels include chemiluminescent compounds, e.g., acridinium ester ("AE") compounds that include standard AE and derivatives (see, e.g., U.S. Pat. Nos. 5,656,207; 5,658,737; and 5,639,604; each incorporated by reference herein). Synthesis and methods of attaching labels to nucleic acids and detecting labels are well known. (See, e.g., Sambrook et al. *Molecular Cloning. A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Laboratory

Press, Cold Spring Harbor, N Y, 1989), Chapter 10, incorporated by reference herein. See also U.S. Pat. Nos. 5,658,737; 5,656,207; 5,547,842; 5,283,174; and 4,581,333; each incorporated by reference herein). More than one label, and more than one type of label, may be present on a particular probe, or detection may use a mixture of probes in which each probe is labeled with a compound that produces a detectable signal (see. e.g., U.S. Pat. Nos. 6,180,340 and 6,350,579, each incorporated by reference herein).

[00115] "Capture probe," "capture oligonucleotide," "capture oligomer," and "capture probe oligomer" are used interchangeably to refer to a nucleic acid oligomer that specifically hybridizes to a target sequence in a target nucleic acid by standard base pairing and joins to a binding partner on an immobilized probe to capture the target nucleic acid to a support. One example of a capture oligomer includes two binding regions: a sequence-binding region (e.g., target-specific portion) and an immobilized probe-binding region, usually on the same oligomer, although the two regions may be present on two different oligomers joined together by one or more linkers. Another embodiment of a capture oligomer uses a target-sequence binding region that includes random or non-random poly-GU, poly-GT, or poly U sequences to bind non-specifically to a target nucleic acid and link it to an immobilized probe on a support.

[00116] As used herein, an "immobilized oligonucleotide," "immobilized probe," "immobilized binding partner," "immobilized oligomer," or "immobilized nucleic acid" refers to a nucleic acid binding partner that joins a capture oligomer to a support, directly or indirectly. An immobilized probe joined to a support facilitates separation of a capture probe bound target from unbound material in a sample. One embodiment of an immobilized probe is an oligomer joined to a support that facilitates separation of bound target sequence from unbound material in a sample. Supports may include known materials, such as matrices and particles free in solution, which may be made of nitrocellulose, nylon, glass, polyacrylate, mixed polymers, polystyrene, silane, polypropylene, metal, or other compositions, of which one embodiment is magnetically attractable particles. Supports may be monodisperse magnetic spheres (e.g., uniform size+5%), to which an immobilized probe is joined directly (via covalent linkage, chelation, or ionic interaction), or indirectly (via one or more linkers), where the linkage or interaction between the probe and support is stable during hybridization conditions.

[00117] By "complementary" is meant that the nucleotide sequences of similar regions of two single-stranded nucleic acids, or two different regions of the same single-stranded nucleic acid, have a nucleotide base composition that allow the single-stranded regions to hybridize together in a stable double-stranded hydrogen-bonded region under stringent hybridization or amplification conditions. Sequences that hybridize to each other may be completely complementary or partially complementary to the intended target sequence by standard nucleic acid base pairing (e.g., G:C, A:T, or A:U pairing). By "sufficiently complementary" is meant a contiguous sequence that is capable of hybridizing to another

sequence by hydrogen bonding between a series of complementary bases, which may be complementary at each position in the sequence by standard base pairing or may contain one or more residues, including abasic residues, that are not complementary. Sufficiently complementary contiguous sequences typically are at least 80%, or at least 90%, complementary to a sequence to which an oligomer is intended to specifically hybridize. Sequences that are "sufficiently complementary" allow stable hybridization of a nucleic acid oligomer with its target sequence under appropriate hybridization conditions, even if the sequences are not completely complementary. When a contiguous sequence of nucleotides of one single-stranded region is able to form a series of "canonical" or "Watson-Crick" hydrogen-bonded base pairs with an analogous sequence of nucleotides of the other single-stranded region, such that A is paired with U or T and C is paired with G, the nucleotides sequences are "completely" complementary (see, e.g., Sambrook et al., *Molecular Cloning. A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y., 1989) at §§1.90-1.91, 7.37-7.57, 9.47-9.51 and 11.47-11.57, particularly §§9.50-9.51, 11.12-11.13, 11.45-11.47 and 11.55-11.57, incorporated by reference herein). It is understood that ranges for percent identity are inclusive of all whole and partial numbers (e.g., at least 90% includes 90, 91, 93.5, 97.687, etc.). Reference to "the complement" of a particular sequence generally indicates a completely complementary sequence unless the context indicates otherwise.

[00118] "Wobble" base pairs refer to a pairing of a G to either a U or a T.

[00119] By "preferentially hybridize" or "specifically hybridize" is meant that under stringent hybridization assay conditions, probes hybridize to their target sequences, or replicates thereof, to form stable probe:target hybrids, while at the same time formation of stable probe:non-target hybrids is minimized. Thus, a probe hybridizes to a target sequence or replicate thereof to a sufficiently greater extent than to a non-target sequence, to enable one having ordinary skill in the art to accurately detect or quantitate RNA replicates or complementary DNA (cDNA) of the target sequence formed during the amplification. Appropriate hybridization conditions are well-known in the art, may be predicted based on sequence composition, or can be determined by using routine testing methods (see, e.g., Sambrook et al., *Molecular Cloning. A Laboratory Manual*, 2nd ed. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y., 1989) at §§1.90-1.91, 7.37-7.57, 9.47-9.51 and 11.47-11.57, particularly §§9.50-9.51, 11.12-11.13, 11.45-11.47 and 11.55-11.57, incorporated by reference herein).

[00120] By "nucleic acid hybrid," "hybrid," or "duplex" is meant a nucleic acid structure containing a double-stranded, hydrogen-bonded region wherein each strand is complementary to the other, and wherein the region is sufficiently stable under stringent hybridization conditions to be detected by means including, but not limited to, chemiluminescent or fluorescent light detection, autoradiography, or gel electrophoresis. Such hybrids may comprise RNA:RNA, RNA:DNA, or DNA:DNA duplex molecules.

[00121] "Sample preparation" refers to any steps or method that treats a sample for subsequent amplification and/or detection of HCV nucleic acids present in the sample. Samples may be complex mixtures of components of which the target nucleic acid is a minority component. Sample preparation may include any known method of concentrating components, such as microbes or nucleic acids, from a larger sample volume, such as by filtration of airborne or waterborne particles from a larger volume sample or by isolation of microbes from a sample by using standard microbiology methods. Sample preparation may include physical disruption and/or chemical lysis of cellular components to release intracellular components into a substantially aqueous or organic phase and removal of debris, such as by using filtration, centrifugation or adsorption. Sample preparation may include use of a nucleic acid oligonucleotide that selectively or non-specifically capture a target nucleic acid and separate it from other sample components (e.g., as described in U.S. Pat. No. 6,110,678 and International Patent Application Pub. No. WO 2008/016988, each incorporated by reference herein).

[00122] "Separating" or "purifying" means that one or more components of a sample are removed or separated from other sample components. Sample components include target nucleic acids usually in a generally aqueous solution phase, which may also include cellular fragments, proteins, carbohydrates, lipids, and other nucleic acids. "Separating" or "purifying" does not connote any degree of purification. Typically, separating or purifying removes at least 70%, or at least 80%, or at least 95% of the target nucleic acid from other sample components.

[00123] As used herein, a "DNA-dependent DNA polymerase" is an enzyme that synthesizes a complementary DNA copy from a DNA template. Examples are DNA polymerase I from *E. coli*, bacteriophage T7 DNA polymerase, or DNA polymerases from bacteriophages T4, Phi-29, M2, or T5. DNA-dependent DNA polymerases may be the naturally occurring enzymes isolated from bacteria or bacteriophages or expressed recombinantly, or may be modified or "evolved" forms which have been engineered to possess certain desirable characteristics, e.g., thermostability, or the ability to recognize or synthesize a DNA strand from various modified templates. All known DNA-dependent DNA polymerases require a complementary primer to initiate synthesis. It is known that under suitable conditions a DNA-dependent DNA polymerase may synthesize a complementary DNA copy from an RNA template. RNA-dependent DNA polymerases typically also have DNA-dependent DNA polymerase activity.

[00124] As used herein, a "DNA-dependent RNA polymerase" or "transcriptase" is an enzyme that synthesizes multiple RNA copies from a double-stranded or partially double-stranded DNA molecule having a promoter sequence that is usually double-stranded. The RNA molecules ("transcripts") are synthesized in the 5'-to-3' direction beginning at a specific position just downstream of the promoter.

Examples of transcriptases are the DNA-dependent RNA polymerase from *E. coli* and bacteriophages T7, T3, and SP6.

[00125] As used herein, an "RNA-dependent DNA polymerase" or "reverse transcriptase" ("RT") is an enzyme that synthesizes a complementary DNA copy from an RNA template. All known reverse transcriptases also have the ability to make a complementary DNA copy from a DNA template; thus, they are both RNA- and DNA-dependent DNA polymerases. RTs may also have an RNase H activity. A primer is required to initiate synthesis with both RNA and DNA templates.

[00126] "Thermophilic" indicates that an enzyme, e.g., a polymerase, exhibits optimal activity at a temperature greater than about 45°C, e.g., at a temperature in the range from about 50°C to 99°C. In some embodiments, a thermophilic enzyme does not lose more than 50% of its activity upon incubation for 20 minutes at 60°C. In some embodiments, a thermophilic enzyme is obtained or derived from a thermophilic organism, e.g., an organism whose optimal growth temperature is greater than or equal to about 45°C, e.g., greater than or equal to about 50°C.

[00127] As used herein, a "selective RNase" is an enzyme that degrades the RNA portion of an RNA:DNA duplex but not single-stranded RNA, double-stranded RNA or DNA. An exemplary selective RNase is RNase H. Enzymes possessing the same or similar activity as RNase H may also be used. Selective RNases may be endonucleases or exonucleases. Most reverse transcriptase enzymes contain an RNase H activity in addition to their polymerase activities. However, other sources of the RNase H are available without an associated polymerase activity. The degradation may result in separation of RNA from a RNA:DNA complex. Alternatively, a selective RNase may simply cut the RNA at various locations such that portions of the RNA melt off or permit enzymes to unwind portions of the RNA. Other enzymes that selectively degrade RNA target sequences or RNA products of the present disclosure will be readily apparent to those of ordinary skill in the art.

[00128] As used herein, a "standard curve" is a representation that relates (1) a pre-amplification amount of a polynucleotide, and (2) some time-dependent indicia of a post-amplification amount of a corresponding amplicon. For example, a standard curve can be a graph having known numbers of input template molecules plotted on the x-axis, and a time value required for the amplification reaction to achieve some level of detectable amplicon production plotted on the y-axis. Standard curves typically are produced using control polynucleotide standards containing known numbers of polynucleotide templates. Standard curves can be stored in electronic form or can be represented graphically. The pre-amplification amount of an analyte polynucleotide in a test sample can be determined by comparing a measured time-dependent value obtained for the test sample with a standard curve, as will be familiar to those having an ordinary level of skill in the art.

[00129] The term "specificity," in the context of an amplification and/or detection system, is used herein to refer to the characteristic of the system which describes its ability to distinguish between target and non-target sequences dependent on sequence and assay conditions. In terms of nucleic acid amplification, specificity generally refers to the ratio of the number of specific amplicons produced to the number of side-products (e.g., the signal-to-noise ratio). In terms of detection, specificity generally refers to the ratio of signal produced from target nucleic acids to signal produced from non-target nucleic acids.

[00130] The term "sensitivity" is used herein to refer to the precision with which a nucleic acid amplification reaction can be detected or quantitated. The sensitivity of an amplification reaction is generally a measure of the smallest copy number of the target nucleic acid that can be reliably detected in the amplification system, and will depend, for example, on the detection assay being employed, and the specificity of the amplification reaction, e.g., the ratio of specific amplicons to side-products.

[00131] As used herein, the terms "relative light unit" ("RLU") and "relative fluorescence unit" ("RFU") represent arbitrary units of measurement indicating the relative number of photons emitted by the sample at a given wavelength or band of wavelengths. A measurement of RLU or RFU varies with the characteristics of the detector used for the measurement.

[00132] As used herein, the terms "TTime," "emergence time," and "time of emergence" are interchangeable and represent the threshold time or time of emergence of signal in a real-time plot of the assay data. TTime values estimate the time at which a particular threshold indicating amplicon production is passed in a real-time amplification reaction. TTime and an algorithm for calculating and using TTime values are described in Light et al., U.S. Pub. No. 2006/0276972, paragraphs [0517] through [0538], the disclosure of which is incorporated by reference herein. A curve fitting procedure is applied to normalized and background-adjusted data. The curve fit is performed for only a portion of the data between a predetermined low bound and high bound. The goal, after finding the curve that fits the data, is to estimate the time corresponding to the point at which the curve or a projection thereof intersects a predefined threshold value. In one embodiment, the threshold for normalized data is 0.11. The high and low bounds are determined empirically as that range over which curves fit to a variety of control data sets exhibit the least variability in the time associated with the given threshold value. For example, in one embodiment, the low bound is 0.04 and the high bound is 0.36. The curve is fit for data extending from the first data point below the low bound through the first data point past the high bound. Next, there is made a determination whether the slope of the fit is statistically significant. For example, if the p value of the first order coefficient is less than 0.05, the fit is considered significant, and processing continues. If not, processing stops. Alternatively, the validity of the data can be determined by the R^2 value. The slope m and intercept b of the linear curve $y=mx+b$ are determined for the fitted curve. With that information, TTime can be determined as follows: $TTime=(Threshold-b)/m$.

[00133] Unless otherwise indicated, oligomer sequences appearing in tables below follow the conventions that lower case letters indicate 2'-O-methyl RNA for oligomers or RNA for viral sequences, and upper case letters indicate DNA. "(c9)" indicates a $-(CH_2)_9-$ linker. In vitro transcript (IVT) sequences are RNA unless otherwise indicated.

[00134] References, particularly in the claims, to "the sequence of SEQ ID NO: X" refer to the base sequence of the corresponding sequence listing entry and do not require identity of the backbone (e.g., RNA, 2'-O-Me RNA, or DNA) unless otherwise indicated. Furthermore, T and U residues are to be considered interchangeable for purposes of sequence listing entries unless otherwise indicated, e.g., a sequence can be considered identical to SEQ ID NO: 2 regardless of whether the residue at the sixth position is a T or a U.

B. Oligomers, compositions, and kits

[00135] The present disclosure provides oligomers, compositions, and kits, useful for amplifying, detecting, or quantifying HCV from a sample.

[00136] In some embodiments, amplification oligomers are provided. Amplification oligomers generally comprise a target-hybridizing region, e.g., configured to hybridize specifically to an HCV nucleic acid. While oligomers of different lengths and base composition may be used for amplifying HCV nucleic acids, in some embodiments oligomers in this disclosure have target-hybridizing regions from 10 to 60 bases in length, between 14 and 50 bases in length, or between 15 and 40 bases in length. In some embodiments, an initial amplification oligomer is used having a relatively long target hybridizing region such as about 30-50 nucleotides, e.g., 35-45, and at a later stage amplification oligomers with shorter target-hybridizing regions are used, e.g., about 14-35 nucleotides, such as about 15-30 nt.

[00137] In certain embodiments, an amplification oligomer as described herein is a promoter primer further comprising a promoter sequence located 5' to the target-hybridizing sequence and which is non-complementary to the HCV target nucleic acid. For example, in some embodiments of an oligomer combination as described herein for amplification of an HCV target region, an amplification oligomer as described above in (b) (e.g., an amplification oligomer comprising or consisting of an antisense target-hybridizing sequence as shown in Table 1) is a promoter primer further comprising a 5' promoter sequence. In particular embodiments, the promoter sequence is a T7 RNA polymerase promoter sequence such as, for example, a T7 promoter sequence having the sequence shown in SEQ ID NO:8. In specific variations, a promoter primer comprises the non-HCV sequence including a T7 promoter shown in one of SEQ ID NOs:9, SEQ ID NO:10, or, In some embodiments, SEQ ID NO:11. Alternatively, an amplification oligomer can be a promoter provider.

[00138] In some embodiments, an amplification oligomer is not a promoter primer or does not comprise a promoter sequence. For example, in PCR-based approaches the primers are generally not promoter primers, and in TMA-based approaches at least one primer that is not a promoter primer is typically used (while at least one promoter primer is also used).

[00139] In some embodiments, a first amplification oligomer is provided which is a forward amplification oligomer, i.e., it is configured to hybridize specifically to (-) strand HCV nucleic acid and its target-hybridizing sequence corresponds to the "sense" sequence of HCV.

[00140] In some embodiments, the target sequence of the first amplification oligomer comprises position 65 of an HCV genomic nucleic acid such as SEQ ID NO: 75, e.g., positions 64-66, 63-67, 62-68, 61-69, 60-70, 59-71, 58-72, 57-73, 56-74, 55-75, 54-76, 53-77, or 52-78. In some embodiments, the first amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 2. In some embodiments, the first amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 3 or 215. In some embodiments, the first amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to one of SEQ ID NOs: 76-107. Various embodiments of the first amplification oligomer, including with respect to its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00141] In some embodiments, a second amplification oligomer is provided which is an additional forward amplification oligomer different from the first amplification oligomer. As described in the examples, using a second forward amplification oligomer can improve the relative accuracy of quantification of HCV nucleic acid despite sequence variation between genotypes.

[00142] In some embodiments, the target sequence of the second amplification oligomer comprises position 65 of an HCV genomic nucleic acid such as SEQ ID NO: 75, e.g., positions 64-66, 63-67, 62-68, 61-69, 60-70, 59-71, 58-72, 57-73, 56-74, 55-75, 54-76, 53-77, or 52-78. In some embodiments, the second amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 3. In some embodiments, the second amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 2 or 215. In some embodiments, the first amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to one of SEQ ID NOs: 76-107. Various embodiments of the second amplification oligomer, including with respect to its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00143] It should be noted that when only one forward amplification oligomer is used, it can have the features attributed either to a first or a second amplification oligomer herein. This note applies *mutatis*

mutandis to other instances where ordinal numerals are used, e.g., if only one capture oligomer is used, it can have the features attributed either to a first or a second capture oligomer herein.

[00144] In some embodiments, a third amplification oligomer is provided which is a reverse amplification oligomer, i.e., it is configured to hybridize specifically to (+) strand HCV nucleic acid and its target-hybridizing sequence corresponds to the "antisense" sequence of HCV.

[00145] In some embodiments, the target sequence of the third amplification oligomer comprises position 106 of an HCV genomic nucleic acid such as SEQ ID NO: 75, e.g., positions 105-107, 104-108, 103-109, 102-110, 101-111, 100-112, 99-113, 98-114, 97-115, 96-116, 95-117, 94-118, or 93-119. In some embodiments, the third amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 7. In some embodiments, the third amplification oligomer comprises a sequence of SEQ ID NO: 218 or 219, or a sequence having up to 1 or 2 mismatches relative thereto. In some embodiments, the third amplification oligomer comprises a sequence of SEQ ID NO: 147 or 220 or a sequence having up to 1 or 2 mismatches relative thereto. In some embodiments, the third amplification oligomer comprises a target-hybridizing sequence comprising the complement of positions N-119 of SEQ ID NO: 75, where N is 87, 88, 89, 90, 91, 92, 93, 94, or 95 or a sequence having up to 1 or 2 mismatches relative thereto, e.g., one of SEQ ID NOs: 114-128.

[00146] Various embodiments of the third amplification oligomer, including with respect to its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00147] It should be noted that the presence of a third amplification oligomer does not necessarily imply the presence of both first and second amplification oligomers. For example, it is possible to perform an exponential amplification in the presence only of first and third amplification oligomers. Additionally, a linear amplification can be performed in the presence of a third amplification oligomer without requiring any forward amplification oligomer. In some embodiments, the third amplification oligomer is a promoter primer, such that it may have any of the features of promoter primers discussed above. This note applies *mutatis mutandis* to other instances where ordinal numerals are used, e.g., the presence of a second capture oligomer does not necessarily imply the presence of a first capture oligomer.

[00148] In some embodiments, an initial amplification oligomer is provided. The initial amplification oligomer can be different from the first, second, and third amplification oligomers to the extent that they are present or used. In some embodiments, the initial amplification oligomer has a longer target-hybridizing region than at least one other amplification oligomer, such as the third amplification oligomer, or than the first, second, and third AOs. As described in the examples, it was found that using an initial amplification oligomer comprising a long target-hybridizing region can improve subsequent

amplification and quantification of certain HCV genotypes and thereby improve overall detection and quantification performance.

[00149] In some embodiments, the target sequence of the initial amplification oligomer comprises position 99 of an HCV genomic nucleic acid such as SEQ ID NO: 75, e.g., positions 98-100, 97-101, 96-102, 95-103, 94-104, 93-105, 92-106, 91-107, 90-108, 89-109, 88-110, 87-111, 86-112, 85-113, 84-114, 83-115, 82-116, 81-117, 80-118, or 80-119. In some embodiments, the initial amplification oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 6. In some embodiments, the initial amplification oligomer comprises a sequence of SEQ ID NO: 218 or 219, or a sequence having up to 1 or 2 mismatches relative thereto. In some embodiments, the initial amplification oligomer comprises a target-hybridizing sequence comprising the complement of positions N-119 of SEQ ID NO: 75, where N is 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, or 95, or a sequence having up to 1 or 2 mismatches relative thereto. Various embodiments of the initial amplification oligomer, including with respect to its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00150] In some embodiments, at least one probe oligomer is provided. Some embodiments of detection probes that hybridize to complementary amplified sequences may be DNA or RNA oligomers, or oligomers that contain a combination of DNA and RNA nucleotides, or oligomers synthesized with a modified backbone, e.g., an oligomer that includes one or more 2'-methoxy substituted ribonucleotides. Probes used for detection of the amplified HCV sequences may be unlabeled and detected indirectly (e.g., by binding of another binding partner to a moiety on the probe) or may be labeled with a variety of detectable labels. A detection probe oligomer may contain a 2'-methoxy backbone at one or more linkages in the nucleic acid backbone.

[00151] In some embodiments, a detection probe oligomer in accordance with the present disclosure further includes a label. Particularly suitable labels include compounds that emit a detectable light signal, e.g., fluorophores or luminescent (e.g., chemiluminescent) compounds that can be detected in a homogeneous mixture. More than one label, and more than one type of label, may be present on a particular probe, or detection may rely on using a mixture of probes in which each probe is labeled with a compound that produces a detectable signal (see, e.g., U.S. Pat. Nos. 6,180,340 and 6,350,579, each incorporated by reference herein). Labels may be attached to a probe by various means including covalent linkages, chelation, and ionic interactions, but in some embodiments the label is covalently attached. For example, in some embodiments, a detection probe has an attached chemiluminescent label such as, e.g., an acridinium ester (AE) compound (see, e.g., U.S. Pat. Nos. 5,185,439; 5,639,604; 5,585,481; and 5,656,744; each incorporated by reference herein), which in typical variations is attached to the probe by

a non-nucleotide linker (see, e.g., U.S. Pat. Nos. 5,585,481; 5,656,744; and 5,639,604, each incorporated by reference herein).

[00152] A detection probe oligomer in accordance with the present disclosure may further include a non-target-hybridizing sequence. In some applications, probes exhibiting at least some degree of self-complementarity are desirable to facilitate detection of probe:target duplexes in a test sample without first requiring the removal of unhybridized probe prior to detection. Specific embodiments of such detection probes include, for example, probes that form conformations held by intramolecular hybridization, such as conformations generally referred to as hairpins. Particularly suitable hairpin probes include a "molecular torch" (see, e.g., U.S. Pat. Nos. 6,849,412; 6,835,542; 6,534,274; and 6,361,945, each incorporated by reference herein) and a "molecular beacon" (see, e.g., Tyagi et al., supra; U.S. Pat. No. 5,118,801 and U.S. Pat. No. 5,312,728, supra). In yet other embodiments, a detection probe is a linear oligomers that does not substantially form conformations held by intramolecular bonds.

[00153] By way of example, structures referred to as "molecular beacons" comprise nucleic acid molecules having a target complementary sequence, an affinity pair (or nucleic acid arms) holding the probe in a closed conformation in the absence of a target nucleic acid sequence, and a label pair that interacts when the probe is in a closed conformation. Hybridization of the target nucleic acid and the target complementary sequence separates the members of the affinity pair, thereby shifting the probe to an open conformation. The shift to the open conformation is detectable due to reduced interaction of the label pair, which may be, for example, a fluorophore and a quencher (e.g., DABCYL and EDANS). Molecular beacons are fully described in U.S. Pat. No. 5,925,517, the disclosure of which is hereby incorporated by reference. Molecular beacons useful for detecting HCV specific nucleic acid sequences may be created by appending to either end of one of the probe (e.g., target-hybridizing) sequences disclosed herein, a first nucleic acid arm comprising a fluorophore and a second nucleic acid arm comprising a quencher moiety. In this configuration, the HCV specific probe sequence disclosed herein serves as the target-complementary "loop" portion of the resulting molecular beacon, while the self-complementary "arms" of the probe represent the "stem" portion of the probe.

[00154] Another example of a self-complementary hybridization assay probe that may be used in conjunction with the disclosure is a structure commonly referred to as a "molecular torch" (sometimes referred to simply as a torch). These self-reporting probes are designed to include distinct regions of self-complementarity (coined "the target binding domain" and "the target closing domain") which are connected by a joining region (e.g., a $-(CH_2)_9$ - linker) and which hybridize to one another under predetermined hybridization assay conditions. When exposed to an appropriate target or denaturing conditions, the two complementary regions (which may be fully or partially complementary) of the molecular torch melt, leaving the target binding domain available for hybridization to a target sequence

when the predetermined hybridization assay conditions are restored. Molecular torches are designed so that the target binding domain favors hybridization to the target sequence over the target closing domain. The target binding domain and the target closing domain of a molecular torch include interacting labels (e.g., fluorescent/quencher) positioned so that a different signal is produced when the molecular torch is self-hybridized as opposed to when the molecular torch is hybridized to a target nucleic acid, thereby permitting detection of probe:target duplexes in a test sample in the presence of unhybridized probe having a viable label associated therewith. Molecular torches are fully described in U.S. Pat. No. 6,361,945, the disclosure of which is hereby incorporated by reference.

[00155] Molecular torches and molecular beacons in some embodiments are labeled with an interactive pair of detectable labels. Examples of detectable labels that are members of an interactive pair of labels include those that interact with each other by FRET or non-FRET energy transfer mechanisms. Fluorescence resonance energy transfer (FRET) involves the radiationless transmission of energy quanta from the site of absorption to the site of its utilization in the molecule, or system of molecules, by resonance interaction between chromophores, over distances considerably greater than interatomic distances, without conversion to thermal energy, and without the donor and acceptor coming into kinetic collision. The "donor" is the moiety that initially absorbs the energy, and the "acceptor" is the moiety to which the energy is subsequently transferred. In addition to FRET, there are at least three other "non-FRET" energy transfer processes by which excitation energy can be transferred from a donor to an acceptor molecule.

[00156] When two labels are held sufficiently close that energy emitted by one label can be received or absorbed by the second label, whether by a FRET or non-FRET mechanism, the two labels are said to be in "energy transfer relationship" with each other. This is the case, for example, when a molecular beacon is maintained in the closed state by formation of a stem duplex, and fluorescent emission from a fluorophore attached to one arm of the probe is quenched by a quencher moiety on the opposite arm.

[00157] Exemplary label moieties for the disclosed molecular torches and molecular beacons include a fluorophore and a second moiety having fluorescence quenching properties (i.e., a "quencher"). In this embodiment, the characteristic signal is likely fluorescence of a particular wavelength, but alternatively could be a visible light signal. When fluorescence is involved, changes in emission are In some embodiments due to FRET, or to radiative energy transfer or non-FRET modes. When a molecular beacon having a pair of interactive labels in the closed state is stimulated by an appropriate frequency of light, a fluorescent signal is generated at a first level, which may be very low. When this same probe is in the open state and is stimulated by an appropriate frequency of light, the fluorophore and the quencher moieties are sufficiently separated from each other that energy transfer between them is substantially precluded. Under that condition, the quencher moiety is unable to quench the fluorescence from the

fluorophore moiety. If the fluorophore is stimulated by light energy of an appropriate wavelength, a fluorescent signal of a second level, higher than the first level, will be generated. The difference between the two levels of fluorescence is detectable and measurable. Using fluorophore and quencher moieties in this manner, the molecular beacon is only "on" in the "open" conformation and indicates that the probe is bound to the target by emanating an easily detectable signal. The conformational state of the probe alters the signal generated from the probe by regulating the interaction between the label moieties.

[00158] Examples of donor/acceptor label pairs that may be used in connection with the disclosure, making no attempt to distinguish FRET from non-FRET pairs, include fluorescein/tetramethylrhodamine, IAEDANS/fluorescein, EDANS/DABCYL, coumarin/DABCYL, fluorescein/fluorescein, BODIPY FL/BODIPY FL, fluorescein/DABCYL, lucifer yellow/DABCYL, BODIPY/DABCYL, eosine/DABCYL, erythrosine/DABCYL, tetramethylrhodamine/DABCYL, Texas Red/DABCYL, CY5/BH1, CY5/BH2, CY3/BH1, CY3/BH2 and fluorescein/QSY7 dye. Those having an ordinary level of skill in the art will understand that when donor and acceptor dyes are different, energy transfer can be detected by the appearance of sensitized fluorescence of the acceptor or by quenching of donor fluorescence. When the donor and acceptor species are the same, energy can be detected by the resulting fluorescence depolarization. Non-fluorescent acceptors such as DABCYL and the QSY7 dyes advantageously eliminate the potential problem of background fluorescence resulting from direct (i.e., non-sensitized) acceptor excitation. Exemplary fluorophore moieties that can be used as one member of a donor-acceptor pair include fluorescein, ROX, and the CY dyes (such as CY5). Exemplary quencher moieties that can be used as another member of a donor-acceptor pair include DABCYL and the BLACK HOLE QUENCHER moieties which are available from Biosearch Technologies, Inc., (Novato, Calif.).

[00159] Oligomers that are not intended to be extended by a nucleic acid polymerase, e.g., probe oligomers and capture oligomers, can include a blocker group that replaces the 3' OH to prevent enzyme-mediated extension of the oligomer in an amplification reaction. For example, blocked amplification oligomers and/or detection probes present during amplification in some embodiments do not have a functional 3' OH and instead include one or more blocking groups located at or near the 3' end. A blocking group near the 3' end is in some embodiments within five residues of the 3' end and is sufficiently large to limit binding of a polymerase to the oligomer, and other embodiments contain a blocking group covalently attached to the 3' terminus. Many different chemical groups may be used to block the 3' end, e.g., alkyl groups, non-nucleotide linkers, alkane-diol dideoxynucleotide residues, and cordycepin.

[00160] While oligonucleotide probes of different lengths and base composition may be used for detecting HCV nucleic acids, some embodiments of probes in this disclosure are from 10 to 60 bases in length, or between 14 and 50 bases in length, or between 15 and 30 bases in length.

[00161] In some embodiments, the target sequence of the probe oligomer comprises position 88 or 89 of an HCV genomic nucleic acid such as SEQ ID NO: 75, e.g., positions 88-89, 87-90, 86-91, 85-92, 84-93, 83-94, 82-95, or 81-96. In some embodiments, the probe oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 13. In some embodiments, the probe oligomer comprises a sequence of positions 1-19 of SEQ ID NO: 216 or positions 1-19 of SEQ ID NO: 217, or a sequence having up to 1 or 2 mismatches relative thereto. In some embodiments, the probe oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 12. In some embodiments, the probe oligomer comprises a sequence of SEQ ID NO: 216 or 217, or a sequence having up to 1 or 2 mismatches relative thereto. Various embodiments of the probe oligomer, including with respect to its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00162] In some embodiments, at least one capture oligomer is provided. The capture oligomer comprises a target-hybridizing sequence configured to specifically hybridize to HCV nucleic acid, e.g., from 10 to 60 bases in length, or between 14 and 50 bases in length, or between 15 and 30 bases in length. The target-hybridizing sequence is covalently attached to a sequence or moiety that binds to an immobilized probe, e.g., an oligomer attached to a solid substrate, such as a bead.

[00163] In more specific embodiments, the capture probe oligomer includes a tail portion (e.g., a 3' tail) that is not complementary to the HCV target sequence but that specifically hybridizes to a sequence of the immobilized binding partner (e.g., immobilized probe), thereby serving as the moiety allowing the target nucleic acid to be separated from other sample components, such as previously described in, e.g., U.S. Pat. No. 6,110,678, incorporated herein by reference. Any sequence may be used in a tail region, which is generally about 5 to 50 nt long, and certain embodiments include a substantially homopolymeric tail ("poly-N sequence") of at least about 10 nt, e.g., about 10 to 40 nt (e.g., A₁₀ to A₄₀), such as about 14 to 33 nt (e.g., A₁₄ to A₃₀ or T₃A₁₄ to T₃A₃₀), that bind to a complementary immobilized sequence (e.g., poly-T) attached to a solid support, e.g., a matrix or particle. For example, in specific embodiments of a capture probe comprising a 3' tail, the capture probe has a sequence selected from SEQ ID NO:16 or 17.

[00164] In some embodiments, a first capture oligomer is provided. In some embodiments, the target sequence of the first capture oligomer comprises position 307 of an HCV genomic nucleic acid such as SEQ ID NO: 75, e.g., positions 306-308, 305-309, 304-310, 303-311, 302-312, 301-313, 300-314, 299-315, or 298-316. In some embodiments, the first capture oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 54. In some embodiments, the first capture oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 16. In some embodiments, the first capture oligomer comprises a sequence having up to 1 or 2 mismatches relative to positions 1-19 of one of SEQ ID NOS: 161-165. Various embodiments of the first capture oligomer, including with respect to

its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00165] In some embodiments, a second capture oligomer different from the first capture oligomer is provided. In some embodiments, the target sequence of the second capture oligomer comprises position 335 or 336 of an HCV genomic nucleic acid such as SEQ ID NO: 75, e.g., positions 335-336, 334-337, 333-338, 332-339, 331-340, 330-341, 329-342, 328-343, or 327-344. In some embodiments, the second capture oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 55. In some embodiments, the second capture oligomer comprises a sequence having up to 1 or 2 mismatches relative to SEQ ID NO: 17. In some embodiments, the first capture oligomer comprises a sequence having up to 1 or 2 mismatches relative to positions 1-19 of one of SEQ ID NOS: 161-165. Various embodiments of the second capture oligomer, including with respect to its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00166] Various embodiments of the second capture oligomer, including with respect to its sequence, are disclosed in the summary above, any of which can be combined to the extent feasible with the features discussed above in this section.

[00167] Internal control oligomers can be provided, e.g., for confirming that a negative result is valid by establishing that conditions were suitable for amplification. An exemplary control target capture oligomer is SEQ ID NO: 15. Exemplary control amplification oligomers are SEQ ID NOS: 18 and 19. An exemplary control probe oligomer is SEQ ID NO: 20. A control template that can be amplified by the control amplification oligomers can also be provided. Control templates may be prepared according to known protocols. See, e.g., U.S. Patent No. 7,785,844, which is incorporated herein by reference, and which describes an internal control consisting of an in vitro synthesized transcript containing a portion of HIV-1 sequence and a unique sequence targeted by the internal control probe.

[00168] In certain aspects of the disclosure, a combination of at least two oligomers is provided for determining the presence or absence of HCV or quantifying HCV in a sample. In some embodiments, the oligomer combination includes at least two amplification oligomers suitable for amplifying a target region of an HCV target nucleic acid, e.g., having the sequence of SEQ ID NO: 1, 75, an HCV strain referred to in Table 5, the HCV-derived sequence of any of SEQ ID NO: 63-74, or an HCV construct described in Example 10. In such embodiments, at least one amplification oligomer comprises a target-hybridizing sequence in the sense orientation ("sense THS") and at least one amplification oligomer comprises a target-hybridizing sequence in the antisense orientation ("antisense THS"), where the sense THS and antisense THS are each configured to specifically hybridize to a target sequence within an HCV sequence. It is understood that the target-hybridizing sequences are selected such that the HCV sequence targeted by

antisense THS is situated downstream of the HCV sequence targeted by the sense THS (i.e., the at least two amplification oligomers are situated such that they flank the target region to be amplified).

[00169] The oligomers can be provided in various combinations (e.g., kits or compositions), e.g., comprising 2, 3, 4, 5, 6, or 7 of a first amplification oligomer, second amplification oligomer, third amplification oligomer, initial amplification oligomer, probe oligomer, first capture oligomer, and second capture oligomer, such as an initial amplification oligomer and at least one capture oligomer; a first capture oligomer and second capture oligomer, optionally further comprising an initial amplification oligomer; a first amplification oligomer and a third amplification oligomer, optionally further comprising a probe oligomer; a first, second, and third amplification oligomer, optionally further comprising a probe oligomer; an initial amplification oligomer, at least one capture oligomer, a first amplification oligomer, and a third amplification oligomer, optionally further comprising a probe oligomer; an initial amplification oligomer, a first capture oligomer, a second capture oligomer, a first amplification oligomer, and a third amplification oligomer, optionally further comprising a probe oligomer; an initial amplification oligomer, at least one capture oligomer, a first amplification oligomer, a second amplification oligomer, and a third amplification oligomer, optionally further comprising a probe oligomer; or an initial amplification oligomer, a first capture oligomer, a second capture oligomer, a first amplification oligomer, a second amplification oligomer, and a third amplification oligomer, optionally further comprising a probe oligomer. Combinations can further comprise a control oligomer or combination thereof, e.g., two control AOs, a control target capture oligomer, and/or a control probe oligomer. In some embodiments, both first and second AOs are present. In some embodiments, both initial and third AOs are present. In some embodiments, both an initial amplification oligomer and a probe oligomer are present, wherein the initial amplification oligomer and probe oligomer anneal to at least one common position, such as at least 5, 10, or 15 common positions, in an HCV nucleic acid.

[00170] In some embodiments, a combination does not comprise more than 8, 7, 6, or 5 distinct oligomers, not including control oligomers. In such embodiments, variants present in trace amounts (e.g., about 15 mol% or less or about 10 mol% or less relative to a major species of oligomer, such as the oligomer with the most similar sequence to the variant), such as may result from misincorporation, double incorporation, omission, or other errors during oligomer synthesis, are not considered a distinct oligomer.

[00171] In some embodiments, a combination of oligomers is provided as described below in any of the examples or individual reactions described in the examples.

[00172] In some embodiments, a combination of oligomers, e.g., in a kit or composition, is configured to specifically hybridize to nucleic acid of at least three, four, five, or six HCV genotypes (e.g., types 1a, 1b, 2b, 3a, 3b, 4h, 5a, 6a), optionally with minimal cross-reactivity to other, non-HCV nucleic acids suspected of being in a sample (e.g., other bloodborne pathogens). In certain variations, compositions of

the disclosure further allow detection of HCV sequences that vary from the 5' UTR of the foregoing types, e.g., at least 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, or all HCV strains comprising a sequence of SEQ ID NO: 166-213 or 214 (e.g., strains listed in Table 5). In some embodiments, a combination of oligomers can be used to quantify such strains within 1 log of HCV 1a. In some embodiments, a combination of oligomers can be used to quantify such strains within 0.5 log of HCV 1a. In some aspects, the compositions of the instant disclosure are configured to specifically hybridize to HCV nucleic acid with minimal cross-reactivity to one or more, or all, of Hepatitis A, Hepatitis B, Herpes simplex 1, Herpes simplex 2, HIV, Parvovirus, Rubella, Dengue 2, Dengue 3, Dengue 4, Epstein-Barr, and West Nile viruses. In some embodiments, the compositions of the instant disclosure are configured to specifically hybridize to HCV nucleic acid with minimal cross-reactivity to one or more, or all, of *C. albicans*, *C. diphtheriae*, *P. acnes*, *S. aureus*, *S. epidermis*, *S. pneumoniae*. In one aspect, the compositions of the instant disclosure are part of a multiplex system that further includes components and methods for detecting one or more of these organisms.

[00173] Also provided by the disclosure is a reaction mixture for determining the presence or absence of an HCV target nucleic acid or quantifying the amount thereof in a sample. A reaction mixture in accordance with the present disclosure at least comprises one or more of the following: an oligomer combination as described herein for amplification of an HCV target nucleic acid; a capture probe oligomer as described herein for purifying the HCV target nucleic acid; a detection probe oligomer as described herein for determining the presence or absence of an HCV amplification product; and a probe protection oligomer as described herein for detuning sensitivity of an assay for detecting the HCV target nucleic acid. In some embodiments, any oligomer combination described above is present in the reaction mixture. The reaction mixture may further include a number of optional components such as, for example, arrays of capture probe nucleic acids. For an amplification reaction mixture, the reaction mixture will typically include other reagents suitable for performing in vitro amplification such as, e.g., buffers, salt solutions, appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP, dTTP, ATP, CTP, GTP and UTP), and/or enzymes (e.g., reverse transcriptase, and/or RNA polymerase), and will typically include test sample components, in which an HCV target nucleic acid may or may not be present. In addition, for a reaction mixture that includes a detection probe together with an amplification oligomer combination, selection of amplification oligomers and detection probe oligomers for a reaction mixture are linked by a common target region (i.e., the reaction mixture will include a probe that binds to a sequence amplifiable by an amplification oligomer combination of the reaction mixture).

[00174] Also provided by the subject disclosure are kits for practicing the methods as described herein. A kit in accordance with the present disclosure at least comprises one or more of the following: an amplification oligomer combination as described herein for amplification of an HCV target nucleic acid; a

capture probe oligomer as described herein for purifying the HCV target nucleic acid; a detection probe oligomer as described herein for determining the presence or absence of an HCV amplification product; and a probe protection oligomer as described herein for detuning sensitivity of an assay for detecting the HCV target nucleic acid. In some embodiments, any oligomer combination described above is present in the kit. The kits may further include a number of optional components such as, for example, arrays of capture probe nucleic acids. Other reagents that may be present in the kits include reagents suitable for performing in vitro amplification such as, e.g., buffers, salt solutions, appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP, dTTP, ATP, CTP, GTP and UTP), and/or enzymes (e.g., reverse transcriptase, and/or RNA polymerase). Oligomers as described herein may be packaged in a variety of different embodiments, and those skilled in the art will appreciate that the disclosure embraces many different kit configurations. For example, a kit may include amplification oligomers for only one target region of an HCV genome, or it may include amplification oligomers for multiple HCV target regions. In addition, for a kit that includes a detection probe together with an amplification oligomer combination, selection of amplification oligomers and detection probe oligomers for a kit are linked by a common target region (i.e., the kit will include a probe that binds to a sequence amplifiable by an amplification oligomer combination of the kit). In certain embodiments, the kit further includes a set of instructions for practicing methods in accordance with the present disclosure, where the instructions may be associated with a package insert and/or the packaging of the kit or the components thereof.

C. Methods and Uses

[00175] Any method disclosed herein is also to be understood as a disclosure of corresponding uses of materials involved in the method directed to the purpose of the method. Any of the oligomers comprising HCV sequence and any combinations (e.g., kits and compositions) comprising such an oligomer are to be understood as also disclosed for use in detecting or quantifying HCV, and for use in the preparation of a composition for detecting or quantifying HCV.

[00176] Broadly speaking, methods can comprise one or more of the following components: target capture, in which HCV nucleic acid is annealed to a capture oligomer and optionally to an initial amplification oligomer; isolation, e.g., washing, to remove material not associated with a capture oligomer; linear amplification; exponential amplification; and amplicon detection, e.g., amplicon quantification, which may be performed in real time with exponential amplification. Certain embodiments involve each of the foregoing steps. Certain embodiments involve exponential amplification without linear amplification. Certain embodiments involve washing, isolation, and linear amplification. Certain embodiments involve exponential amplification and amplicon detection. Certain embodiments involve any two of the components listed above. Certain embodiments involve any two components listed

adjacently above, e.g., washing and linear amplification, or linear amplification and exponential amplification.

[00177] In some embodiments, amplification comprises contacting the sample with at least two oligomers for amplifying an HCV nucleic acid target region corresponding to an HCV target nucleic acid, where the oligomers include at least two amplification oligomers as described above (e.g., one or more oriented in the sense direction and one or more oriented in the antisense direction for exponential amplification); (2) performing an in vitro nucleic acid amplification reaction, where any HCV target nucleic acid present in the sample is used as a template for generating an amplification product; and (3) detecting the presence or absence of the amplification product, thereby determining the presence or absence of HCV in the sample, or quantifying the amount of HCV nucleic acid in the sample.

[00178] A detection method in accordance with the present disclosure can further include the step of obtaining the sample to be subjected to subsequent steps of the method. In certain embodiments, "obtaining" a sample to be used includes, for example, receiving the sample at a testing facility or other location where one or more steps of the method are performed, and/or retrieving the sample from a location (e.g., from storage or other depository) within a facility where one or more steps of the method are performed.

[00179] In certain embodiments, the method further includes purifying the HCV target nucleic acid from other components in the sample, e.g., before an amplification, such as before a capture step. Such purification may include methods of separating and/or concentrating organisms contained in a sample from other sample components, or removing or degrading non-nucleic acid sample components, e.g., protein, carbohydrate, salt, lipid, etc. In some embodiments, DNA in the sample is degraded, e.g., with DNase, and optionally removing or inactivating the DNase or removing degraded DNA.

[00180] In particular embodiments, purifying the target nucleic acid includes capturing the target nucleic acid to specifically or non-specifically separate the target nucleic acid from other sample components. Non-specific target capture methods may involve selective precipitation of nucleic acids from a substantially aqueous mixture, adherence of nucleic acids to a support that is washed to remove other sample components, or other means of physically separating nucleic acids from a mixture that contains HCV nucleic acid and other sample components.

[00181] Target capture typically occurs in a solution phase mixture that contains one or more capture probe oligomers that hybridize specifically to the HCV target sequence under hybridizing conditions, usually at a temperature higher than the T_m of the tail-sequence:immobilized-probe-sequence duplex. For embodiments comprising a capture probe tail, the HCV-target:capture-probe complex is captured by adjusting the hybridization conditions so that the capture probe tail hybridizes to the immobilized probe. Certain embodiments use a particulate solid support, such as paramagnetic beads.

[00182] Isolation can follow capture, wherein the complex on the solid support is separated from other sample components. Isolation can be accomplished by any appropriate technique, e.g., washing a support associated with the HCV-target-sequence one or more times (e.g., 2 or 3 times) to remove other sample components and/or unbound oligomer. In embodiments using a particulate solid support, such as paramagnetic beads, particles associated with the HCV-target may be suspended in a washing solution and retrieved from the washing solution, In some embodiments by using magnetic attraction. To limit the number of handling steps, the HCV target nucleic acid may be amplified by simply mixing the HCV target sequence in the complex on the support with amplification oligomers and proceeding with amplification steps.

[00183] Linear amplification can be performed, e.g., by contacting the target nucleic acid sequence with a first phase amplification reaction mixture that supports linear amplification of the target nucleic acid sequence and lacks at least one component that is required for its exponential amplification. In some embodiments, the first phase amplification reaction mixture includes an amplification enzyme selected from a reverse transcriptase, a polymerase, and a combination thereof. The polymerase is typically selected from an RNA-dependent DNA polymerase, a DNA-dependent DNA polymerase, a DNA-dependent RNA polymerase, and a combination thereof. In some embodiments, the first phase amplification reaction mixture further includes a ribonuclease (RNase), such as an RNase H or a reverse transcriptase with an RNase H activity. In some embodiments, the first phase amplification mixture includes a reverse transcriptase with an RNase H activity and an RNA polymerase.

[00184] In some embodiments, the first phase amplification mixture may also include an amplification oligonucleotide. The amplification oligonucleotide can include a 5' promoter sequence for an RNA polymerase, such as T7 RNA polymerase, and/or a blocked 3' terminus that prevents its enzymatic extension. In addition, the first phase amplification mixture may sometimes include a blocker oligonucleotide to prevent enzymatic extension of the target nucleic sequence beyond a desired end-point.

[00185] As noted above, the key feature of the first phase amplification reaction is its inability to support an exponential amplification reaction because one or more components required for exponential amplification are lacking, and/or an agent is present which inhibits exponential amplification, and/or the temperature of the reaction mixture is not conducive to exponential amplification, etc. Without limitation, the lacking component required for exponential amplification and/or inhibitor and/or reaction condition may be selected from the following group: an amplification oligonucleotide (e.g., an amplification oligonucleotide comprising a 5' promoter sequence for an RNA polymerase, a non-promoter amplification oligonucleotide, or a combination thereof), an enzyme (e.g., a polymerase, such as an RNA polymerase), a nuclease (e.g., an exonuclease, an endonuclease, a cleavase, an RNase, a phosphorylase, a glycosylase, etc), an enzyme co-factor, a chelator (e.g., EDTA or EGTA), ribonucleotide triphosphates

(rNTPs), deoxyribonucleotide triphosphates (dNTPs), Mg^{2+} , a salt, a buffer, an enzyme inhibitor, a blocking oligonucleotide, pH, temperature, salt concentration and a combination thereof. In some cases, the lacking component may be involved indirectly, such as an agent that reverses the effects of an inhibitor of exponential amplification which is present in the first phase reaction.

[00186] Exponentially amplifying an HCV target sequence utilizes an in vitro amplification reaction using at least two amplification oligomers that flank a target region to be amplified. In some embodiments, first and second amplification oligomers as described above are provided in the forward orientation and a third amplification oligomer is provided in the reverse orientation. In particular embodiments, the target region to be amplified substantially corresponds to a region of SEQ ID NO:75 including nucleotide position 79, e.g., about positions 74-84, 69-89, 64-94, 59-99, 59-109, or 52-119 (including oligomer sequences incorporated into the amplification product). Particularly suitable amplification oligomer combinations for amplification of these target regions are described above. Suitable amplification methods include, for example, replicase-mediated amplification, polymerase chain reaction (PCR), ligase chain reaction (LCR), strand-displacement amplification (SDA), and transcription-mediated or transcription-associated amplification (TMA).

[00187] For example, some amplification methods that use TMA amplification include the following steps. Briefly, the target nucleic acid that contains the sequence to be amplified is provided as single-stranded nucleic acid (e.g., ssRNA such as HCV RNA). Those skilled in the art will appreciate that, alternatively, DNA can be used in TMA; conventional melting of double stranded nucleic acid (e.g., dsDNA) may be used to provide single-stranded target nucleic acids. A promoter primer (e.g., a third amplification oligomer comprising a promoter as described above) binds specifically to the target nucleic acid at its target sequence and a reverse transcriptase (RT) extends the 3' end of the promoter primer using the target strand as a template to create a cDNA extension product, resulting in an RNA:DNA duplex if ssRNA was the original template. An RNase digests the RNA strand of the RNA:DNA duplex and a second primer binds specifically to its target sequence, which is located on the cDNA strand downstream from the promoter primer end. RT synthesizes a new DNA strand by extending the 3' end of the other primer using the first cDNA template to create a dsDNA that contains a functional promoter sequence. An RNA polymerase specific for the promoter sequence then initiates transcription to produce RNA transcripts that are about 100 to 1000 amplified copies ("amplicons") of the initial target strand in the reaction. Amplification continues when the other primer binds specifically to its target sequence in each of the amplicons and RT creates a DNA copy from the amplicon RNA template to produce an RNA:DNA duplex. RNase in the reaction mixture digests the amplicon RNA from the RNA:DNA duplex and the promoter primer binds specifically to its complementary sequence in the newly synthesized DNA. RT extends the 3' end of the promoter primer to create a dsDNA that contains a functional promoter to which

the RNA polymerase binds to transcribe additional amplicons that are complementary to the target strand. The autocatalytic cycles of making more amplicon copies repeat during the course of the reaction resulting in about a billion-fold amplification of the target nucleic acid present in the sample. The amplified products may be detected in real-time during amplification, or at the end of the amplification reaction by using a probe that binds specifically to a target sequence contained in the amplified products. Detection of a signal resulting from the bound probes indicates the presence of the target nucleic acid in the sample.

[00188] In some embodiments, the method utilizes a "reverse" TMA reaction. In such variations, the initial or "forward" amplification oligomer is a priming oligonucleotide that hybridizes to the target nucleic acid in the vicinity of the 3'-end of the target region. A reverse transcriptase (RT) synthesizes a cDNA strand by extending the 3'-end of the primer using the target nucleic acid as a template. The other or "reverse" amplification oligomer is a promoter primer or promoter provider having a target-hybridizing sequence configured to hybridize to a target-sequence contained within the synthesized cDNA strand. Where the second amplification oligomer is a promoter primer, RT extends the 3' end of the promoter primer using the cDNA strand as a template to create a second, cDNA copy of the target sequence strand, thereby creating a dsDNA that contains a functional promoter sequence. Amplification then continues essentially as described above in the preceding paragraph for initiation of transcription from the promoter sequence utilizing an RNA polymerase. Alternatively, where the second amplification oligomer is a promoter provider, a terminating oligonucleotide, which hybridizes to a target sequence that is in the vicinity to the 5'-end of the target region, is typically utilized to terminate extension of the priming oligomer at the 3'-end of the terminating oligonucleotide, thereby providing a defined 3'-end for the initial cDNA strand synthesized by extension from the priming oligomer. The target-hybridizing sequence of the promoter provider then hybridizes to the defined 3'-end of the initial cDNA strand, and the 3'-end of the cDNA strand is extended to add sequence complementary to the promoter sequence of the promoter provider, resulting in the formation of a double-stranded promoter sequence. The initial cDNA strand is then used a template to transcribe multiple RNA transcripts complementary to the initial cDNA strand, not including the promoter portion, using an RNA polymerase that recognizes the double-stranded promoter and initiates transcription therefrom. Each of these RNA transcripts is then available to serve as a template for further amplification from the first priming amplification oligomer.

[00189] The detection step may be performed using any of a variety of known techniques to detect a signal specifically associated with the amplified target sequence, such as, e.g., by hybridizing the amplification product with a labeled detection probe and detecting a signal resulting from the labeled probe. The detection step may also provide additional information on the amplified sequence, such as, e.g., all or a portion of its nucleic acid base sequence. Detection may be performed after the amplification

reaction is completed, or may be performed simultaneously with amplifying the target region, e.g., in real time. In one embodiment, the detection step allows homogeneous detection, e.g., detection of the hybridized probe without removal of unhybridized probe from the mixture (see, e.g., U.S. Pat. Nos. 5,639,604 and 5,283,174, each incorporated by reference herein). In some embodiments, the nucleic acids are associated with a surface that results in a physical change, such as a detectable electrical change. Amplified nucleic acids may be detected by concentrating them in or on a matrix and detecting the nucleic acids or dyes associated with them (e.g., an intercalating agent such as ethidium bromide or cyber green), or detecting an increase in dye associated with nucleic acid in solution phase. Other methods of detection may use nucleic acid detection probes that are configured to specifically hybridize to a sequence in the amplified product and detecting the presence of the probe:product complex, or by using a complex of probes that may amplify the detectable signal associated with the amplified products (e.g., U.S. Pat. Nos. 5,424,413; 5,451,503; and 5,849,481; each incorporated by reference herein). Directly or indirectly labeled probes that specifically associate with the amplified product provide a detectable signal that indicates the presence of the target nucleic acid in the sample. In particular, the amplified product will contain a target sequence in or complementary to a sequence in the HCV genomic RNA, and a probe will bind directly or indirectly to a sequence contained in the amplified product to indicate the presence of HCV nucleic acid in the tested sample.

[00190] In embodiments that detect the amplified product near or at the end of the amplification step, a linear detection probe may be used to provide a signal to indicate hybridization of the probe to the amplified product. One example of such detection uses a luminescently labeled probe that hybridizes to target nucleic acid. Luminescent label is then hydrolyzed from non-hybridized probe. Detection is performed by chemiluminescence using a luminometer. (see, e.g., International Patent Application Pub. No. WO 89/002476, incorporated by reference herein). In other embodiments that use real-time detection, the detection probe may be a hairpin probe such as, for example, a molecular beacon, molecular torch, or hybridization switch probe that is labeled with a reporter moiety that is detected when the probe binds to amplified product. Such probes may comprise target-hybridizing sequences and non-target-hybridizing sequences. Various forms of such probes have been described previously (see, e.g., U.S. Pat. Nos. 5,118,801; 5,312,728; 5,925,517; 6,150,097; 6,849,412; 6,835,542; 6,534,274; and 6,361,945; and US Patent Application Pub. Nos. 20060068417A1 and 20060194240A1; each incorporated by reference herein).

[00191] In some embodiments, a molecular torch (sometimes referred to simply as a torch) is used for detection. In some embodiments, the torch is a probe oligomer as disclosed above.

[00192] In general, the disclosed methods can involve the step of consulting a standard curve that relates pre-amplification amounts of analyte polynucleotide and post-amplification amounts of analyte amplicon.

[00193] Since real-time amplification reactions advantageously feature quantitative relationships between the number of analyte polynucleotides input into the reaction and the number of analyte amplicons synthesized as a function of time, the number of analyte polynucleotides present in a test sample can be determined using a standard curve. For example, a plurality of amplification reactions containing known amounts of a polynucleotide standard can be run in parallel with an amplification reaction prepared using a test sample containing an unknown number of analyte polynucleotides. Alternatively, a standard curve can be prepared in advance so that it is unnecessary to prepare a curve each time an analytical procedure is carried out. Such a curve prepared in advance can even be stored electronically in a memory device of a testing instrument. A standard curve having pre-amplification amounts of the polynucleotide standard on a first axis and some indicia of the time required to effect a certain level of nucleic acid amplification (such as a time-of-emergence above a background signal) on a second axis is then prepared. The post-amplification amount of analyte amplicon measured for the test reaction is then located on the post-amplification axis of the standard curve. The corresponding value on the other axis of the curve represents the pre-amplification amount of analyte polynucleotide that was present in the test reaction. Thus, determining the number of molecules of analyte polynucleotide present in the test sample is accomplished by consulting the standard curve, or more particularly by comparing the quantitative results obtained for the test sample with the standard curve, a procedure that will be familiar to those having an ordinary level of skill in the art.

[00194] The procedures described herein can easily be used to quantify analyte polynucleotides (e.g., HCV nucleic acid) present in a test sample. Indeed, if a plurality of standard control amplification reactions are initiated using known numbers of an analyte polynucleotide standard, and if a test reaction that includes an unknown number of analyte polynucleotide molecules is carried out, then it becomes possible after measuring the time required to effect a certain level of amplification in each reaction to determine the number of analyte polynucleotide molecules that must have been present in the test sample. The relationship between the number of analyte polynucleotide molecules input into standard amplification reaction and the time required to effect a certain level of amplification is conveniently established using a graph. Determining the number of analyte polynucleotide molecules present in a test sample is simply a matter of determining from the standard graph the number of analyte polynucleotide molecules that correspond to a measured analyte amplicon signal strength. This illustrates how analyte polynucleotide standards can be used in connection with polynucleotide amplification reactions to quantify pre-amplification amounts of analyte polynucleotide contained in test samples.

[00195] In some embodiments, a method or use can provide substantially equivalent quantification (e.g., within 1, 0.5, or 0.25 logs) of at least three, four, five, or six HCV genotypes (e.g., types 1a, 1b, 2b, 3a, 3b, 4h, 5a, 6a), optionally with minimal cross-reactivity to other, non-HCV nucleic acids suspected of being in a sample (e.g., other bloodborne pathogens). In certain variations, methods and uses of the disclosure further allow quantification of HCV sequences that vary from the 5' UTR of the foregoing types, e.g., at least 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, or all HCV strains comprising a sequence of SEQ ID NO: 166-213 or 214 (e.g., strains listed in Table 5), e.g., substantially equivalent quantification (e.g., within 1, 0.5, or 0.25 logs) to HCV genotype 1a (e.g., SEQ ID NO: 75). In some aspects, the methods and uses of the instant disclosure show minimal cross-reactivity to one or more, or all, of Hepatitis A, Hepatitis B, Herpes simplex 1, Herpes simplex 2, HIV, Parvovirus, Rubella, Dengue 2, Dengue 3, Dengue 4, Epstein-Barr, and West Nile viruses. In some embodiments, the the methods and uses of the instant disclosure show minimal cross-reactivity to one or more, or all, of *C. albicans*, *C. diphtheriae*, *P. acnes*, *S. aureus*, *S. epidermis*, *S. pneumoniae*. In one aspect, the methods and uses of the instant disclosure are multiplexed with methods for detecting one or more of the foregoing viruses or microbes. In general, minimal cross-reactivity is understood as showing at least about 95% specificity, e.g., at least about 96%, 97%, 98%, or 99%.

EXAMPLES

[00196] The following examples are provided to illustrate certain disclosed embodiments and are not to be construed as limiting the scope of this disclosure in any way.

[00197] *General Reagents and Methods.* Unless otherwise indicated, amplifications were performed isothermally using transcription-mediated amplification with T7 RNA polymerase and reverse transcriptase. Standard transcription mediated amplification (TMA) reactions were carried out essentially as described by Kacian et al., in U.S. Pat. No. 5,399,491, which is incorporated herein by reference. Biphasic TMA was carried out essentially as described in U.S. Pat. No. 9,139,870, which is incorporated herein by reference. In general, the last primer added in the biphasic procedures was the T7 primer, or the shorter T7 primer where a combination of two different T7 primer sequences were used.

[00198] Amplification reactions were conducted for various primer combinations using about 5 to 10 pmoles per reaction of T7 primer and nonT7 primer.

[00199] Detection used molecular torches as probe oligomers which contained a 5'-fluorophore (e.g., FAM or ROX) and a 3'-quencher (e.g., DABCYL) ("5F3D" for FAM and DABCYL or "5R3D" for ROX and DABCYL). Torches are discussed in detail in U.S. Pat. No. 6,849,412, which is incorporated by reference. Torches generally contained a $-(CH_2)_9$ - linker near the 3'-end (e.g., between the 5th and 6th or

between the 4th and 5th nucleotides from the 3'-end). Target capture was performed essentially as described in U.S. Pat. No. 8,034,554, which is incorporated herein by reference.

[00200] Exemplary internal control oligomers and template are discussed in U.S. Pat. No. 7,785,844, which is incorporated herein by reference.

Example 1 – HCV *In Vitro* Transcripts for HCV Genotypes and Exemplary Oligomers

[00201] The 5' untranslated region (UTR) non-coding region of HCV was chosen as the assay target for detecting HCV across genotypes. It was thought that the conserved nature of this region could allow for a genetic test capable of detecting multiple genotypes of HCV using similar primer and detection probes. The length of the 5'-UTR is 341 bases long with ~ 90% homology between HCV genotypes. The 5' UTR is required for viral RNA replication but is not essential for translation.

[00202] An HCV 1a *in vitro* transcript (IVT) was produced using a pBluescript II SK (+) vector with a transcript length of 926 bases, and a sequence insert length of 837 base pairs including the HCV 1a 5'-UTR region. Sequence information for this and subsequent IVTs is shown in the Table of Sequences below.

[00203] The HCV 2b IVT was originally placed into the pBluescript II SK (+) with a transcript length of 998 bases, and a sequence insert length of ~850 base pairs of the HCV 2b 5'-UTR region.

[00204] An aliquot of IVT stock made from a HCV 3a clinical sample was used to reverse-transcribe the IVT into a cDNA clone which was inserted into a pBluescript II SK (+) vector suitable for IVT manufacture. The plasmid insert was sequenced and compared to sequences from the Los Alamos HCV DB, thereby confirming that the clone was consistent with known HCV 3a genotype sequences. IVT from this new plasmid was generated using the T7 promoter resulting in a 861 base IVT containing a large portion of the 5' UTR region and 5'- coding region of HCV 3a. Following initial experiments suggestive that the 3' region of the IVT was forming an inhibitory structure (not shown), the 3' open reading frame (ORF) region was removed from the HCV 3a IVT so that it more closely matches the HCV 3b IVT.

[00205] The new Version 2 IVT (3aV2) of HCV 3a had the end of the 3' IVT removed just past the binding site for target capture oligomer HCV0297(-)dT3dA30 (SEQ ID NO: 16) and near the ORF start point resulting in an approximately 400-base-shorter IVT with a final length of 351 bases. This length and region is more similar to the HCV 3b IVT sequence of 322 bases.

[00206] An additional type 3a Version 3 (3aV3) was made that differed slightly from the 3a V2 IVT by removing a high GC rich region just 5' of the 52-78 (+) non-T7 primer. The V2 version showed better amplification and detection performance versus the HCV 3b IVT than the V1 or V3 versions of HCV 3a.

[00207] A PCR product of the HCV 3b 5'-UTR was inserted into a TOPO cloning plasmid and transcribed off of a SP6 promoter with a transcript length of 422 bases. Subsequently this insert was

transferred to a pBluescript II SK (+) plasmid with a 325 base pair length. The original insert had a mutation that was introduced by the original RT-PCR primers. This mutation was corrected to match the Los Alamos DB for HCV 3b genotype sequences.

[00208] An HCV 4h insert sequence with a length of 422 base pairs was originally placed into a TOPO vector containing an SP6 promoter. To be more consistent with other IVTs, the insert was moved into a pBluescript II SK (+) plasmid with IVT length of 325 bases using a T7 promoter to generate IVT's.

[00209] The original TOPO HCV 4h IVT produced was over-quantitating compared to HCV 1a regardless of mismatches. The optical density (OD), molecular weight, and sequence of the HCV 4h IVT were rechecked and found to be correct. Thus, it was concluded that the over-quantitation relative to HCV 1a is intrinsic to the 4h IVT sequence. The effect is less than 0.15 log difference (not shown).

[00210] The HCV 5a sequence was originally placed into the TOPO clone ID 100007 with a length of 435 base pairs and IVT generated off the T7 TOPO promoter. The sequence was moved into the pBluescript II SK (+) vector so that it will have a similar IVT sequence to HCV 3a, 3b, 4h and 6a. IVT's were again made using pBluescript II SK (+) T7 promoter. The resulting IVT length of the pBluescript II (+) plasmid generates a 325-base IVT with the 5' UTR region of HCV 5a.

[00211] The HCV 6a sequence was originally placed into the TOPO clone ID 100008 with a base pair length of 438 base pairs and generated using the T7 promoter. The sequence was moved into the pBluescript II SK (+) vector using a T7 promoter to generate IVT. The resulting IVT length of the pBluescript II SK (+) vector generates a 328-base IVT with the 5' UTR region of HCV 6a.

[00212] An alignment of selected pBluescript IVT sequences with exemplary oligomers is shown in **Figure 1**.

Example 2 – Initial Assay design

[00213] An alignment was created from HCV sequences to identify the sequence differences among various HCV genotypes including sequences from the Los Alamos database (2008) [hcv.lanl.gov]. An initial set of oligomers was designed to target the 5'UTR region of Hepatitis C virus polyprotein precursor (HCV-1), a region that is ~90% homologous among the genotypes, starting at about base 50 from the 5' end. The primer sequences described here align to the HCV-1a mRNA genome sequence (GenBank Accession No. M62321; SEQ ID NO: 75) without mismatches.

[00214] This original HCV oligomer set had the following characteristics (circled in Figure 1). The torch 68-86 oligomer has 2 mismatches for HCV type 3a/b and had poor amplification kinetics, with large differences among the genotypes. The nonT7 50-66 oligomer has 1 mismatch in HCV type 3a and the T7 95-119 has 1 mismatch in each of HCV types 2b, 3a, and 4h. Amplification curves from tests of the original oligomer set are shown in **Figure 2**, clearly demonstrating differences in quantitation of different HCV genotypes with this oligomer set. For example, under the CAL02 condition (10^2 copies/ml), HCV

1a amplified about 5 minutes later than the CAL04 condition (10^4 copies/ml); HCV 2b did not meaningfully amplify; and the other tested genotypes showed inconsistent amplification kinetics.

Example 3 – HCV nonT7 primer selection

[00215] New oligomer designs were made. Alternate regions were targeted, including the left boxed region in Figure 1 for the probe, which matched to all HCV genotypes. NonT7s and T7s were designed around this probe region. A poor region for oligomer design containing a C-rich string is shown in the right-most boxed region in Figure 1. Oligomers in or amplifying across this region did not amplify or showed very poor amplification.

[00216] New sequences for the nonT7 primer were compared with the original sequence. Calibration curves using the original HCV NT7 50-66 oligomers with genotypes 1a and 3a (second highest and highest lines in **Fig. 3**) compared with HCV NT7 52-78 (green & gold) for HCV 1a and 3a showed that using the NT7 52-78 sequence gave faster emergence time and the genotypes are more similar (lines in the lower group of four in **Fig. 3**).

[00217] Sequence mismatches that affect the nonT7 primer design are mainly in the HCV 3a/3b sequences. In an experiment performed with the HCV 3a IVT, using standard transcription mediated amplification (TMA), new torch and T7 HCV 93-119 (-), a 50:50 mixture of HCV 52-78 NT7 sequences that matched genotypes 1a and 3a showed more equal quantitation than either 52-78 NT7 sequence alone (**Figures 4A-4C**). These oligomers were retested with all genotypes.

[00218] All HCV genotypes were tested with different nonT7 primer conditions, including new oligomer HCV nonT7 52-78t (5'-GGAAGTTCTGTCTTCACGCAGAAAGCG; SEQ ID NO: 215). The HCV 3a is under quantitated with the HCV nonT7 52-78t (only) (arrow in **Figure 5A**) whereas the HCV nonT7 52-78tg (only) shows similarity in quantitation across genotypes (**Figure 5B**). HCV 5a is slightly under-quantitated; however, this sequence has two mismatches in the T7 region. These experiments used the TOPO IVT sequences for HCV 4h, 5a and 6a. The HCV NT7 52-78 genotype 3a sequence ("52-78tg", also referred to as 52-78-1; SEQ ID NO: 2) was selected for inclusion in the oligomer set.

[00219] Shown in **Figure 6** are confirmatory experimental results for the HCV primer set including the HCV nonT7 52-78 tg (only) in biphasic TMA format (including internal control [IC]). 7 HCV genotypes were tested at 10k copies/ml ("04" items in Fig. 6) and 1M copies/ml ("07" items in Fig. 6) for genotypes 2-6 are shown as log differences relative to target. "CAL" entries in Fig. 6 used genotype 1a; genotypes of other items are indicated by the last two characters, e.g., "2B." IVTs for this experiment were from TOPO plasmids for HCV genotypes 4h, 5a, and 6a; and pBluescript IVTs for HCV 1a, 2b, 3a (version 1) and 3b.

Example 4 – HCV Torch selection experiments

[00220] With the original oligomer set, the HCV torch 68-86 had two mismatches to the HCV 3a and HCV 3b sequences. Several sequences were tested in the perfect match region (left box in Fig. 1), some with matches to the C's at the edges of the match regions with sequence and without. The original torch HCV 68-86 sequence was compared side-by-side with HCV 80-98 5st a (+) (5'-CUAGCCAUGGCGUUAGUAU-(c9)-gcuag, SEQ ID NO: 216), and the comparison shows that emergence curves are dramatically different for HCV 3a (**Figure 7**).

[00221] The emergence time calibration curves for 3 torches tested with two IVTs, HCV 1a and 3a, are shown in **Figure 8**. There is a clear delay of the HCV 3a genotype with the original oligomer set (condition 3; top calibration curve in Fig. 8, indicated with straight arrow). Two HCV torches with the 80-98 target binding region with different stem lengths (torches 80-98_5st (5'-gCUAGCCAUGGCGUUAGUAU-(c9)-cuage, SEQ ID NO: 217) and 80-98_5st_a) move the kinetics closer together for HCV 1a and 3a, relative to the HCV 1a (indicated with curved arrow) and HCV 3a calibration curves for 68-86 (cnd3, control [cnt] set) (**Figure 8**).

[00222] An exact match to all HCV genotypes with HCV torch 81-96 and 81-97 with pure system (no target capture) shows no difference to HCV torch 80-98 control for HCV 1a (**Figure 9**). HCV torch 81-96 was selected for further use and is 3 bases shorter in the target binding region than HCV torch 80-98 5st a.

Example 5 – Selection of HCV T7 primer and initial amplification oligomer

[00223] Experiments testing T7 sequences with the original oligomer set, HCV Torch 68-86, and HCV NonT7 50-66 were performed in uniplex HCV amplification using a standard TMA format. The calibration curves for HCV 1a were performed with variations in the T7 sequences, revealing a dependence on the emergence time with the T7 sequence as shown in **Figure 10**. The T7 99-119 (5'-AATTTAATACGACTCACTATAGGGAGACCTGGAGGCTGCACGACACTC, SEQ ID NO: 218, target-hybridizing sequence italicized) has 4 bases removed from the target binding region relative to T7 95-119 resulting in a 5-minute delay in the emergence time at the low end of the assay. T7 99-119I (5'-AATTTAATACGACTCACTATAGGGAGACCTGGAGGCTGIACGACACTC, SEQ ID NO: 219, target-hybridizing sequence italicized) showed a further delay.

[00224] A series of standard T7 primers matching all subtypes, testing singles and mixtures were tested in TCR and AMP2. The HCV 5a genotype was always delayed, unless matched perfectly. However, the primer perfectly matched to 5a delayed HCV 1a, likely due to the AA mismatch in the center of the target binding region of the T7 region (data not shown). Standard T7 primers with inosine bases were also tested attempting to balance amplification among genotype, as indicated by the box in the alignment in

Figure 11. All 7 genotypes were tested in a biphasic TMA format (using TOPO IVTs for HCV 4, 5, and 6 genotypes).

[00225] A series of emergence curves for 3 copy levels comparing 3 T7 primers revealed a collapse of the lower concentrations when an inosine base was present as indicated by the arrows in **Figures 12A-12D**. No further studies were performed with inosine bases in primers as no improvements were observed.

[00226] T7 primers designed in the C-rich region were also tested in combination with torches and nonT7 primers; however, the level of sensitivity observed did not justify further studies (data not shown).

[00227] A series of HCV T7 initial amplification oligomers to eliminate mismatches on first round of initiation were tested where the T7 initial amplification oligomer was added to the TCR with all target capture oligomers (TCOs) and the shortest standard T7 HCV 93-119 (match to HCV 1a) was added to the Promoter AMP2 reagent. HCV genotypes 1a, 2b and 5a were initially screened with two candidate initial amplification oligomers T7 89-119 and T7 80-119 versus the control T7 93-119 present in both TCR and AMP2. For the data presented in **Figures 13A-13C**, the calibrators for HCV 1a are Cal02 = 2.0, Cal04 = 4.0 and Cal06 = 6.0 log copies/ml. For the HCV genotypes 2b and 5a, the concentrations are CTR01 = 2.3, CTR02 = 4.3 and CTR03 = 6.3 log copies/ml. The emergence curves show all cals and controls at three levels. The Control Condition (T7 93-119, Fig. 13A) shows the least defined groups of levels among all the genotypes whereas T7 89-119 (Fig. 13B) and T7 80-119 (Fig. 13C) conditions show separated levels (even though T7 89-119 and T7 80-119 have slightly different levels) (**Figures 13A-13C**).

[00228] The HCV 2b and 5a log difference from HCV 1a for each T7 initial amplification oligomer is shown in **Figure 14**, with the largest difference for HCV 5a (IVT from TOPO plasmid). There are two AA mismatches in the T7 target binding region of all three primers, but the longer T7 sequences 89-119 and 80-119 overcomes the mismatch for initiation of amplification.

[00229] To compare all HCV 6 genotypes to HCV 1a, the same three T7 initial amplification oligomers HCV T7 93-119, T7 89-119, and 80-119 (control and AMP2 for all) were tested with HCV genotypes 1a, 2b, 3a/b, 4h, 5a, and 6a (in TOPO plasmid for HCV genotypes 4-6). The ratio calibration curves for all genotypes plotted as calibrators (same levels as previous experiment) show that the longer initial amplification oligomers (T7 89-119 or 80-119) clearly bring HCV 5a amplification curves more in-line with those of the other genotypes (**Figures 15A-15C**).

[00230] This same data set plotted as the difference in quantitation for the genotypes relative to the HCV 1a calibrators is shown in **Fig. 16**, also illustrating improvement with longer initial amplification oligomers such as the HCV T7 89-119 initial amplification oligomer (center bar in each set of three).

[00231] During the original standard TMA screening of HCV T7 primers, HCV T7 89-119 was identified to have a primer interaction with the internal control (IC) primers (not shown). Due to this

interaction, its use in standard TMA format was avoided, although HCV T7 89-119 can be used in biphasic TMA format.

[00232] To further characterize the log copy difference among the genotypes, a series of T7 initial amplification oligomers was designed and is shown in the alignment next to the diagonal line in **Figure 17**.

[00233] A portion of this series of T7 initial amplification oligomers were tested in biphasic format with the A3 amp reagent with HCV 1a calibrator and HCV genotypes 1-6 (using IVTs from TOPO plasmids for genotypes 4-6). All HCV genotypes 2-6 were tested at 3 levels: 100, 10k and 1M copies per ml. Again, T7 89-119 as an initial amplification oligomer performed well, among others. T7 89-119 gave the smallest difference relative to HCV 1a for other HCV genotypes with T7 93-119 present in AMP2 (**Figure 18**).

[00234] A subset of this data is presented in **Figure 19** for the 10k copies per ml conditions to more clearly show the relative performance of the T7 initial amplification oligomers.

Example 6 – Exemplary HCV Oligomer set

[00235] Based in part on the foregoing results, an exemplary HCV oligomer set containing the oligomers listed in Table 1 was designed.

Table 1: Exemplary HCV biphasic oligomers and IVT sequences	
Non-T7 Primer: HCV(+)-52-78-1	5'-GGAACCTTCTGTCTTCACGCGGAAAGCG-3' (SEQ ID NO: 2)
T7 Primer: HCV(-)93-119	3'ATCATACTCACAGCACGTCGGAGGTCCAGAGGGATATCACTCAGCATAATTAA-5' (SEQ ID NO: 5)
T7 initial amplification oligomer: HCV(-)89-119	3'CGCAATCATACTCACAGCACGTCGGAGGTCCAGAGGGATATCACTCAGCAT AATTTAA-5' (SEQ ID NO: 220)
Target Capture Oligomer: HCV0297 (-)dT3dA30	3'-AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTUCCACGAACGCUCA CGGG-5' (SEQ ID NO: 16)
Probe oligomer 81-96 5F3D	5'-uagccauggcgguagu-(c9)-ggcua-3' (SEQ ID NO: 12)

[00236] The oligomer sequences align as follows to the IVT and sequences for different HCV genotypes.

[00237] Two mismatched "A" base pairs exist in the non-T7 binding region of the type 1A IVT relative to the (+)52-78 primer. The probe oligomer, initial amplification oligomer, and T7 primers match the rest of the sequence. The type 1a IVT is used as a reference for comparison to the IVTs for the rest of the genotypes;

[00238] Two mismatched "A" base pairs exist in the non-T7 binding region for the 52-78 (+) primer and a single "A" mismatch in the T7 binding region. These "A"s are bolded in the entry for the type 2b IVT in the Table of Sequences.

[00239] HCV 4h is characterized by two mismatches in the non-T7 52-78 (+) region and a single point U to G mutation in the initiator/T7 region. The torch and target capture oligomers match the HCV 1a genotype sequence.

[00240] HCV 5a IVT is characterized by two "A" mismatches in the non-T7 52-78 (+) region and two side by side "AA" mismatches in the middle of the T7 primer.

[00241] Initial experiments, without an initiator primer, resulted in poor performance using the HCV 5a genotype. Under-quantitation relative to HCV 1a standard was very apparent due to the double "AA" mismatches in the T7 primer binding region. However, once an initial amplification oligomer was included in the target capture reagent (TCR), the performance of the HCV 5a IVT was comparable to those of other IVT genotypes

[00242] HCV 6a IVT is characterized by two "A" mismatches in the non-T7 52-78 (+) region and one "A" base mismatch in the middle portion of the T7 binding domain.

Example 7 – Internal control oligomer primer selection

[00243] Incorporation of the internal control oligomers was tested with the following set of oligomers: T7 95-119; NT7 52-78; and 80-98-a Torch.

[00244] Oligomers according to SEQ ID NO: 15 and 18-20 were evaluated for use as an internal control (a.k.a. general internal control [GIC], IC). The IC oligomers were spiked into the early HCV amp system using standard TMA format on the OEM platform to determine if any primer interactions exist. Spiking one or all of the IC oligomers resulted in some expected slowing based on resource competition (between 1-2 minute difference in emergence time at the low end; data not shown). It was also confirmed that internal control amplification was successful in the presence of the HCV oligomer set (not shown).

Example 8 – HCV genotype detection with the biphasic TMA HCV/IC assay

[00245] HCV genotype quantitation of the pBluescript IVTs for HCV genotypes 2b, 3a, 3b, 4h, 5a and 6a with oligomer set of **Table 2** were plotted as the difference in quantitation from the HCV 1a calibrators (**Figure 20**). HCV genotype quantitation at $\square 0.25$ log difference from the HCV 1a calibrators was achieved.

[00246] Two T7 amplification oligomers HCV T7 93-119 (SEQ ID NO: 5) and HCV T7 80-119 (SEQ ID NO: 4) in the TCR were tested with negative serum and it was confirmed that the emergence time for internal control amplification was not affected (not shown). The HCV T7 80-119 initial amplification oligomer was also tested to determine if there are false positives in experiments with serum due to T7

carryover from a TCR that overlaps the torch sequence because of its greater overlap with the HCV torch sequence. One false positive (N=140, specificity = 99.3%) occurred at a very low concentration and may be due to operator error during preparation of spiked serum samples; data were excluded due to apparent degradation.

Example 9 – Summary and Further Development of HCV Quantification Assay

[00247] An HCV quantification assay was designed and performed using biphasic TMA in combination with specific target capture and real time detection. The assay uses the long HCV T7 initial amplification oligomer in the Target capture reagent (TCR) and two HCV NT7 oligomers in the amplification reagent for first round extension and linear amplification. A second HCV T7 in the promoter reagent is used for exponential amplification of the HCV target. An HCV probe in the promoter reagent, labeled with FAM and quenched with Dabcyl is used for real time fluorescent detection.

[00248] General internal control (GIC) oligomers were as described in the Sequence Table below (SEQ ID NOs: 15 and 18-20).

[00249] Following development of the biphasic format of the assay to detect and equally quantitate the six HCV genotypes, further development of the oligomer set addressed specific HCV sequence mutations, and addition of a second HCV TCO (0327b, SEQ ID NO: 17) addressed target capture from the sample. The Los Alamos HCV sequence database, which provides annotated HCV sequences, was used as an analysis tool.

[00250] Oligomers used in the HCV quantification are presented in **Table 2**.

[00251] The amplification primers are targeted to the 5'UTR region of Hepatitis C virus polyprotein precursor (HCV-1), a region with ~90% homology among the genotypes.

[00252] HCV primers from the endpoint Procleix® Ultrio® Assay were also tested in the real-time TMA format. None performed well enough to proceed with further.

[00253] As discussed above, the earlier HCV oligomer set had mismatches against HCV genotypes (shown in ovals in **Figure 1**). The torch 68-86 has 2 mismatches for HCV 3a/b and had poor amplification kinetics, with large differences among the genotypes. The nonT7 50-66 has 1 mismatch in HCV 3a and the T7 95-119 has 1 mismatch in each of HCV 2b, 3a, and 4h. The original set of oligomers did not equally quantitate all genotypes.

[00254] New oligomers were designed in alternate regions and in the Torch boxed region shown in **Figure 21** for the torch sequence with a complete match to all HCV genotypes. NonT7s (NT7) and T7s were designed around this torch region.

[00255] Preliminary oligomers chosen for the HCV-Quant Assay are listed in **Table 2** with alignment data in **Figure 21**.

Table 2: Oligomers used in an exemplary HCV Quantification Assay (lower case = 2'-methoxy RNA, uppercase = DNA, underlined = T7 promoter)				
Target and Class	Description	bases	MW (g/mol)	Sequence
HCV NT7	DNA, HCV(+) 52-78-1, NT7	27	8300	5' GGA ² ACTTCTGTCTTCACGCGGAAAGCG 3' (SEQ ID NO: 2)
HCV NT7	DNA, HCV(+) 52-78-2, NT7	27	8347	5' GGA ² ATTACTGTTTTAACGCAGAAAGCG 3' (SEQ ID NO: 3)
HCV T7 initial amplification oligomers	DNA, HCV(-) 80-119 T7	67	20628	5' <u>AATTTAATACGACTCACTATAGGGAGACCTGGAGGC</u> TGCACGACACTCATACTAACGCCATGGCTAG 3' (SEQ ID NO: 4)
HCV T7	DNA, HCV(-) 93-119 T7	54	16607	5' <u>AATTTAATACGACTCACTATAGGGAGACCTGGAGGC</u> TGCACGACACTCATACTA 3' (SEQ ID NO: 5)
HCV Torch	RNA, HCV(-)81-96 C9(16,17) 5F3D Torch	21	8238	5'-FAM uagccaugggcguuagu(c9)ggcua 3'-DABCYL (SEQ ID NO: 12)
HCV TCO	RNA/DNA, HCV(-)0297 dT3dA30 TCO	52	16610	5' gggcacucgcaagcaccuTTTAAAAAAAAAAAAA 3' (SEQ ID NO: 16)
HCV TCO	RNA/DNA, HCV0327b(-) dT3dA30 TCO	51	16309	5' cauggugcacggucucgTTTAAAAAAAAAAAAA 3' (SEQ ID NO: 17)
GIC NT7	DNA, GIC(+) 4102 NT7	19	5885	5' GATTATATAGGACGACAAG 3' (SEQ ID NO: 18)
GIC T7	DNA, GIC(-) 4203, T7	49	15134	5' <u>AATTTAATACGACTCACTATAGGGAGAGATGA</u> TTGACTTGTGATTCCGC 3' (SEQ ID NO: 19)
GIC Torch	RNA, GIC(+)4180-4197 C9(5-6) 5A3R Torch	23	9532	5'-ACRIDINE gcaug(c9)gugcgauugggacaugc 3'-ROX (SEQ ID NO: 20)
GIC TCO	DNA, IC CAP (-) 4277 dT3A30 TCO	57	18150	5' cguucacuaauuggucucugcauucTTTAAAAA 3' (SEQ ID NO: 15)

(5F3D: 5'-FAM, 3'- DABCYL. 5A3R: 5'-acridine, 3'-ROX.)

[00256] The oligomers in **Table 2** were found to perform well with multiple HCV subtypes. However, several were found to have mismatches within the oligomer binding region to certain HCV sequences, which could result in poor quantitation. The sequences were gathered from database sources including HCVdB.org, Genbank, and Los Alamos. Genotype prevalence in these databases is reported below in **Table 3**, and is similar to US prevalence.

Table 3: Genotype prevalence in HCV database sequences

genotype	n	Prevalence in Database
1	422	49.4%
2	63	7.4%
3	120	14.0%
4	50	5.8%
5	10	1.2%
6	70	8.2%
7	1	0.1%
unknown	119	13.9%
total	855	

[00257] The goal was to provide quantification within ± 0.5 log c/ml of expected concentration regardless of genotype. Out of 855 sequences found from the source databases, there were 81 unique sequences (including perfect matches) in the relevant region for the oligomer set in **Table 2**. The frequency of mismatches was highest in the T7 and torch sequences as shown in **Table 4** below, under effective mismatches. The TCO also had a high prevalence of mismatches (over 5%) but were mostly single-base mismatches, which are not believed to have more than minimal impact on performance.

Table 4: Summary of mismatch frequency between preliminary oligomer set and HCV mutant sequences

# of mismatches	NT7	T7 (corrected for built-in mismatches)	Torch	torch (no overlap w/ T7)	TCO
total mismatches	84.1%	15.0%	4.3%	0.9%	5.6%
1 mismatch	0.7%	6.6%	3.1%	0.5%	5.4%
2 mismatch	81.3%	7.4%	0.7%	0.2%	0.1%
3 mismatch	1.7%	0.5%	0.3%	0.1%	0.1%
≥ 4 mismatch	0.3%	0.5%	0.0%	0.0%	0.0%

perfect matches	15.9%	69.3%	95.7%	99.1%	94.4%
N	860	748	860	860	728
Effective Mismatches	2.8% (note 2)	15.0% (note 1)	4.3%	0.9%	5.6%

Note 1: T7 primer has inherent single base mismatch (G-A) that is common to the HCV-1a, -2b, -5a and -6a used to design the assay (Figure 21), and is also prevalent in sequences from the databases (see T7 primer box in the far right of Figure 23). The oligomer set is designed around this specific mismatch, and therefore it was not counted in the table.

Note 2: NT7 has a (T-A and G-A) mismatch common to the HCV-1a, -2b, -4h, -5a and -6a used to design the assay (Figure 21), and is also prevalent in 81% of the sequences from the databases. This oligomer set is designed around this specific mismatch and therefore it was not included in the 'Effective Mismatches'.

[00258] Fifty of the 81 unique mutant sequences were chosen for synthesis based on the following criteria:

1. >2 mismatches within a given primer or the oligomer sequence
2. All mutant sequences occurring more than once in databases were built and tested.
3. Common mutations. If for example, a "g" was commonly seen instead of a "t" at position "x", then a subset of these types of mutation were made. As this type of single base mutation was very common, only a subset was made.
4. Select deletions and insertions were made and tested.

[00259] The identified mutations were incorporated into parental HCV clones by site directed mutagenesis (PCR of the plasmid using primers which contain the base changes). The *in vitro* transcripts were then made off of these new mutant clones. **Table 5** lists the mutants that were synthesized and tested. In Table 5, the "subtype" column indicates the subtype in which the mutation was initially identified, and the clone name includes a designation of the subtype of the parental clone from which the construct for testing was derived.

Table 5: <i>In vitro</i> transcript mutants							
SEQ ID NO	Clone name	Sub type	Mutation location	Partial sequence including mutation(s) (underlined)	frequency*	# of mutations	Accession ref (GenBank)
166	HCV-1a NT7 A Clone	6m	NT7	GGAAC <u>T</u> AATGT CTTCACGCAGA AAGCG	7	3	DQ835766
167	HCV-1a T7 C-T-A-A Clone	6q	T7	GCGTTAGTATG AGCGTTGTACA ACCTCCAGG	1	4	EF424625
168	HCV-1a T7 T-A	4	T7	GCGTTAGTATG AGTGT <u>T</u> GTACA GCCTCCAGG	35	2	EF392175

Table 5: <i>In vitro</i> transcript mutants							
SEQ ID NO	Clone name	Sub type	Mutation location	Partial sequence including mutation(s) (underlined)	frequency*	# of mutations	Accession ref (GenBank)
169	HCV-1a T7 A-A	7a	T7	<u>ACGTT</u> AGTATG AGTGT <u>CGTACA</u> GCCTCCAGG	1	2	EF108306
170	HCV-1a NT7 T-T-A	1b	NT7	GGAATTACTGT <u>TTTAACGCAGA</u> AAGCG	1	5	AF165050
171	HCV-5a NT7 T	5	NT7	GGA <u>ACTACTTT</u> CTTCACGCAGA AAGCG	1	3	AM502711
172	HCV-5a NT7 C-C	7a	NT7	GGAAC <u>CACTGT</u> CCTCAGCAGA AAGCG	1	4	EF108306
173	HCV-1a NT7 T	1b	NT7	GGA <u>ACTACTGT</u> CTTCACGCAGA AAGTG	1	3	X65924
174	HCV-1a T7 T-C	2a	T7	GCGTTAGTATG AGTGT <u>TGCACA</u> GCCTCCAGG	1	3	D31604
175	HCV-1a T7 A-C-G	3a	T7	GCGTTAATACG AGTGT <u>CGTGCA</u> GCCTCCAGG	1	2	AJ621226
176	HCV-1a T7 C-C-C-G	3a	T7	GCGTTA <u>CCACG</u> AGTGT <u>CGTGCA</u> GCCTCCAGG	1	3	AJ621237
177	HCV-1a Teh A-C	3	Torch	TA <u>ACCCTGGCG</u> T <u>TAGT</u>	contrived	2	AJ621232 **
178	HCV-1a Teh C	3	Torch	TAGCC <u>CTGGCG</u> T <u>TAGT</u>	1	1	AJ621232
179	HCV-1a NT EF424625	6q	NT	GGA <u>ACTATTGT</u> CTTCACGCAGA AAGCG	3	3	EF424625
180	HCV-1a NT DQ295833	4a	NT	GGT <u>ACTACTGT</u> CTTCACGCAGA AAGCG	1	3	DQ295833
181	HCV-1a T7 DQ295833	4a	T7	GCAGTTAGTAT <u>AGAGTGT</u> <u>CGTA</u> CAGCCTCCAGG	1	3	DQ295833
182	HCV-1a TCO DQ295833	4a	TCO	AAGGTGCTTGC GAGTCGCC	1	3	DQ295833
183	HCV-1a Teh AJ621232	3a	torch	TAGCC <u>CCCTGGC</u> GTTAGT	1	2	AJ621232
184	HCV-1a NT EU360317	1a	NT	GGA <u>ACTGCTGT</u> CTTCCCGCAGA AAGCG	1	3	EU360317

Table 5: <i>In vitro</i> transcript mutants							
SEQ ID NO	Clone name	Sub type	Mutation location	Partial sequence including mutation(s) (underlined)	frequency*	# of mutations	Accession ref (GenBank)
185	HCV-3a NT AJ621233	3a	NT	GAAC <u>TTTT</u> GTT TTCACG <u>GAAAA</u> GCG	2	4	AJ621233
186	HCV-1a T7 FJ696476	1	T7/torch	GCGTCTGTATG AGT <u>TT</u> CGGGCA GCCTCCAGG	1	4	FJ696476
187	HCV-1a Tch FJ696480	1	torch/T7	TAGCCATGGCG CTAGT	13	1	FJ696480
188	HCV-1a Tch FJ696498	1	torch/T7	TAGCCATGGCG <u>CT</u> TGT	2	2	FJ696498
189	HCV-1a T7 FJ696503	1	T7/torch	GCGCT <u>TTTT</u> ATG AGCGTCGTGCA GCCTCCAGG	1	4	FJ696503
190	HCV-1a Tch EU360323	1b	torch	TAGCCATGGCG <u>T</u> CAGT	3	1	EU360323
191	HCV-3a Tch FJ696423	3	torch	TAGCTATGGC- GTTAGT	1	1	FJ696423
192	HCV-1a T7 AJ621237	3a	T7	GCGTTATCCAC GAGTGTCGTGC AGCCTCCAGG	1	4	AJ621237
193	HCV-1a TCO DQ071885	1b	TCO	AGGGTGCGTGC <u>AAGT</u> GCCC	1	2	DQ071885
194	HCV-1a T7 FJ696420	3	T7	GC- GTTAGT <u>AC</u> - GAGTGTCGTGC ACCCTCTAGG	1	3	FJ696420
195	HCV-1a Tch GU451220	1b	torch	TAGTGCTGGCG TTAGT	1	3	GU451220
196	HCV-1a TCO EU360321	1b	TCO	AGGTTGCTTGC GAGTGCCC	2	1	EU360321
197	HCV-3a TCO HM043011	3	TCO	AGGGCGCTTGC GAGTGCCC	32	1	HM043011
221	HCV-1a T7-NT DQ295833	4a	NT & T7 mutated	(NT mutant region) GGT <u>ACTACT</u> GTT CTTCACGCAG <u>A</u> AAGCG	1	6	DQ295833

Table 5: <i>In vitro</i> transcript mutants							
SEQ ID NO	Clone name	Sub type	Mutation location	Partial sequence including mutation(s) (underlined)	frequency*	# of mutations	Accession ref (GenBank)
				(T7 mutant region) GCAGTTAGTAT <u>AGAGTGT</u> CGTA CAGCCTCCAGG			
199	HCV-1a T7 FJ696429 E(12)	1	T7	GCGTTAGTATG AGTGT <u>CGT</u> GCA GCCTCCAAG	12	1	FJ696429
200	HCV-1a T7 FJ696458 G(10)	1	T7	GCGCTAGTATG AGTGT <u>CGT</u> GCA GCCTCCAGG	10	1	FJ696458
201	HCV-1a T7 FJ696439 I(4)	1	T7	GCGTTAGTATG AATGT <u>CGT</u> GCA GCCTCCAGG	4	1	FJ696439
202	HCV-1a T7 FJ696473 J(3)	1	T7	GCGT <u>C</u> AGTATG AGTGT <u>CGT</u> GCA GCCTCCAGG	3	1	FJ696473
203	HCV-1a T7 AJ621233 K(2)	3a	T7	GCGTTAGACGA GTGT <u>CGT</u> GCA CCTCCAGG	2	1	AJ621233
204	HCV-1a T7 DQ071885 L(2)	1b	T7	GCGTTAGTATG AGTGT <u>CGT</u> GCA GCCTCCATG	2	1	DQ071885
205	HCV-1a T7 AJ621234 M(2)	3a	T7	GCGTTAGTACG AGTGT <u>CGT</u> GCA GCATCCAGG	2	2	AJ621234
206	HCV-1a T7 FJ696431 N(2)	1	T7	GCGTTAGTATG AGAGT <u>CGT</u> GCA GCCTCCAGG	2	1	FJ696431
207	HCV-1a T7 EU360320 O(2)	1b	T7	GCGTTAGTATG AGTGACGTGCA GCCTCCAGG	2	1	EU360320
208	HCV-1a T7 FJ696486	1	T7	GCGCTAGTATG AGCGT <u>CGT</u> GCA GCCTCCAGG	1	1	FJ696486
209	HCV-1a T7 FJ696498	1	T7	GCGCTTGTATG AGTGT <u>CGT</u> GCA GCCTCCAGG	1	2	FJ696498
210	HCV-1a T7 FJ696503 mod	1	T7	GCGTTTTTATG AGCGT <u>CGT</u> GCA GCCTCCAGG	contrived	3	FJ696503
211	HCV-1a T7 AJ621237 mod	3a	T7	GCGTTATCCAT GAGTGT <u>CGT</u> GCA AGCCTCCAGG	contrived	3	AJ621237

Table 5: <i>In vitro</i> transcript mutants							
SEQ ID NO	Clone name	Sub type	Mutation location	Partial sequence including mutation(s) (underlined)	frequency*	# of mutations	Accession ref (GenBank)
212	HCV-1a T7 FJ696428	1	T7	GCGTTAGTATG AGAGTCGTGCA GCCCCCAGG	1	2	FJ696428
213	HCV-3a NT FJ790793 F(2)	3a	NT	GGAATTTCTGT CTTCACGCGGA AAGCG	2	1	FJ790793
214	HCV-1a TCO EU360322 H(2)	1	TCO	AGGGTGCTTGC GAATGCCC	2	1	EU360322

[00260] The 50 *in vitro* transcript mutants were tested with the initial assay feasibility oligomer system (Table 2) and 8 mutants recovered outside 0.5log c/ml from expected results (**Figures 22A and 22B**) which represent ~1% of the population (8/850). 13 mutants under quantified by >0.4 log c/mL.

[00261] Six of the 8 mutants with a log difference of >0.5 logs were located in the T7 and torch region, 1 in the NT7 region, and a single mutant had mutations in T7, NT7 and TCO region (Table 6).

Table 6: Mismatches to oligomer set in selected mutants

Mutation location	#
T7	3
T7/torch	2
torch	1
NT	1
multiple area	1

[00262] **Figure 23** shows a sequence alignment including the 13 mutants that under quantified by >0.4 log c/mL.

[00263] To improve quantitation of mutant HCV, changes were made to the initial oligomer set. The chosen modifications to the initial oligomer set were (1) lengthening the T7 initial amplification oligomer to address the T7 and torch mismatches and (2) adding a second, different NT7 oligomer. The oligomers screened are listed in **Table 7**.

Table 7: Oligomers screened to improve mutant quantitation			
name	type	sequence 5'-3'	SEQ ID NO
DNA, HCV(+)245-266 NT7_1a mtc	NT7	ATT TGG GCG TGC CCC CGC AAG A	76
DNA, HCV(+)245-266 NT7_3a mtc	NT7	ATT TGG GCG TGC CCC CGC GAG A	77

Table 7: Oligomers screened to improve mutant quantitation			
name	type	sequence 5'-3'	SEQ ID NO
DNA, HCV(+)270-289 NT7 2 mism	NT7	CTA GCC GAG TAG TGT TGG GT	78
DNA, HCV(+)278-304 NT7 3 mism	NT7	AGT AGT GTT GGG TCG CGA AAG GCC TTG	79
DNA, HCV(+)50-69_TG NT7_64A	NT7	GAGGAACTACTGTCTTCACG	80
DNA, HCV(+)52-78_TG NT7_64A	NT7	GGAAGTACTGTCTTCACGCGGAAAGCG	81
DNA, HCV(+)50-78_TG NT7_64 A	NT7	GAGGAACTACTGTCTTCACGCGGAAAGCG	82
DNA, HCV(+)292-318 NT7	NT7	GCGAAAGGCCTTGTGGTACTGCCTGAT	83
DNA, HCV(+)298-324 NT7	NT7	GGCCTTGTGGTACTGCCTGATAGGGTG	84
DNA, HCV(+)66-78_TG NT7 shrt	NT7	TGTCTTCACGCGGAAAGCG	85
DNA, HCV(+)245-266 NT7_1a mtch	NT7	ATTTGGGCGTGCCCCCGCAAGA	86
DNA, HCV(+)245-266 NT7_3a mtch	NT7	ATTTGGGCGTGCCCCCGCGAGA	87
DNA, HCV(+)270-289 NT7 2 mismatches	NT7	CTAGCCGAGTAGTGTGGGT	88
DNA, HCV(+)271-295 NT73 mismatches	NT7	TAGCCGAGTAGTGTGGGTGCGGAA	89
DNA, HCV(+)278-304 NT7 3 mismatches	NT7	AGTAGTGTGGGTGCGGAAAGGCCTTG	90
DNA, HCV(+)284-311 NT7 2 mismatches	NT7	GTTGGGTGCGGAAAGGCCTTGTGGTACT	91
DNA, HCV(+)292-318 NT7	NT7	GCGAAAGGCCTTGTGGTACTGCCTGAT	92
DNA, HCV(+)298-324 NT7	NT7	GGCCTTGTGGTACTGCCTGATAGGGTG	93
DNA, HCV(+)50-78_TG NT7	NT7	GAGGAACTTCTGTCTTCACGCGGAAAGCG	94
DNA, HCV(+)66-78_TG NT7 shrt	NT7	TGTCTTCACGCGGAAAGCG	95
DNA, HCV(+)52-78_TG NT7_71A	NT7	GGAAGTCTGTCTTCACGCAGAAAGCG	96
DNA, HCV(+)52-78_TG NT7_71Ino	NT7	GGAAGTCTGTCTTCACGCIGAAAGCG	97
DNA, HCV(+)66-78_TG NT7_71A	NT7	TGTCTTCACGCAGAAAGCG	98
DNA, HCV(+)50-69_TG NT7	NT7	GAGGAACTTCTGTCTTCACG	99
DNA, HCV(+)52- 78_NT7_A64,71	NT7	GGAAGTACTGTCTTCACGCAGAAAGCG	100

Table 7: Oligomers screened to improve mutant quantitation			
name	type	sequence 5'-3'	SEQ ID NO
DNA, HCV(+)52-78_NT7_mut TTA_1	NT7	GGAATTACTGTTTTAACGCAGAAAGCG	3
DNA, HCV(+)271-295 NT7 mtch 2a	NT7	TAGCCTAGTAGCGTTGGGTTGCGAA	101
DNA, HCV(+)271-296 mtch 2a	NT7	TAGCCTAGTAGCGTTGGGTTGCGAAC	102
DNA, HCV(+)271-295 NT7 mtch 291T	NT7	TAGCCGAGTAGTGTTGGGTTGCGAA	103
DNA, HCV(+)271-295 NT7 mtch 2a 271T	NT7	TAGCCTAGTAGTGTTGGGTCGCGAA	104
DNA, HCV(+)271-295 NT7 mtch 2a 283C	NT7	TAGCCGAGTAGCGTTGGGTCGCGAA	105
DNA, HCV(+)271-295 NT7 mtch 2a, 283, 291	NT7	TAGCCGAGTAGCGTTGGGTTGCGAA	106
DNA, HCV(+)271-295 NT7 mtch 3a	NT7	TAGCCGAGTAGTGCTGTGTCGCGAA	107
HCV T7 79-119 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CCA TGG CTA GA	108
HCV T7 80-119 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CCA TGG CTA G	109
HCV T7 81-119 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CCA TGG CTA	110
HCV T7 82-119 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CCA TGG CT	111
HCV T7 83-119 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CCA TGG C	112
HCV T7 84-119 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CCA TGG	113
DNA, HCV(-)87-119 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CCA	114
DNA, HCV(-)88-119 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG CC	115
DNA, HCV(-)89-119 T7_3_ino	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGI ACI ACA CTC ATA CTA ICG C	116
DNA, HCV(-)89-119 T7_A105	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACA ACA CTC ATA CTA ACG C	117

Table 7: Oligomers screened to improve mutant quantitation			
name	type	sequence 5'-3'	SEQ ID NO
DNA, HCV(-)89-119 T7_G92	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA GCG C	118
DNA, HCV(-)89-119 T7_I105	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACI ACA CTC ATA CTA ACG C	119
DNA, HCV(-)89-119 T7_I92	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ICG C	120
DNA, HCV(-)89-119 T7_Ino108	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGI ACG ACA CTC ATA CTA ACG C	121
DNA, HCV(-)89-119 T7_mut CTAA	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGT TGT ACA ACG CTC ATA CTA ACG C	122
DNA, HCV(-)89-119 T7_T108	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGT ACG ACA CTC ATA CTA ACG C	123
DNA, HCV(-)89-119 T7_T108_A105	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGT ACA ACA CTC ATA CTA ACG C	124
DNA, HCV(-)90-119 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC ATA CTA ACG	125
DNA, HCV(-)93-119 T7_A105	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACA ACA CTC ATA CTA	126
DNA, HCV(-)93-119 T7_mut CTAA_	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGT TGT ACA ACG CTC ATA CTA	127
DNA, HCV(-)93-119 T7_T108	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGT ACG ACA CTC ATA CTA	128
DNA, HCV(-)109-119 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGC ACG ACA CTC	129
DNA, HCV(-)109-119 T7_T108_A10	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCT GGA GGC TGT ACA ACA CTC	130
DNA, HCV(-)127-157 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA GTT CCG CAG ACC ACT ATG GCT CTC CCG GGA G	131
DNA, HCV(-)133-163 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA TCA CCG GTT CCG CAG ACC ACT ATG GCT CTC C	132
T7 HCV1a 134-158(-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA GGT TCC GCA GAC CAC TAT GGC TCT C	133
T7 HCV1a 136-157(-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA GTT CCG CAG ACC ACT ATG GCT C	134
T7 HCV1a 139-162 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CAC CGG TTC CGC AGA CCA CTA TGG	135
T7 HCV 1a 143-166 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA TAC TCA CCG GTT CCG CAG ACC ACT	136

Table 7: Oligomers screened to improve mutant quantitation			
name	type	sequence 5'-3'	SEQ ID NO
T7 HCV 1a 144-167 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA GTA CTC ACC GGT TCC GCA GAC CAC	137
T7 HCV 1a 146-175 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA ATT CCG GTG TAC TCA CCG GTT CCG CAG ACC	138
T7 HCV 1a 149-172 (-)	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CCG GTG TAC TCA CCG GTT CCG CAG	139
DNA, HCV(-)303-333 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA ACT CGC AAG CAC CCT ATC AGG CAG TAC CAC A	140
DNA, HCV(-)308-333 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA ACT CGC AAG CAC CCT ATC AGG CAG TA	141
DNA, HCV(-)316-345 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA ACC TCC CGG GGC ACT CGC AAG CAC CCT ATC	142
DNA, HCV(-)327-354 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA GTC TAC GAG ACC TCC CGG GGC ACT CGC A	143
DNA, HCV(-)329-355 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA GGT CTA CGA GAC CTC CCG GGG CAC TCG	144
DNA, HCV(-)333-360 T7	T7	AAT TTA ATA CGA CTC ACT ATA GGG AGA CAC GGT CTA CGA GAC CTC CCG GGG CA	145
DNA, T7AHCV0263(-)	T7	AATTTAATACGACTCACTATAGGGAGAAGTACCAC AAGGCCTTTCGCIACCCAAC	146
DNA, HCV(-)89-108 T7	T7	AATTTAATACGACTCACTATAGGGAGAGACACTCA TACTAACGC	147
HCV Torch 80-96 5F3D	Tch	CUAGCCAUGGCGUUAGUGCUAG	148
HCV Torch 81-96 5F3D_93C	Tch	UAGCCCUGGCGUUAGUGGCUA	149
HCV Torch 81-94 5F3D	Tch	UAGCCAUGGCGUUAGGCUA	150
HCV Torch 80-94 5F3D	Tch	CUAGCCAUGGCGUUAGCUAG	151
HCV Torch 292-309 5F3D	Tch	GCGAAAGGCCUUGUGGUUAUUCGC	152
HCV Torch 325-340 5F3D	Tch	CUUGCGAGUGCCCCGGGCAAG	153
HCV Torch 321-336 5F3D	Tch	GGUGCUUGCGAGUGCCGCACC	154
HCV Torch 316-331 5F3D	Tch	GAUAGGGUGCUUGCGACUAUC	155
HCV Torch 314-329 5F3D	Tch	CUGAUAGGGUGCUUGCAUCAG	156
HCV Torch 310-325 5F3D	Tch	CUGCCUGAUAGGGUGCGGCAG	157
HCV Torch 307-322 5F3D	Tch	GUACUGCCUGAUAGGGAGUAC	158
HCV Torch 306-321 5F3D	Tch	GGUACUGCCUGAUAGGGUACC	159

Table 7: Oligomers screened to improve mutant quantitation			
name	type	sequence 5'-3'	SEQ ID NO
HCV Torch 300-314 5F3D	Tch	CCUUGUGGUACUGCCCAAGG	160
HCV0168-186(-)dT3dA30	TCO	AUUCGGUGUACUCACCGGTTTAAAAAAAAAAAAA AAAAAAAAAA	161
HCV0157-174(-)dT3dA30	TCO	UCACGGUUCGCGACACCTTTAAAAAAAAAAAAA AAAAAAAAAA	162
HCV0154-173(-)dT3dA30	TCO	CACCGGUUCCGCGACACACUTTTAAAAAAAAAAAAA AAAAAAAAAA	163
HCV0143-161(-)dT3dA30	TCO	AGACCACUAUGGCUCUCCCTTTAAAAAAAAAAAAA AAAAAAAAAA	164
HCV0141-159(-)dT3dA30	TCO	ACCACUAUGGCUCUCCCGGTTTAAAAAAAAAAAAA AAAAAAAAAA	165

[00264] NT7 oligomer HCV (+)52-78_NT7_mut TTA_1, also referred to as 52-78-2 (SEQ ID NO: 3), was found to improve quantification in the presence of certain mutations. With the addition of this oligomer to address mutations, there were 2 NT7 primers (HCV (+) 52-78-1, SEQ ID NO: 2; and HCV (+) 52-78-2, SEQ ID NO: 3) in the oligomer set.

[00265] Detection results for genotypes including subtype 3a, subtype 3b, and the subtype 1a NT7 TTAA mutant at varying proportions of the two NT7 primers are in Table 8 (given as log difference from target; bold italics indicate more than 0.5 log difference for the NT7 T-T-A mutant or greater than 0.25 log difference for the 3a and 3b genotypes). Using 75% or 50% of the 52-78-2 NT7 oligomer resulted in quantification of all tested sequences within 0.5 logs of target. Using 25% of the 52-78-2 NT7 oligomer resulted in quantification of all tested sequences except the T-T-A mutant within 0.5 logs of target. It was also concluded that a manufacturing tolerance around primer concentrations of approximately +/-10% was acceptable. At 50% 52-78-2, subtype 3a and 3b were quantified within +/-0.25 log difference of target, and the 1a NT7 TTA mutant was quantified within +/- 0.5log c/ml.

Table 8: Effect of NT7 oligomer concentrations						
% HCV (+) 52-78-2 /total NT7 primer concentration						
	100%	75%	50%	25%	11%	0%
CAL02	0.13	0.05	0.15	0.13	0.15	0.11
CAL03	-0.05	0.02	-0.02	-0.01	-0.06	0.06
CAL04	-0.14	-0.11	-0.18	-0.17	-0.17	-0.30
CAL06	0.01	0.01	-0.05	-0.03	0.04	0.10
CAL08	0.05	0.03	0.10	0.08	0.04	0.02
CTRL30-1A	0.01	0.15	0.09	0.07	0.26	0.30
SEQ ID 170 at 1e4 c/ml	0.12	0.44	-0.37	-1.18	-1.50	-1.35
SEQ ID 172 at 1e4 c/ml	-0.07	-0.08	-0.28	-0.23	-0.29	-0.20
SEQ ID 173 at 1e4 c/ml	-0.24	-0.23	-0.34	-0.27	-0.33	-0.26

HCV GENOTYPE 2B	-0.19	-0.10	-0.12	-0.24	-0.17	-0.09
HCV GENOTYPE 3A	-0.70	-0.33	-0.21	-0.15	-0.28	-0.21
HCV GENOTYPE 3B	-0.58	-0.18	0.03	0.05	0.02	0.06
HCV GENOTYPE 4H	-0.08	-0.02	-0.03	0.03	0.02	0.06
HCV GENOTYPE 5A	-0.03	0.04	0.05	0.02	0.01	0.14
HCV GENOTYPE 6A	-0.12	-0.01	-0.09	-0.05	-0.15	0.05

[00266] A longer T7 initial amplification oligomer (HCV (-) 80-119 T7) was designed to address the T7 and torch mutants. By increasing the length of the T7 sequence, oligomer binding overcame isolated mismatches in the T7 region. As a result, the new T7 initial amplification oligomer completely overlaps the torch.

[00267] The T7 initial amplification oligomer is located in the target capture reagent. The T7 initial amplification oligomer design overlaps the torch region. Accordingly, to minimize the risk of false positives, free T7 initial amplification oligomer should be removed during the wash step. Spiking T7 initial amplification oligomer directly into the amplification reaction resulted in false positives (data not shown).

[00268] **Figure 24** is a sequence alignment of the oligonucleotides in the HCV oligomer set corresponding to the oligomers listed in **Error! Reference source not found..** With these changes, all IVT mutants recovered within +/- 0.5log c/ml of targeted concentration (**Figure 25A**) and subtype detection was within +/- 0.25 log c/ml of expected value (**Figure 25B**). The sequence for the second HCV TCO (0327), which was added during reagent formulation is also shown in **Figure 24**.

Example 10 – Analytical specificity studies

[00269] These data were generated using the set of oligomers as presented in Table 2 except that the HCV 0327b(-) capture oligomer was not used.

[00270] Several specificity studies were conducted on a series of different instruments using HCV-negative serum prepared in-house, internal amplification control (IAC) buffer, and clinical negative samples, including more viscous clinical samples. No false positives (FP) were seen in 1468 negatives tested resulting in a specificity of 100% (95% CI: 99.7 to 100%) (**Table 9**).

Table 9: Analytical specificity studies			
Instrument#	# of Neg	#FP*	Description
1	45	0	negative serum
1	105	0	IAC buffer
1	105	0	negative serum
2	85	0	IAC buffer

Table 9: Analytical specificity studies			
Instrument#	# of Neg	#FP*	Description
3	200	0	Clinical negative plasma
4	92	0	auto-immune clinical negatives
3	104	0	negative serum
5	105	0	negative serum
4	102	0	negative serum
1	105	0	negative serum
6	105	0	negative serum
7	105	0	negative serum
8	105	0	negative serum
2	105	0	negative serum
total	1468	0	

* RFU range threshold: 1000

Example 11 – Analytical sensitivity and analysis of clinical samples

[00271] The data in this example were generated using the set of oligomers in Table 2 except that the HCV0327b(-) capture oligomer was not used.

[00272] The studies presented below were performed with virus in plasma, IVT in IAC buffer, and also an artificial AcroMetrix HCV-S virus panel similar to armored RNA. The AcroMetrix HCV-S panel is a synthetic sequence of HCV 1b, embedded in a recombinant BVDV (bovine viral diarrhea virus) protein using the SynTura Technology by AcroMetrix, calibrated in IU/mL (Applied Biosystems cat #950350).

[00273] Based on preliminary experiments, using the WHO HCV 2nd Standard, the HCV assay has a 5 copy/IU conversion factor. Preliminary sensitivity studies were performed with *in vitro* transcripts indicated in **Table 10** in IAC. The positivity rate at 60c/ml was 100%. Using PROBIT analysis, the limit of detection at 95% probability, was 19.58 c/ml or 3.9IU/ml. Probit analysis was performed using R statistical computing software, using a generalized linear model with binomial error distribution, along with the Probit function for response variable. See **Tables 10 and 11**.

Table 10: Analytical sensitivity of <i>in vitro</i> transcript, Sample data					
IVT	copies/ml	N	Negatives	Positives	% Positive
HCV 1A	100	35	0	35	100%
HCV 1A	60	35	0	35	100%
HCV 1A	37	35	1	34	97%
HCV 1A	10	35	4	31	89%
HCV 1A	5	35	14	21	60%
Neg. Control	0	4	4	0	0%

Table 11: Analytical sensitivity for IVT - Limit of detection using PROBIT analysis				
Probability	Conc (Copy/mL)	LowerLimit- 95% (Copy/mL)	UpperLimit- 95% (Copy/mL)	R- squared
50%	3.54	1.49	5.20	0.997
95%	19.58	13.22	48.22	0.997

[00274] A study was also performed with the Acrometrix panel in serum. The positivity rate at 12 IU/ml was 100%. Using PROBIT analysis, the limit of detection at 95% probability was 3.13 IU/ml. See **Tables 12 and 13.**

Table 12: Analytical Sensitivity of Acrometrix panel, Sample data					
IU/ml of Acrometrix panel	Reps	# Neg	# Pos	% positive	R_Avg_HCV LogCopy c/ml
12 IU/mL	30	0	30	100%	1.96
8 IU_mL	30	0	30	100%	1.42
6 IU_mL	30	0	30	100%	1.45
4 IU_mL	30	1	29	97%	1.14
2 IU_mL	30	5	25	83%	1.14
1 IU_mL	30	10	20	67%	0.80

Table 13: Analytical Sensitivity of Acrometrix panel, Limit of detection using PROBIT analysis				
Probability	Conc (IU/mL)	LowerLimit- 95% (IU/mL)	UpperLimit- 95% (IU/mL)	R- squared
50%	0.74	0.34	1.05	0.997
95%	3.13	2.30	5.74	0.997

[00275] Precision was assessed with various low copy-level panels over 3 instruments and 3 days for a total of 60 replicates. The total error was less than 1 log c/ml at 12IU/ml or 1.78 log c/ml. See **Table 14.**

Table 14: Assay precision ≤ 100c/ml								
type	n	target log c/ml	target IU/ml	% positi ve	Observed average LogCopy	log differe nce	total sd (log c/ml)	total error*
HCV 1a IVT/IAC	60	1.48		100%	1.65	0.27	0.27	0.76
HCV 1a virus/serum	60	1.21		98%	1.48	0.30	0.33	0.92

artificial HCV 1b virus/serum	60		12	100%	2.04	0.16	0.16	0.45
artificial HCV 1b virus/serum	60		2	93%	1.21	0.50	0.49	1.39

*total error = $\sqrt{2} \times 2 \times \text{standard deviation}$

[00276] The precision of the QC calibrators were also assessed at 5 different concentrations in this study. Total error was below 1 log c/ml and sdlog c/ml was <0.20 from 2 log c/ml (~20IU/ml) to 9 log c/ml (~2e8 IU/ml). See **Table 15**.

Table 15: Precision from 100 c/ml to 1e9 c/ml					
type	n	target log c/ml	Observed average Log Copy	total sdlog c/ml	total error*
HCV 1a transcript/IAC	12	1.96	2.04	0.12	0.34
HCV 1a transcript/IAC	12	4.18	4.02	0.10	0.28
HCV 1a transcript/IAC	12	5.89	5.95	0.08	0.23
HCV 1a transcript/IAC	12	8.3	8.32	0.09	0.25
HCV 1a transcript/IAC	12	9.1	9.05	0.06	0.17

*total error = $\sqrt{2} \times 2 \times \text{standard deviation}$

[00277] **Figure 26** demonstrates that the assay was linear from 1.47 log c/ml (~6IU/ml) to 9 log c/ml (~2e8 IU/ml).

[00278] HCV viral load for 91 clinical samples were determined using the assay as described in Example 11 and compared to results from commercial HCV assays from Abbott Molecular Inc. and Roche Molecular Systems Inc. A 5 copy/IU conversion was determined as discussed above. The results of the instant assay were all within one log c/ml of the Abbott results (not shown). When compared to the Roche assay, 2 HCV subtype 4 samples gave more than 1 log over-quantification. The Roche assay is known to under-quantitate HCV subtype 4. See Chevaliez et al., *Journal of Hepatology*, Volume 44, Supplement 2, April 2006, Pages S195-S196.

Example 12 – Addition of second target capture oligomer

[00279] A second TCO, HCV 0327b(-)dT3dA30 (SEQ ID NO: 17), was evaluated as to whether it impacts performance with respect to target capture. All experiments below were tested with HCV 0327b(-)dT3dA30 at 6 pmol/reaction unless otherwise stated.

[00280] The following conditions were tested to evaluate the impact of the addition of the second TCO and determine the optimal concentration of the second TCO. Six mutant transcripts that have mutations in the TCO (0297) region and genotype transcript panels were tested at 1e4 copies/ml (n = 5). The

addition of the second TCO (0327b) at 6 and 12 pmol/reaction had similar log copy and precision. All positive panels were 100% positive and within ± 0.5 logs of target log copy. The control (single TCO system, 0297 only) had slightly higher log copy values in the initial run; however, results from the same condition repeated on a different day had results that aligned with the rest of the conditions (not shown), indicating slight day-to-day variability. The second TCO (0327b) alone had delayed emergence times for HCV and GIC by approximately 3 minutes for both (data not shown). The additional second TCO (0327b) at 6 pmol/reaction is thus an acceptable concentration.

[00281] The WHO HCV panel was tested with the addition of the second TCO. The study was completed on multiple instruments with total replicates ranging from 15-45 per panel (3 runs). The previous limit of detection (LoD) (95% positive) was determined to be 3.76 IU/mL (3 instruments, $n = 30-90$ per panel or 6 runs). The LoD slightly increased to 5.06 IU/mL which may be variability between experiments, as the previous value of 3.76 IU/ml is within the 95% confidence interval (**Table 16**).

Table 16: Limit of Detection (95% positivity) of HCV WHO 2nd Standard			
Condition	Concentration (IU/mL)	Lower Limit 95%	Upper Limit 95%
WHO in plasma (with 2 nd TCO)	5.06	3.46	10.56

[00282] The calculated LoQ (limit of quantification, i.e., concentration where the total error equals 1) was 9.748 IU/ml, similar when the single TCO was used (single TCO TE = 9.02 IU/mL), demonstrating equivalent precision near the LoD of the assay (**Table 17**).

Table 17: LoQ or Total Error (TE) determination of WHO with addition of second TCO		
Sample	Target IU/mL	TE (log IU/mL)
WHO0	0	--
WHO1	1	0.792
WHO2	2	1.358
WHO3	3	1.358
WHO6	6	1.273
WHO12	12	0.764
WHO20	20	0.537
Interpolated based on linear regression line (1 IU/mL excluded)	9.748 IU/ml	1

[00283] The LoD for the same clinical specimens of six HCV genotypes previously tested with only the 0297 TCO were re-tested near the LoD (12 IU/ml) with the second TCO, 0327b (NB3+TCO). The

clinical specimens were serially diluted in appropriate plasma or serum diluents beyond the 5 IU/ml from initial testing. For all tested genotypes with the exception of HCV genotype 4, the percent positive results and average log copy at the lowest target concentration were greater with the addition of the second TCO (**Table 18**). That is, at 1 IU/ml, each of 1b, 2a, 3a, 5a, and 6c showed improved % positives (gains of 13, 20, 26, 13, and 13 percentage points). Specimens of HCV genotype 4 had similar results with addition of the second TCO compared to the single TCO system. All percent positive results were $\geq 95\%$ at 12 IU/mL and ≤ 0.25 SD log copy at 100 IU/ml.

Table 18: Log Copy Results for Clinical Genotype Specimens +/- second TCO (0327b)								
Genotype/sample	Target (IU/mL)	Reps	0297 TCO only			0297 + 0327b TCOs		
			% Positive	SD IU/mL	Observed LogIU	% Positive	SD IU/mL	Observed LogIU
1b Plasma	1E+03	5	100%	0.01	3.03	100%	0.02	3.08
	1E+02	5	100%	0.08	2.14	100%	0.05	2.15
	2E+01	20	100%	0.30	1.18	100%	0.17	1.41
	12	30	100%	0.32	0.93	100%	0.28	1.24
	5	20	100%	0.39	0.41	100%	0.40	0.68
	3	20	85%	0.48	0.36	100%	0.52	0.18
	1	15	47%	0.61	0.02	60%	0.49	0.18
2a Serum	1E+03	5	100%	0.06	2.91	100%	0.10	3.03
	1E+02	5	100%	0.14	2.11	100%	0.09	2.17
	2E+01	20	100%	0.17	1.35	100%	0.17	1.52
	12	30	100%	0.23	0.99	100%	0.23	1.29
	5	20	100%	0.38	0.50	100%	0.22	0.81
	3	20	90%	0.54	0.21	100%	0.52	0.47
	1	15	53%	0.49	0.01	73%	0.49	-0.06
3a Plasma	1E+03	5	100%	0.07	3.10	100%	0.05	3.22
	1E+02	5	100%	0.12	2.13	100%	0.08	2.27
	2E+01	20	100%	0.19	1.31	100%	0.12	1.65
	12	30	100%	0.25	0.97	100%	0.15	1.40
	5	20	95%	0.24	0.48	100%	0.24	0.96
	3	20	100%	0.30	0.46	95%	0.37	0.54
	1	15	67%	0.30	-0.42	93%	0.49	0.30
4 Plasma	1E+03	5	100%	0.03	2.59	100%	0.04	2.72
	1E+02	5	100%	0.17	1.62	100%	0.10	1.80
	2E+01	20	95%	0.32	0.84	100%	0.42	0.96
	12	30	100%	0.38	0.43	100%	0.50	0.40
	5	19	89%	0.48	0.22	85%	0.48	0.01
	3	20	65%	0.41	-0.04	65%	0.42	-0.01
	1	15	27%	0.40	-0.22	20%	0.66	-0.01
5a Plasma	1E+03	5	100%	0.05	3.03	100%	0.05	3.07
	1E+02	5	100%	0.17	1.96	100%	0.06	2.08
	2E+01	20	100%	0.27	1.30	100%	0.18	1.40
	12	30	100%	0.24	1.13	100%	0.16	1.12

Table 18: Log Copy Results for Clinical Genotype Specimens +/- second TCO (0327b)								
Genotype/sample	Target (IU/mL)	Reps	0297 TCO only			0297 + 0327b TCOs		
			% Positive	SD IU/mL	Observed LogIU	% Positive	SD IU/mL	Observed LogIU
	5	20	100%	0.42	0.59	100%	0.44	0.60
	3	20	100%	0.52	0.32	100%	0.43	0.41
	1	15	67%	0.51	-0.05	80%	0.42	0.08
6c Serum	1E+03	5	100%	0.06	3.10	100%	0.08	3.43
	1E+02	5	100%	0.13	2.19	100%	0.11	2.48
	2E+01	20	100%	0.19	1.37	100%	0.21	1.80
	12	30	100%	0.22	1.12	100%	0.19	1.58
	5	20	100%	0.36	0.63	100%	0.31	1.05
	3	20	95%	0.48	0.51	100%	0.29	0.72
	1	15	60%	0.43	-0.24	73%	0.52	0.22

[00284] To further confirm performance at low concentration with and without the second TCO, the genotype IVTs were tested with panels at 30, 8 and 5 copies/ml. Each panel was tested using 0297 TCO only (n = 10) or 0297 and 0327b TCOs (n = 20). The percent positive results were comparable for HCV genotypes 2b, 3a, 3b and 4h, and results were improved with 0297 and 0327b TCOs for genotypes 5a and 6a (**Figures 27A-B**). All conditions produced 100% positive results at 30 copies/mL. The average log copy results were comparable between the conditions for genotypes 2b, 3a and 3b and slightly higher for genotypes 4h, 5a and 6a (not shown). The increase trend in percent positivity with the second TCO at low concentrations for genotypes such as 5a and 6a was confirmed with another 30 replicates of the 8 and 5 copies/ml panel and a separate lot of 0297 TCO (not shown). Data are summarized in **Table 19**.

Table 19: HCV genotype IVT percent positive, average log copy, and standard deviation log copy results with 0297 +/- 0327b TCO

HCV Genotype	Copies/ml	Percent Positive		Average Observed Log Copy		Standard Deviation of Observed Log Copy	
		0297 TCO (N=10)	0297 + 0327b TCO (N=20)	0297 TCO (N=10)	0297 + 0327b TCO (N=20)	0297 TCO (N=10)	0297 + 0327b TCO (N=20)
2B	30C	100%	100%	1.50	1.62	0.22	0.27
	8C	90%	89%	0.78	0.79	0.53	0.57
	5C	50%	55%	0.68	0.72	0.43	0.58
3A	30C	100%	100%	1.46	1.41	0.20	0.21
	8C	100%	80%	1.04	0.73	0.34	0.44
	5C	67%	60%	0.81	0.67	0.45	0.49
3B	30C	100%	100%	1.31	1.58	0.66	0.22
	8C	70%	68%	0.83	0.83	0.56	0.47
	5C	44%	47%	1.19	0.69	0.18	0.51
4H	30C	100%	100%	1.71	1.48	0.31	0.47
	8C	70%	95%	1.01	0.88	0.49	0.53
	5C	100%	58%	0.45	0.82	0.53	0.44
5A	30C	100%	100%	1.37	1.56	0.55	0.23
	8C	70%	90%	0.43	0.92	0.50	0.60
	5C	40%	47%	1.22	1.07	0.27	0.39
6A	30C	100%	100%	1.66	1.37	0.28	0.32
	8C	80%	89%	0.83	1.00	0.60	0.56
	5C	30%	74%	0.57	0.57	0.56	0.47

Example 13 – Cross-Reactivity, Analytical specificity, and Clinical specificity

[00285] Testing was done with the 0327b TCO included for microorganism cross-reactivity to a panel of viruses (Hepatitis A, Hepatitis B, Herpes simplex 1, Herpes simplex 2, HIV, Parvovirus, Rubella, Dengue 2, Dengue 3, Dengue 4, Epstein-Barr, and West Nile) and microbes (*C. albicans*, *C. diphtheriae*, *P. acnes*, *S. aureus*, *S. epidermis*, *S. pneumoniae*) spiked into IAC (internal control buffer) at 10^5 particle-forming units (PFU)/mL or 50% tissue culture infective dose (TCID₅₀) for viruses and 10^6 colony-forming units (CFU)/mL for microbes. No positive results were obtained in the absence of HCV nucleic acid. In the presence of HCV (2.3 log copies/ml), there was no significant interference from any virus or microbe in the panel (i.e., quantification was within 0.25 log of control for all spiked samples).

[00286] Clinical specificity was repeated using the oligomer set including the 0297 and 0327b TCOs with 961 frozen uninfected specimens (420 individual human serum and 541 individual human plasma). Eight positives occurred during testing, giving a specificity of 99% and a lower bound (95% CI) of

98.4%. Analytical specificity was repeated for informational purposes with a small number of IAC and negative serum samples at n = 150 total. No positives occurred for the IAC and negative serum samples (specificity was 100%; lower bound (95% CI) was 98.4%).

[00287] No positives had occurred in earlier testing with 1 TCO using the same samples. Testing was repeated with 1 TCO and with 2 TCOs in parallel to determine whether the increase of positives was attributable to addition of the second TCO or an extraneous source such as environmental contamination at the time of testing. Of 410 clinical negative specimens tested in each condition, 2 positives occurred with 2 TCOs and no positives occurred in the control 1 TCO condition. Of 408 IAC negative samples, 2 positives occurred in the control 1 TCO condition and none for 2 TCOs. Thus, both the 1 TCO and 2 TCOs conditions had similar results, and these data confirmed that the addition of the second TCO did not contribute to a higher rate of false positives.

TABLE OF SEQUENCES

[00288] In the following table, lower case letters indicate RNA (for HCV sequences) or 2'-O-methyl RNA (for oligomer sequences and subsequences) and upper case letters indicate DNA. "(c9)" indicates a - (CH₂)₉- linker. Underlining indicates heterologous fusion sequence, e.g., a promoter or subsequence thereof (underlining not shown for T₃A₃₀ sequences).

SEQ ID NO	Description	Sequence
1	Representative HCV 1b sequence, GenBank Acc. No. AB016785	gcccagccccctgatggggggcgacactccaccatagatcactccccctgtga ggaactactgtcttcacgcagaaagcgtctagccatggcggttagtatgag tgtcgtgcagcctccaggccccccccctccggggagagccatagtgggtctg cggaaccggtgagtacaccggaattgccaggacgaccgggtcccttcttg gatcaatcccgcctcaatgcctggagatttgggcgtgcccccgagactg ctagccgagtagtggttgggtcgcgaaaggccttgtggtagctgcctgatag ggtagcttgcgagtgccccgggagggtctcgtagaccgtgcaccatgagcac aaatcctaaacctcaaagaaaaaccaaactaacaccaaccgcccggccac aggacgtcaagttccccgggcggtgggtcagatcgttgggtggagtttacctg ttgccgcgcaggggccccagggttgggtgtgcgcgcgactaggaagacttc cgagcggtcacaacctcgtggaaggcgacaacctatccccaaggctcgcc ggcccagggcaggacctgggtcagccccgggtacccttggccccctctac ggcaatgagggcctggggtgggcagaatggctcctgtcaccccggtgggtc tcggcccagttggggccccacggacccccggcgtaggtcgcgtaatttgg gtaagggtcatcgataacctcacatgcgggttcgcgcgacctcatggggtac attccgctcgtcggcgccccccctggggggcgctgccaggggccctggcgca tggcgctccgggttctggaggacggcggtgaactacgcaacagggaatctcc ccggttgctctttctctatcttccctcctggcttctgtgctcctgtttgacc atcccagcttccgcttatgaagtgcgcaacgtgtccggggtgtaccatgt cacgaacgactgtccaactcaagtattgtgtatggggcggcggacatga tcatgcacacccccgggtgcgtgccttgcgtccggggagaacaattcctct cgttgctgggtagcgttacccccacgctcgcggccagggaacaggagcat ccccactacgacaatacgcacgccatgtcgatttgcctcgttggggcggtg ctttctgctccgccatgtacgtgggggatctctgcggatctgtcttcctc gtctcccagctgttcactttctcacctcgcgggtatgagacagtacaaga ctgcaattgctcgtctatcccggccacgtatcagggtcatcgcatggctt gggatatgatgatgaactggtcacctacagcagccttgggtggtagtcgag ctactccggatcccacaagccgctcgtggacatgggtgacggggggccactg gggagtcctggcgggccttgccactattccatgggtggggaactgggcta aggctcttgattgtgatgtactctttgccggcggttgacggggagaaccacc catgtaacgggggggcaaacaggccggaccaccctgggcattacggccat gtttgcgtttggccgcacataaaagctccaactcattaacaccaatggca gctggcacatcaacaggacccgcctgaactgcaatgactctctcaacact gggttcctagctgcgtgttttacgcacgcaagttcaactcgtctggatg cccagagcgcacatggccagctgccgccccattgacaagtttgttcagggat ggggtcccatcactcatgctgtgcctgacaacttggaccagaggccttac tgttggcactacgcgcccccaaccgtgcgggtatcatacccgctcacagggt gtgtgggtccagtgattgtttcaccccaagccccgttgtgggtggggacga ccgaccgtttcggcgccccctacttacacctgggggggagaatgagacggac gtgctgctccttaacaacacgcggcgccgcgaaggcaactgggttcggctg tacatggatgaatggcaccgggttcgccaagacgtgcggaggccccccat

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2	amplification oligomer 52-78-1	GGAATTCTGTCTTCACGCGGAAAGCG

3	amplification oligomer 52-78-2	GGAATTACTGTTTTAACGCAGAAAGCG
4	T7 amplification oligomer 80-119	AATTTAATACGACTCACTATAGGGAGACCTGGAGGCTGCACGACACTCAT ACTAACGCCATGGCTAG
5	T7 amplification oligomer 93-119	AATTTAATACGACTCACTATAGGGAGACCTGGAGGCTGCACGACACTCAT ACTA
6	amplification oligomer 80-119	CCTGGAGGCTGCACGACACTCATACTAACGCCATGGCTAG
7	amplification oligomer 93-119	CCTGGAGGCTGCACGACACTCATACTA
8	Exemplary T7 promoter	TAATACGACTCACTATAG
9	Sequence comprising T7 promoter	TAATACGACTCACTATAGGGAGA
10	Sequence comprising T7 promoter	AATTTAATACGACTCACTATAG
11	Sequence comprising T7 promoter	AATTTAATACGACTCACTATAGGGAGA
12	Probe oligomer 81-96	uagccauggcgguagu (c9) ggcua
13	Probe oligomer 81-96 target hybridizing sequence	uagccauggcgguagu
14	HCV 1b subsequence, positions 86-95	uggcgguagu
15	Control capture oligomer	cguucacuaauuggucucugcauucTTTAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAA
16	Capture oligomer 0297	gggcacucgcaagcacccuTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AA
17	Capture oligomer 0327b	cauggugcacggucuacgTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA A
18	Control NT7 amplification oligomer	GATTATATAGGACGACAAG
19	Control T7 amplification oligomer	AATTTAATACGACTCACTATAGGGAGAGATGATTGACTTGTGATTCCGC

20	Control probe oligomer 4180-4197	gcaug (c9) gugcgaaauugggacauge
21	T3A30	TTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
22	A30	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA
23	amplification oligomer 52-78-1 subsequence	GCGGAAAGCG
24	amplification oligomer 52-78-1 subsequence	TTCACGCGGA
25	amplification oligomer 52-78-1 subsequence	CTGTCTTCAC
26	amplification oligomer 52-78-1 subsequence	AACTTCTGTC
27	amplification oligomer 52-78-1 subsequence	GGAATTCTG
28	amplification oligomer 52-78-2 subsequence	GCAGAAAGCG
29	amplification oligomer 52-78-2 subsequence	TTAACGCAGA
30	amplification oligomer 52-78-2 subsequence	CTGTTTTAAC
31	amplification oligomer 52-78-2 subsequence	AATTACTGTT
32	amplification oligomer 52-78-2 subsequence	GGAATTACTG
33	amplification oligomer 93-119 subsequence	ACTCATACTA
34	amplification oligomer 93-119 subsequence	ACGACACTCA

35	amplification oligomer 93-119 subsequence	GCTGCACGAC
36	amplification oligomer 93-119 subsequence	TGGAGGCTGC
37	amplification oligomer 93-119 subsequence	CCTGGAGGCT
38	amplification oligomer 80-119 subsequence	ACGCCATGGCTAG
39	amplification oligomer 80-119 subsequence	CCATGGCTAG
40	amplification oligomer 80-119 subsequence	TAACGCCATG
41	amplification oligomer 80-119 subsequence	TACTAACGCC
42	T7 amplification oligomer 93-119 subsequence	GGAGACCTGG
43	T7 amplification oligomer 93-119 subsequence	TAGGGAGACCTGG
44	T7 amplification oligomer 93-119 subsequence	TAATACGACTCACTATAGGGAGACCTGG
45	T7 amplification oligomer 93-119 subsequence	GGAGACCTGGAGGCT
46	T7 amplification oligomer 93-119 subsequence	TAGGGAGACCTGGAGGCT
47	T7 amplification oligomer 93-119 subsequence	TAATACGACTCACTATAGGGAGACCTGGAGGCT
48	Probe oligomer 81-96 subsequence	uuaguggcua

49	Probe oligomer 81-96 subsequence	uuagu (c9) ggcua
50	Probe oligomer 81-96 subsequence	uggcguuagu
51	Probe oligomer 81-96 subsequence	agccauggcg
52	Probe oligomer 81-96 subsequence	uagccauggc
53	Control capture oligomer target hybridizing sequence	cguucacuaauuggucucugcauuc
54	Capture oligomer 0297 target hybridizing sequence	gggcacucgcaagcacccu
55	Capture oligomer 0327b target hybridizing sequence	cauggugcacggucuacg
56	Control amplification oligomer target hybridizing sequence	GATGATTGACTTGTGATTCCGC
57	Capture oligomer 0297 subsequence	caagcacccu
58	Capture oligomer 0297 subsequence	acucgcaagc
59	Capture oligomer 0297 subsequence	gggcacucgc
60	Capture oligomer 0327b subsequence	acggucuacg
61	Capture oligomer 0327b subsequence	uggugcacgg

62	Capture oligomer 0327b subsequence	cauggugcac
63	HCV 1a Transcript MW= 298,334 g/mol, 926 b	GGGCGAAUUGGAGCUCCACCGCGGUGGCGGCCGCUCUAGAACUAGUGGAU CCCCCGGGCUGCAGGAAUUCGCCC UUUCACUCCCCUGUGAGGAACUACUG UCUUCACGCAGAAAGCGUCUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAG CCUCCAGGACCCCCCUCGCGGGAGAGCCAUAGUGGUCUGCGGAACCGGU GAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUCUUGGAUCAACCCG CUCAAUGCCUGGAGAUUUGGGCGUGCCCCGCAAGACUGCUAGCCGAGUA GUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGA GUGCCCCGGGAGGUCUCGUAGACCGUGCACC AUGAGCACGAAUCCUAAAC CUCAAAAAAAAAACAAACGUAACACCAACCGUCGCCCCACAGGACGUAAG UUCCCCGGUGGCGGUCAGAU CGUUGGUGGAGUUUACUUGUUGCCGCGCAG GGGCCCCUAGAUUGGGUGUGCGCGCGACGAGAAAGACUUCGAGCGGUCGC AACCUCGAGGUAGACGUCAGCCUAUCCCCAAGGUCUGUCGGCCCCGAGGGC AGGACCUGGGCUCAGCCCCGGUACCCUUGGCCCCUCUAUGGCAAUGAGGG CUGCGGGUGGGCGGGAUGGCUCUGUCUCCCCGUGGCUCUCGGCCUAGCU GGGGCCCCACAGACCCCCGGCGUAGGUCGCGCAAUUUGGGUAAGGUAUC GAUACCCUUACGUGCGGCUUCGCCGACCUC AUGGGGUACAUAACCGCUCGU CGGCGCCCCUCUUGGAGGCGUGCCAGGGCCUGGCGCAUGGCGUCCGGG UUCUGGAAGACGGCGUAACUAUGCAACAGGGAACCUUCCUGGUUGCUCU UUCUCUAUCUCCGAAUUCGAUAUCA
64	HCV 2b Transcript MW = 321,358 g/mol, 998 b	GGGCGAAUUGGGUACCGGGCCCCCCCCUCGAGGUCGACGGUAUCGAUAAGC UUGAUUAUCGAAUUCUGCAGCCCCGGGGAUCCACUAGUAACGGCCGCCAG UGUGCUGGAAUUCGCCC UUUCACUCCCCUGUGAGGAACUACUGUCUUCAC GCAGAAAGCGUCUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAG GCCCCCCCCUCCCGGGAGAGCCAUAGUGGUCUGCGGAACCGGUGAGUACA CCGGAAUUGCCGGAAAGACUGGGUCCUUUCUUGGAUAAAACCCACUCUAUG UCCGGUCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCUAGUAGCGUUGG GUUGCGAACCGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC GGGAGGUCUCGUAGACCGUGCAUCAUGAGCACAAAUUCUAAACCUCAAAG AAAAACCAAAGAAACACAAACCGCCGCCACAGGACGUAAGUUCGCCG GUGGCGGCCAGAU CGUUGGCGGAGUUUACUUGCUGCCGCGCAGGGGCCCC AGGUUGGGUGUGCGCGGACAAGGAAGACUUCUGAGCGAUCCAGCCGCG UGGGAGACGCCAGCCAUCCCGAAAGAU CGGCGCUCACCGGCAAGUCCU GGGGAAGCCAGGAUAUCCUUGGCCUCUGUAUGGAAACGAGGGCUGUGGC UGGGCAGGUUGGCUCCUGUCCCCCGCGGGUCUCGUCCUACUUGGGGCCC CACUGACCCCCGGCAUAGAUACGCAAUCUGGGCAGAGUCAUCGAUACCA UUACGUGUGGUUUUGCCGACCUC AUGGGGUACAUCUCCUGUCGUUGGCGCC CCAGUCGGAGGCGUCGCCAGAGCUUUGGCACACGGUGUUAGGGUCCUGGA AGACGGGAUAAAUAUGCAACAGGGAACCUACCUGGUUGCUCUUUUUCUA UCUUUUUGCUUGCUAAGGGCGAAUUCUGCAGAUAUCCAUCACACUGGC
65	pBluescript II SK (+) HCV 3a V1 MW = 277,725 g/mol ; 861 b	GGGCGAAUUGGGUACCGGGCCCCCCCCUCGAGGUCGACGGUAUCGAUAAGC UUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGCCUAGCCAUGGCGUUAG UACGAGUGUCGUGCAGCCUCCAGGCCCCCCCCUCCCGGGAGAGCCAUAGU GGUCUGCGGAACCGGUGAGUACACCGGAAUCGUGGGGUGACCGGGUCCU UUCUUGGAGCAACCCGCUCAAUACCCAGAAAUUUGGGCGUGCCCCCGCA GAUCACUAGCCGAGUAGUGCUGUGUCGCGAAAGGCCUUGUGGUACUGCCU GAUAGGGUGCUUGCGAGUGCCCCGGGAGGUCUCGUAGACCAUGCAACAUG AGCACACUUCUAAACCUCAAAGAAAAACCAAAGAAACACCAUCCGUCG CCCACAGGACGUUAAGUUCGCGGGCGGGACAGAU CGUUGGUGGAGUAU

		ACGUGUUGCCGCGCAGGGGCCACGAUUGGAUGUGCGCGCGACGCGUAAA ACUUCUGAACGGUCGCGAGCCUCGCGGACGACGACAGCCUAUCCCCAAGGC ACGUCGGAGUGAAGGCCGGUCCUGGGGUCAGCCCCGGGUACCCUUGGCCCC UCUAUGGUAAACGAGGGCUGCGGGUGGGCAGGAUGGCUCUGUCCCCACGU GGCUCGCCGUCCAUCUUGGGGCCCAAACGACCCCCGGCGACGGUCCACAA CUUGGGUAAAGUCAUCGAUACCCUACGUACGGAUUCGCCGACCUCUAUGG GGUACAUCCCCGUCGUCGGCGCUCGCCGUAGGAGGCGUCGCAAGAGCCCUC GCACAUGGCGUGAGGGCCCUUGAGGACGGGAUAAAUUUCGCAACAGGGAA CUUGCGGAAUU
66	pBluescript II SK (+) HCV 3a V2 : MW = 113,268 g/mol; 351 b	AUUGGGUACCGGGCCCCCUCGAGGUCGACGGUAUCGAUAAGCUUGUGA GGAACUUCUGUCUUCACGCGGAAAGCGCCUAGCCAUGGCGUAGUACGAG UGUCGUGCAGCCUCCAGGCCCCCCCCUCCGGGAGAGCCAUAUGGGUCUG CGGAACCGGUGAGUACACCGGAUUCGUGGGGUGACCGGGUCCUUUCUUG GAGCAACCCGCUCAAUACCCAGAAAUUUGGGCGUGCCCCCGCGAGAUAC UAGCCGAGUAGUGCUGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGG GUGCUUGCGAGUGCCCCGGGAGGUCUCGUAGACCAUGCAGGAAUU
67	pBluescript II SK (+) HCV 3a V3 : MW = 104,770 g/mol; 325 b	GGGCGAAUUGGGUACCUACUCCCCUGUGAGGAACUUCUGUCUUCACGCG GAAAGCGCCUAGCCAUGGCGUAGUACGAGUGUCGUGCAGCCUCCAGGCC CCCCCUCGCGGGAGAGCCAUAUGGGUCUGCGGAACCGGUGAGUACACCG GAAUCGCGUGGGGUGACCGGGUCCUUUCUUGGAGCAACCCGCUCAAUACCC AGAAAUUUGGGCGUGCCCCCGCGAGAUACUAGCCGAGUAGUGCUGUGUC GCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCCGGG AGGUCUCGUAGACCGUGCAGGAAUU
68	TOPO HCV 3b : MW = 135,874 g/mol, 422 b	GAAUACUCAAGCUAUGCAUCAAGCUUGGUACCGAGCUCGGAUCCACUAGU AACGGCCGCCAGUGUGCUGGAAUUCGCCC UUACUCCCCUGUGAGGAAC UACUGUCUUCACGCGGAAAGCGUCUAGCCAUGGCGUUAUAGAGUGUCG UGCAGCCUCCAGGCCCCCCCUCGCGGAGAGCCAUAUGGGUCUGCGGAA CCGGUGAGUACACCGGAAUCGCCGGGAUGACCGGGUCCUUUCUUGGAACA ACCCGCUCAAUGCCUGGAAAUUUGGGCGUGCCCCCGCGAGAUACUAGCC GAGUAGUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCU UGCGAGUGCCCCGGGAGGUCUCGUAGACCGUGCAAAGGGCGAAUUCUGCA GAUAUCCAUCACACUGGCGGCC
69	pBluescript II SK (+) HCV 3b : MW = 104,810 g/mol, 325 b	GGGCGAAUUGGGUACCUACUCCCCUGUGAGGAACUUCUGUCUUCACGCG GAAAGCGUCUAGCCAUGGCGUAGUACGAGUGUCGUGCAGCCUCCAGGCC CCCCCUCGCGGGAGAGCCAUAUGGGUCUGCGGAACCGGUGAGUACACCG GAAUCGCCGGGAUGACCGGGUCCUUUCUUGGAACAACCCGCUCAAUGCCU GGAAAUUUGGGCGUGCCCCCGCGAGAUACUAGCCGAGUAGUGUUGGGUC GCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCCGGG AGGUCUCGUAGACCGUGCAGGAAUU
70	TOPO HCV 4h: MW = 135,878 g/mol, 422 b	GAAUACUCAAGCUAUGCAUCAAGCUUGGUACCGAGCUCGGAUCCACUAGU AACGGCCGCCAGUGUGCUGGAAUUCGCCC UUACUCCCCUGUGAGGAAC UACUGUCUUCACGCGAGAAAGCGUCUAGCCAUGGCGUUAUAGAGUGUUG UGCAGCCUCCAGGAUCCCCCUCGCGGAGAGCCAUAUGGGUCUGCGGAA CCGGUGAGUACACCGGAAUCGCCGGGAUGACCGGGUCCUUUCUUGGAUUA ACCCGCUCAAUGCCCGGAAAUUUGGGCGUGCCCCCGCGAGACUGCUAGCC GAGUAGUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCU UGCGAGUGCCCCGGGAGGUCUCGUAGACCGUGCAAAGGGCGAAUUCUGCA GAUAUCCAUCACACUGGCGGCC
71	pBluescript II SK (+) HCV 4h :	GGGCGAAUUGGGUACCUACUCCCCUGUGAGGAACUACUGUCUUCACGCA GAAAGCGUCUAGCCAUGGCGUAGUAUGAGUGUUGUGCAGCCUCCAGGAU CCCCCUCGCGGGAGAGCCAUAUGGGUCUGCGGAACCGGUGAGUACACCG

	MW = 104,811 g/mol, 325 b	GAAUCGCCGGGAUGACCGGGUCCUUUCUUGGAUUAACCCGCUCAAUGCCC GGAAAUUUGGGCGUGCCCCCGCGAGACUGCUAGCCGAGUAGUGUUGGGUC GCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUUGCGAGUGCCCCGGG AGGUCUCGUAGACCGUGCAGGAAUU
72	TOPO HCV 5a : MW = 140,284 g/mol, 435 b	GGGCGAAUUGGGCCCUCUAGAUGCAUGCUCGAGCGGCCGCCAGUGUGAUG GAUAUCUGCAGAAUUCGCCCCUUCACUCCCCUGUGAGGAACUACUGUCUU CACGCAGAAAGCGUCUAGCCAUGGCGUUAGUAUGAGUGUCGAACAGCCUC CAGGACCCCCCUCGCGGAGAGCCAUAGUGGUCUGCGGAACCGGUGAGU ACACCGGAAUUGCCGGGACGACCGGGUCCUUUCUUGGAUAAACCCGCUCA AUGCCCGGAGAUUUGGGCGUGCCCCCGCGAGACUGCUAGCCGAGUAGUGU UGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGC CCCGGGAGGUCUCGUAGACCGUGCAAAGGGCGAAUUCAGCACACUGGCG GCCGUUACUAGUGGAUCCGAGCUCGGUACCAAGCU
73	pBluescript II SK (+) HCV-6a : MW = 105,744 g/mol, 328 b	GGGCGAAUUGGGUACCUCACUCCCCUGUGAGGAACUACUGUCUUCACGCA GAAAGCGUCUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCC CCCCCUCGCGGAGAGCCAUAGUGGUCUGCGGAACCGGUGAGUACACCG GAAUUGCCAGGAUGACCGGGUCCUUUCCAUGGAUCAAAACCCGCUCAAUG CCUGGAGAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGAGUAGCGUUGG GUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUUGCGAGUGCCCC GGGAGGUCUCGUAGACCGUGCAGGAAUU
74	pBluescript II SK (+) HCV-5a: MW = 104,881 g/mol, 325 b	GGGCGAAUUGGGUACCUCACUCCCCUGUGAGGAACUACUGUCUUCACGCA GAAAGCGUCUAGCCAUGGCGUUAGUAUGAGUGUCGAACAGCCUCCAGGAC CCCCCUCGCGGAGAGCCAUAGUGGUCUGCGGAACCGGUGAGUACACCG GAAUUGCCGGGACGACCGGGUCCUUUCUUGGAUAAACCCGCUCAAUGCCC GGAGAUUUGGGCGUGCCCCCGCGAGACUGCUAGCCGAGUAGUGUUGGGUC GCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUUGCGAGUGCCCCGGG AGGUCUCGUAGACCGUGCAGGAAUU
75	HCV-1a mRNA genome sequence (GenBank Accession No. M62321)	gccagccccc tgatgggggc gacactccac catgaatcac tcccctgtga ggaactactg tcttcacgca gaaagcgtct agccatggcg ttagtatgag tgcgtgcag cctccaggac ccccctccc gggagagcca tagtggtctg cggaaccggt gagtacaccg gaattgccag gacgaccggg tcccttcttg gatcaacccg ctcaatgcct ggagatttgg gcgtgcccc gcaagactgc tagccgagta gtgttggtc gcgaaaggcc ttgtggtact gctgatagg gtgcttgcca gtgccccggg aggtctcgta gaccgtgcac catgagcacg aatcctaacc ctcaaaaaaa aaacaaacgt aacaccaacc gtcgccacac ggacgtcaag ttcccgggtg

Note: additional sequences numbered higher than SEQ ID NO: 75 appear above, in the specification.

What is claimed is:

1. A composition or kit comprising at least first and second amplification oligomers, wherein:
the first amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 2, including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 2; and
the second amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 3 including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 3; and
the target-hybridizing sequences of the first and second amplification oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

2. The composition or kit of claim 1, further comprising a third amplification oligomer, wherein the third amplification oligomer comprises at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence and is configured to specifically hybridize downstream of HCV genomic position 78.

3. A method of detecting Hepatitis C virus nucleic acid in a sample, comprising:
contacting the sample with at least first, second, and third amplification oligomers, thereby forming a composition,
performing a nucleic acid amplification reaction in the composition which produces one or more amplicons in the presence of a Hepatitis C virus nucleic acid,
and detecting the amplicon,

wherein:
the first amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 2, including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 2;
the second amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 3 including at least one of positions 5, 7, 12, and 15 of SEQ ID NO: 3;
the third amplification oligomer comprises at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence and is configured to specifically hybridize to downstream of HCV genomic position 78;
the target-hybridizing sequences of the first and second amplification oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence; and
the one or more amplicons are produced through extension of the first and third amplification oligomers or second and third amplification oligomers in the presence of the Hepatitis C virus nucleic acid.

4. A composition or kit comprising at least first and second capture oligomers, wherein:
the first capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 54; and
the second capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 55; and
the target-hybridizing sequences of the first and second capture oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

5. A method of isolating Hepatitis C virus nucleic acid from a sample, comprising:
contacting the sample with at least first and second capture oligomers under conditions permissive for annealing of the first and second capture oligomers to the Hepatitis C virus nucleic acid, thereby forming at least one complex of Hepatitis C virus nucleic acid and a capture oligomer; and
isolating the at least one complex, thereby providing a composition comprising the complex;
wherein:
the first capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 54; and
the second capture oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 55; and
the target-hybridizing sequences of the first and second capture oligomers each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

6. The kit, composition, or method of any one of the preceding claims, wherein the composition or kit further comprises an initial amplification oligomer comprising at least 10 contiguous nucleotides of SEQ ID NO: 6.

7. The kit, composition, or method of any one of the preceding claims, wherein the composition or kit further comprises a probe oligomer comprising at least 10 contiguous nucleotides of SEQ ID NO: 13 and at least about 14 contiguous nucleotides of Hepatitis C virus sequence.

8. The kit, composition, or method of claim 7, wherein the initial amplification oligomer and probe oligomer anneal to at least one common position in an HCV nucleic acid.

9. A kit or composition comprising an initial amplification oligomer and a probe oligomer, wherein:
the initial amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 6;
the probe oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 13;
the initial amplification oligomer and probe oligomer each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence; and
the initial amplification oligomer and probe oligomer anneal to at least one common position in an HCV nucleic acid.

10. The kit or composition of claim 4 or 7, or the method of claim 5, wherein the kit or composition further comprises at least 1, 2, or 3 of:
a first amplification oligomer comprising a target-hybridizing sequence comprising at least about 14 contiguous nucleotides of Hepatitis C virus sequence that is configured to specifically hybridize upstream of HCV genomic position 81;
a second amplification oligomer different from the first amplification oligomer comprising at least about 14 contiguous nucleotides of Hepatitis C virus sequence that is configured to specifically hybridize upstream of HCV genomic position 81; and
a third amplification oligomer different from the initial amplification oligomer comprising at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence that is configured to specifically hybridize downstream of HCV genomic position 90.

11. The kit, composition, or method of any one of claims 1 to 3 or 6 to 10, wherein the kit or composition further comprises one or more capture oligomers comprising at least about 14 contiguous nucleotides of antisense Hepatitis C virus sequence.

12. A method of detecting Hepatitis C virus nucleic acid in a sample, comprising:
contacting the sample with one or more capture oligomers and an initial amplification oligomer, thereby associating at least one capture oligomer and amplification oligomer with HCV nucleic acid if present;
removing initial amplification oligomer not associated with the HCV nucleic acid;
performing an extension reaction that extends initial amplification oligomer associated with HCV nucleic acid if present;
performing an amplification reaction with the extended initial amplification oligomer as template if present, thereby producing an amplicon; and
detecting the presence or absence of the amplicon using a probe oligomer;
wherein the initial amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 6;
the probe oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 13 and is configured to specifically hybridize to the amplicon if present;
the initial amplification oligomer and probe oligomer each comprise at least about 14 contiguous nucleotides of Hepatitis C virus sequence; and
the initial amplification oligomer and probe oligomer anneal to at least one common position in an HCV nucleic acid.

13. The method of claim 12, wherein performing the amplification reaction comprises:
adding (i) at least one of first and second amplification oligomers that anneal to the template or amplicon upstream of the probe oligomer and (ii) a third amplification oligomer that is configured to

specifically hybridize to the template or amplicon downstream of the probe oligomer;
and if the template is present, extending the first and second amplification oligomers.

14. The kit, composition, or method of any one of claims 9-11 or 13, wherein the first amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 2.

15. The kit, composition, or method of any one of claims 9-11 or 13-14, wherein the second amplification oligomer comprises at least 10 contiguous nucleotides of SEQ ID NO: 3.

16. The kit, composition, or method of any one of claims 2-15, wherein the third amplification oligomer does not anneal downstream of an HCV genomic position selected from position 120, 125, 130, 135, 140, 145, or 150 in at least one HCV type.

17. The kit, composition, or method of claim 16, wherein the at least one HCV type includes one or more of HCV types 1a, 1b, 2b, 3b, 4b, 5a, and 6a.

18. The kit, composition, or method of any one of claims 2-17, wherein the third amplification oligomer is configured to specifically hybridize to a site comprising at least one of HCV genomic positions 80-119.

19. The kit, composition, or method of claim 18, wherein the third amplification oligomer comprises a target-hybridizing sequence comprising at least 10 contiguous nucleotides of SEQ ID NO: 6 or 7.

20. The composition, kit, or method of claim 19, wherein the third amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, or four of SEQ ID NOs: 33-37.

21. The composition, kit, or method of claim 19 or 20, wherein the third amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31 contiguous nucleotides of SEQ ID NO: 7.

22. The composition, kit, or method of claim 21, wherein the third amplification oligomer comprises the sequence of SEQ ID NO: 7.

23. The composition, kit, or method of any one of claims 2-22, wherein the third amplification oligomer comprises the sequence of at least one, two, three, four, or five of SEQ ID NOs: 42-47.

24. The composition, kit, or method of claim 23, wherein the third amplification oligomer comprises the sequence of SEQ ID NO: 5.

25. The composition, kit, or method of any one of claims 1-3, 6-8, 10-11, or 13-24, wherein the first amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, or four of SEQ ID NOs: 23-27.

26. The composition, kit, or method of any one of claims 1-3, 6-8, 10-11, or 13-25, wherein the first amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or 26 contiguous nucleotides of SEQ ID NO: 2.

27. The composition, kit, or method of claim 26, wherein the first amplification oligomer comprises the sequence of SEQ ID NO: 2.

28. The composition, kit, or method of any one of claims 1-3, 6-8, 10-11, or 13-27, wherein the second amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, or four of SEQ ID NOs: 28-32.

29. The composition, kit, or method of any one of claims 1-3, 6-8, 10-11, or 13-28, wherein the second amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or 26 contiguous nucleotides of SEQ ID NO: 3.

30. The composition, kit, or method of claim 29, wherein the second amplification oligomer comprises the sequence of SEQ ID NO: 3.

31. The composition, kit, or method of any one of claims 1-3, 6-8, 10-11, or 13-30, wherein the first and second amplification oligomers are present in relative molar amounts (first:second) ranging from about 8.5:1.5 to about 1.5:8.5, about 7.5:2.5 to about 2.5:7.5, about 8:2 to about 7:3, about 7:3 to about 6:4, about 6:4 to about 5:5, about 5:5 to about 4:6, about 4:6 to about 3:7, or about 3:7 to about 2:8.

32. The composition, kit, or method of claim 31, wherein the first and second amplification oligomers are present in relative molar amounts (first:second) ranging from about 6:4 to about 1.5:8.5, about 4:6 to about 6:4, or about 4.5:5.5 to about 5.5:4.5.

33. The composition, kit, or method of any one of claims 4 or 7-32, wherein the initial amplification oligomer comprises a target-hybridizing sequence comprising at least one, two, three, four, five, six, or seven of SEQ ID NOs: 33-41.

34. The composition, kit, or method of any one of claims 4 or 7-33, wherein the initial amplification oligomer comprises at least 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, or 44 contiguous nucleotides of SEQ ID NO: 6.

35. The composition, kit, or method of claim 34, wherein the initial amplification oligomer comprises the sequence of SEQ ID NO: 6.

36. The composition, kit, or method of any one of claims 4 or 7-35, wherein the initial amplification oligomer comprises the sequence of at least one, two, three, four, or five of SEQ ID NOs: 42-47.

37. The composition, kit, or method of claim 36, wherein the initial amplification oligomer comprises the sequence of SEQ ID NO: 4.

38. The composition, kit, or method of any one of claims 7-37, wherein the probe oligomer comprises a target-hybridizing sequence comprising at least one or two of SEQ ID NOs: 50-52.

39. The composition, kit, or method of any one of claims 7-38, wherein the probe oligomer comprises the sequence of SEQ ID NO: 48 or 49.

40. The composition, kit, or method of any one of claims 7-39, wherein the probe oligomer comprises at least 11, 12, 13, 14, or 15 contiguous nucleotides of SEQ ID NO: 12.

41. The composition, kit, or method of claim 40, wherein the probe oligomer comprises a target-hybridizing sequence comprising at least 11, 12, 13, 14, or 15 contiguous nucleotides of SEQ ID NO: 13.

42. The composition, kit, or method of any one of claims 7-41, wherein the probe oligomer comprises a first self-complementary region at its 5' end and a second self-complementary region at its 3' end.

43. The composition, kit, or method of claim 42, wherein the self-complementary regions can hybridize to form about 4 to 7 Watson-Crick or wobble base pairs.

44. The composition, kit, or method of claim 43, wherein the self-complementary regions can hybridize to form about 5 Watson-Crick or wobble base pairs.

45. The composition, kit, or method of any one of claims 39-44, wherein the probe oligomer comprises the sequence of SEQ ID NO: 12.

46. The composition, kit, or method of claim 45, wherein the probe oligomer comprises a target-hybridizing sequence comprising the sequence of SEQ ID NO: 13.

47. The composition, kit, or method of any one of claims 7-46, wherein the probe oligomer comprises a non-nucleotide detectable label.

48. The composition, kit, or method of claim 47, wherein the non-nucleotide detectable label is a fluorescent label.

49. The composition, kit, or method of claim 47 or 48, wherein the probe oligomer comprises a quencher.

50. The composition, kit, or method of claim 49, wherein the non-nucleotide detectable label is a fluorescent label and the quencher absorbs fluorescence to a greater extent when the probe is free than when the probe is annealed to a target nucleic acid.

51. The composition, kit, or method of any one of claims 48-50, wherein the fluorescent label is FAM, HEX, or acridine.

52. The composition, kit, or method of any one of claims 49-51, wherein the quencher is DABCYL or ROX.

53. The composition, kit, or method of any one of claims 49-52, wherein the fluorescent label is attached to the 5'-terminus of the probe oligomer and the quencher is attached to the 3'-terminus of the probe oligomer, or the fluorescent label is attached to the 3'-terminus of the probe oligomer and the quencher is attached to the 5'-terminus of the probe oligomer.

54. The composition, kit, or method of any one of claims 7-53, wherein at least about half, at least about 90%, or all of the sugars in the probe oligomer are 2'-O-methyl-ribose.

55. The composition, kit, or method of any one of claims 4-5 or 11-54, wherein the capture oligomers include a first capture oligomer comprising a target-hybridizing sequence comprising at least 10, 11, 12, 13, 14, 15, 16, 17, or 18 contiguous nucleotides of SEQ ID NO: 54.

56. The composition, kit, or method of claim 55, wherein the target-hybridizing sequence of the first capture oligomer comprises at least one or two of SEQ ID NOs: 57-59.

57. The composition, kit, or method of claim 56, wherein the first capture oligomer comprises the sequence of SEQ ID NO: 54.

58. The composition, kit, or method of any one of claims 4-5 or 11-57, wherein the capture oligomers include a second capture oligomer comprising a target-hybridizing sequence comprising at least 10, 11, 12, 13, 14, 15, 16, or 17 contiguous nucleotides of SEQ ID NO: 55.

59. The composition, kit, or method of claim 58, wherein the target-hybridizing sequence of the second capture oligomer comprises at least one or two of SEQ ID NOs: 60-62.

60. The composition, kit, or method of claim 59, wherein the second capture oligomer comprises the sequence of SEQ ID NO: 55.

61. The composition, kit, or method of any one of claims 4-5 or 11-60, wherein at least one of the capture oligomers further comprises a non-nucleotide affinity label.

62. The composition, kit, or method of any one of claims 4-5 or 11-61, wherein at least one of the capture oligomers further comprises a non-HCV sequence.

63. The composition, kit, or method of claim 60, wherein the first and second capture oligomers further comprise a non-HCV sequence.

64. The composition, kit, or method of claim 62 or 63, wherein at least one or two capture oligomers further comprise a poly-N sequence.

65. The composition, kit, or method of claim 64, wherein the poly-N sequence is a poly-A or poly-T sequence.
66. The composition, kit, or method of claim 65, wherein at least one or two capture oligomers comprise the sequence of SEQ ID NO: 21 or SEQ ID NO: 22.
67. The composition, kit, or method of claim 66, wherein the first capture oligomer comprises the sequence of SEQ ID NO: 16.
68. The composition, kit, or method of claim 66 or 67, wherein the second capture oligomer comprises the sequence of SEQ ID NO: 17.
69. The composition, kit, or method of any one of the preceding claims, wherein the kit or composition comprises at least one amplification oligomer that is a promoter-primer.
70. The composition, kit, or method of any one of claims 2-3, 6-8, 10-11, or 13-69, wherein the third amplification oligomer is a promoter-primer.
71. The composition, kit, or method of any one of claims 69-70, wherein one or more of the promoter-primers comprises a T7 promoter located 5' of the target-hybridizing sequence.
72. The composition, kit, or method of claim 71, wherein one or more promoter-primers comprises the sequence of SEQ ID NO: 8, 9, 10, or 11.
73. The composition, kit, or method of any one of claims 1-3 or 6-72, wherein at least one amplification oligomer comprises a non-nucleotide detectable label.
74. The composition, kit, or method of any one of claims 4 or 6-73, wherein the initial amplification and probe oligomers each anneal to at least 1, 2, 3, 4, 5, 6, 7, 8, or 9 of positions 86-95 in an HCV genome or the complement thereof.
75. The composition or method of any one of the preceding claims, wherein the composition further comprises HCV nucleic acid.
76. The composition, kit, or method of any one of the preceding claims, wherein the composition or kit further comprises at least one DNA polymerase.
77. The composition, kit, or method of claim 76, wherein the DNA polymerase is a reverse transcriptase.
78. The composition, kit, or method of claim 76 or 77, wherein the DNA polymerase is thermophilic.
79. The composition, kit, or method of claim 76 or 77, wherein the DNA polymerase is mesophilic.

80. The composition, kit, or method of any one of the preceding claims, wherein the composition or kit further comprises an RNA polymerase.

81. The composition, kit, or method of claim 80, wherein the RNA polymerase is T7 RNA polymerase.

82. The composition, kit, or method of any one of the preceding claims, wherein the composition or kit further comprises at least one, at least two, or each of Mg²⁺, a buffer, and dNTPs.

83. The composition, kit, or method of any one of the preceding claims, wherein the composition or kit further comprises rNTPs.

84. The composition, kit, or method of any one of the preceding claims, wherein the composition or kit further comprises a first control amplification oligomer and a second control amplification oligomer that do not hybridize specifically to HCV.

85. The composition, kit, or method of claim 84, wherein the first control amplification oligomer comprises at least 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19 contiguous nucleotides of the sequence of SEQ ID NO: 18.

86. The composition, kit, or method of claim 84 or 85, wherein the second control amplification oligomer comprises at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or 22 contiguous nucleotides of the sequence of SEQ ID NO: 56.

87. The composition, kit, or method of any one of claims 84 to 86, wherein the first control amplification oligomer or the second control amplification oligomer is a promoter-primer.

88. The composition, kit, or method of any one of claims 84 to 87, wherein the composition or kit further comprises at least one control probe oligomer capable of hybridizing specifically to an amplicon produced from the first and second control amplification oligomers.

89. The composition, kit, or method of claim 88, wherein the control probe oligomer comprises at least 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23 contiguous nucleotides of the sequence of SEQ ID NO: 20.

90. The method, composition, or oligomer of any one of the preceding claims, wherein one, two, three, or more target-hybridizing sequences comprise at least about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides of Hepatitis C virus sequence.

91. The method of any one of claims 12-90, further comprising performing a linear amplification wherein at least one amplification oligomer is extended.

92. The method of claim 91, wherein prior to the linear amplification, the amplification oligomer is associated with a complex of HCV nucleic acid and a capture oligomer and the complex is associated with a solid support, and the method comprises washing the solid support.

93. The method of claim 92, wherein the solid support is a population of microbeads.
94. The method of claim 93, wherein the microbeads of the population are magnetic.
95. The method of any one of claims 91-93, wherein following the washing step, the method comprises adding one or more additional amplification oligomers oppositely oriented to an amplification oligomer associated with the complex of HCV nucleic acid and the capture oligomer.
96. The method of claim 95, wherein one or more oppositely oriented additional amplification oligomer is a promoter-primer.
97. The method of claim 96, wherein one or more oppositely oriented additional amplification oligomer is not a promoter-primer.
98. The method of claim 97, wherein the one or more oppositely oriented additional amplification oligomer includes a first amplification oligomer as recited in any one of claims 1, 10, 13, 14, or 25-27.
99. The method of claim 97 or 98, wherein the one or more oppositely oriented additional amplification oligomer includes a second amplification oligomer as recited in any one of claims 1, 10, 13, 15, or 28-30.
100. The method of any one of claims 90-99, further comprising performing an exponential amplification following the linear amplification.
101. The method of claim 100, wherein the exponential amplification comprises extending a third amplification oligomer as recited in any one of claims 2, 10, 13, 16, or 18-24.
102. The method of claim 100 or 101, wherein the exponential amplification is isothermal amplification.
103. The method of claim 102, wherein the isothermal amplification is transcription-mediated amplification.
104. The method of any one of claims 3, 6-8, or 11-103, further comprising quantifying at least one amplicon produced by the method.
105. The method of claim 104, wherein the amplicon is quantified in real time.
106. An initial amplification oligomer comprising a promoter and a 3'-terminal target-hybridizing sequence, wherein the target-hybridizing sequence comprises at least 10 contiguous nucleotides of SEQ ID NO: 6 and at least about 14 contiguous nucleotides of Hepatitis C virus sequence.
107. The initial amplification oligomer of claim 106, which is an initial amplification oligomer as recited in any one of claims 33-37.

108. The initial amplification oligomer of claim 107, comprising a T7 promoter.
109. The initial amplification oligomer of claim 107, comprising the sequence of SEQ ID NO: 8, 9, 10, or 11.
110. The initial amplification oligomer of any one of claims 106-109, which is configured to specifically hybridize to positions comprising at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 of HCV genomic positions 81-92.
111. The initial amplification oligomer of claim 110, which is configured to specifically hybridize to positions comprising at least 1, 2, 3, 4, 5, 6, 7, 8, or 9 of HCV genomic positions 81-89.
112. A probe oligomer comprising at least 10 contiguous nucleotides of SEQ ID NO: 13 and at least about 14 contiguous nucleotides of Hepatitis C virus sequence.
113. The probe oligomer of claim 112, which is a probe oligomer as recited in any one of claims 38-54.
114. The probe oligomer of claim 112 or 113, which is configured to specifically hybridize to positions comprising at least 6, 7, 8, 9, 10, 11, or 12 of HCV genomic positions 81-92.
115. The probe oligomer of any one of claims 112-114, which is configured to specifically hybridize to positions comprising at least 11, 12, 13, 14, 15, or 16 of HCV genomic positions 81-96.
116. A kit according to any one of claims 1-2, 4, 6-9, or 14-90.
117. A composition according to any one of claims 1-2, 4, 6-9, or 14-90.
118. The composition of claim 117, which is aqueous, frozen, or lyophilized.
119. The composition of claim 117 or 118, further comprising an extension product of an initial amplification oligomer, the extension product comprising a sequence of an initial amplification oligomer recited in any one of claims 106-111 and at least 1, 2, 3, 4, 5, 10, 15, or 20 additional 3'-terminal nucleotides of Hepatitis C nucleic acid sequence.

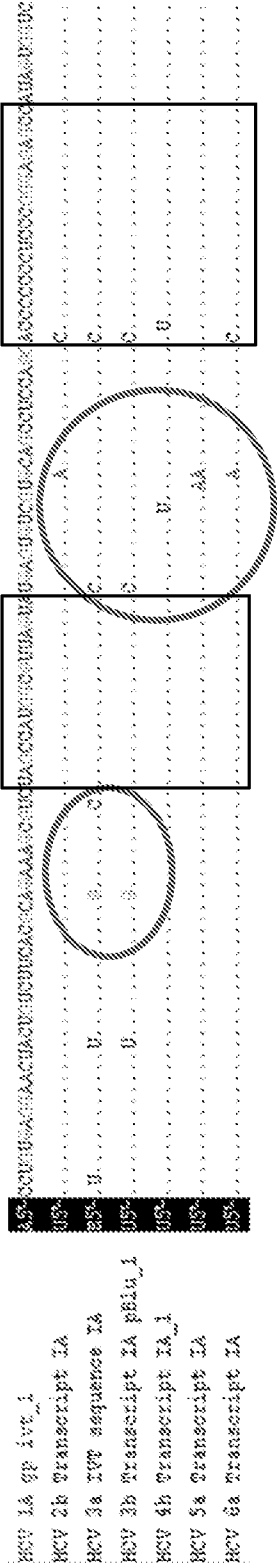


Fig. 1

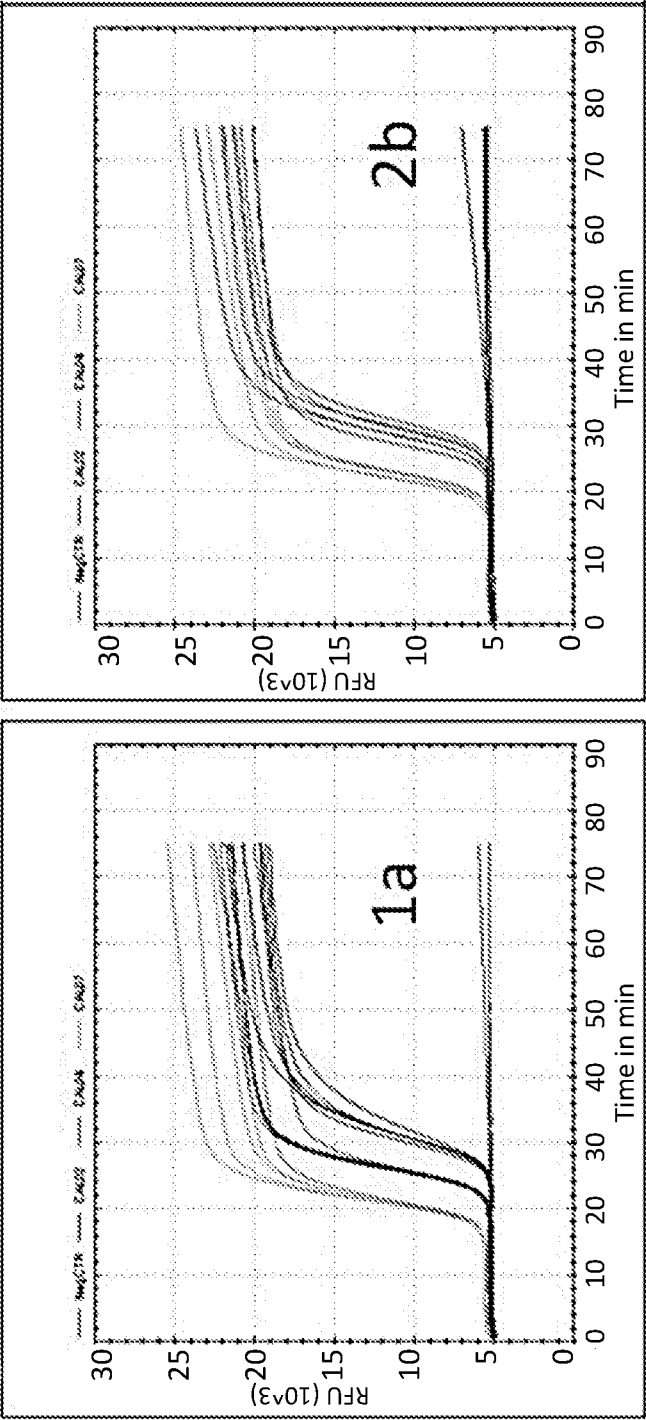


Fig. 2-1

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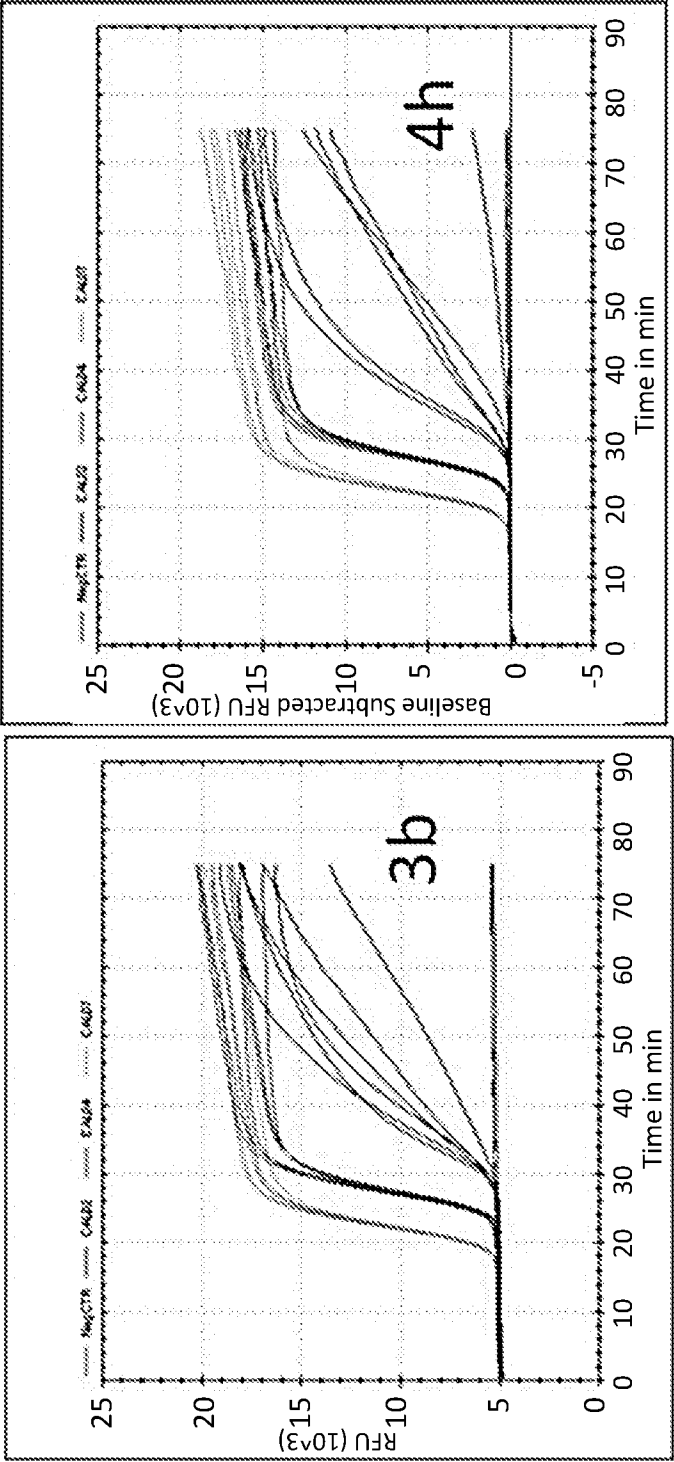


Fig. 2-2

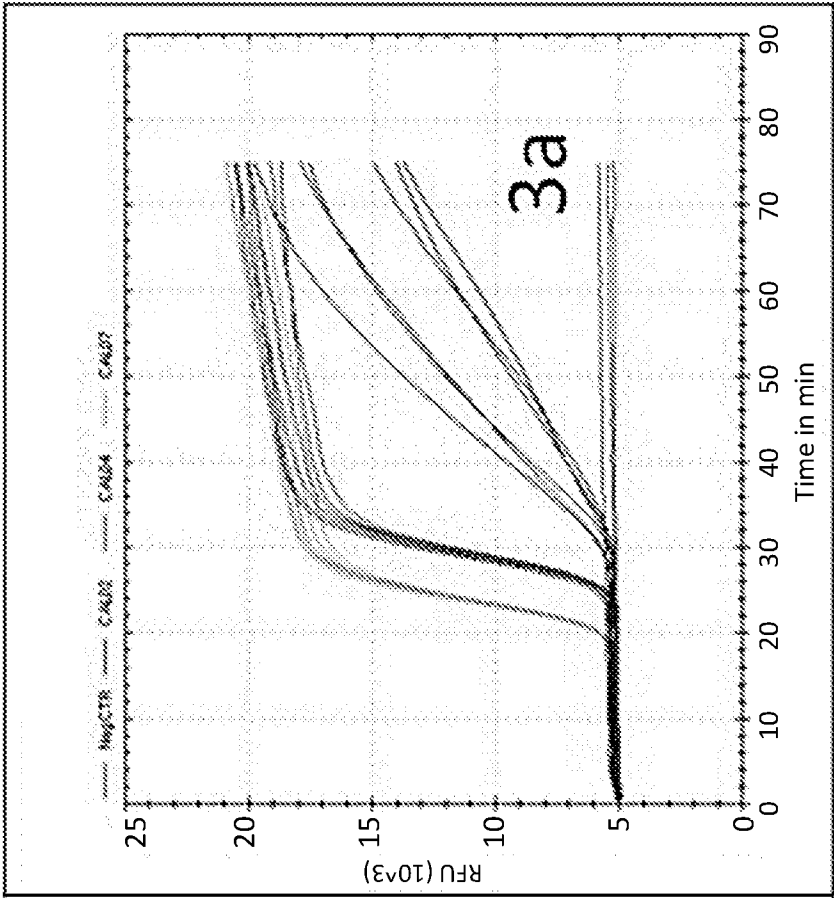


Fig. 2-3

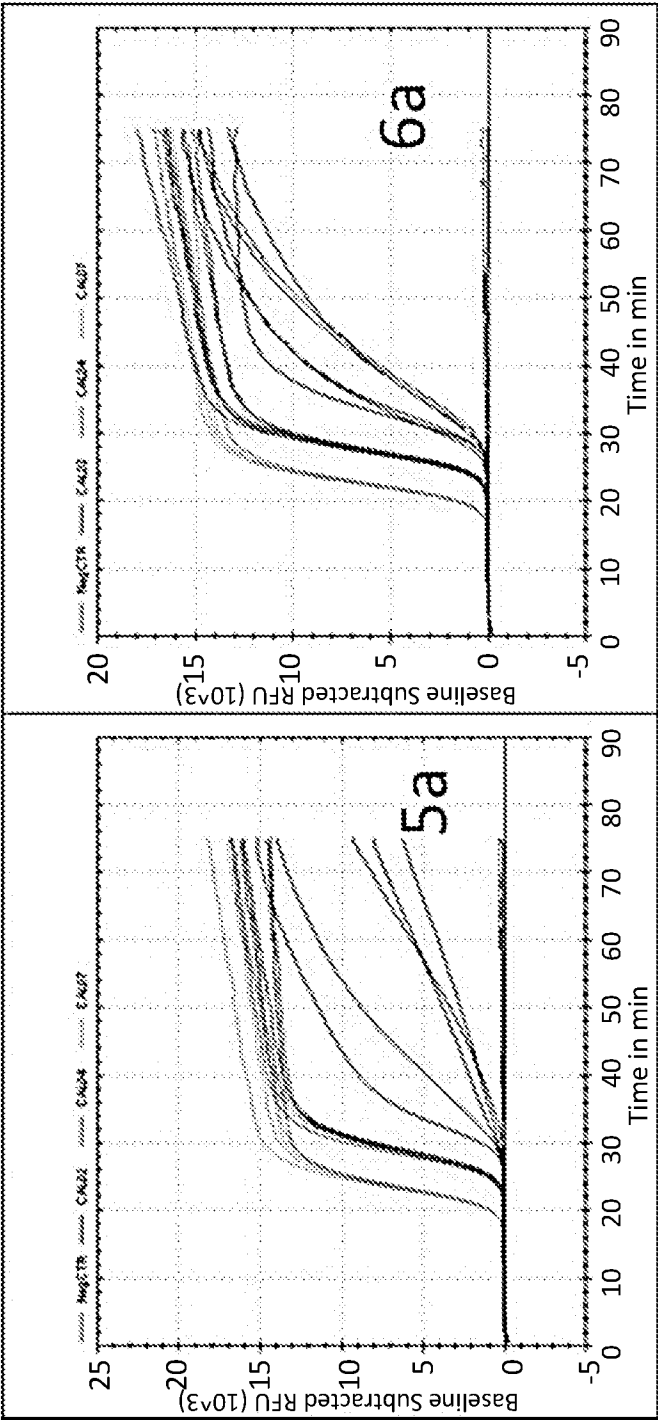


Fig. 2-4

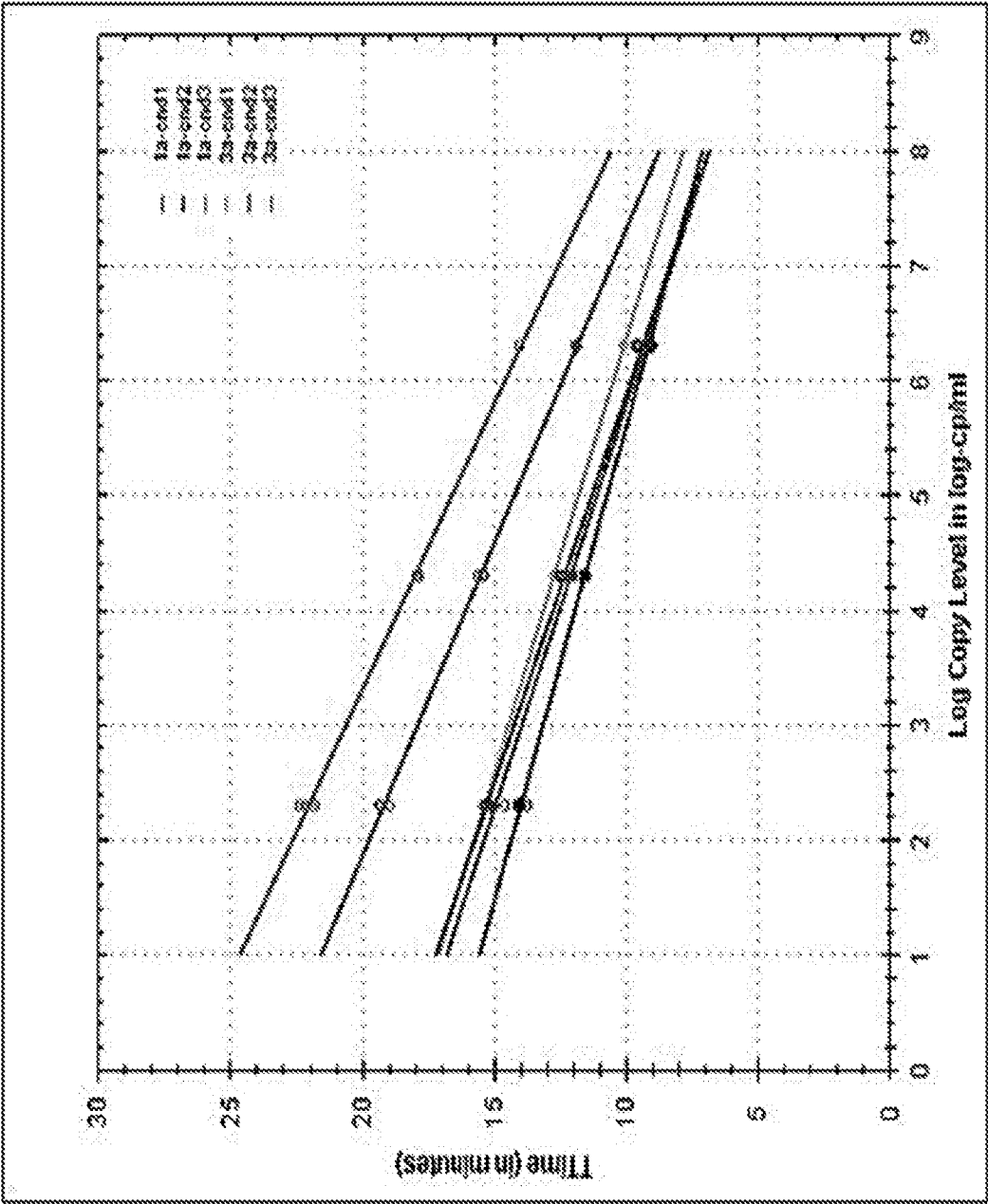


Fig. 3

3a Match NT7 52-78tg

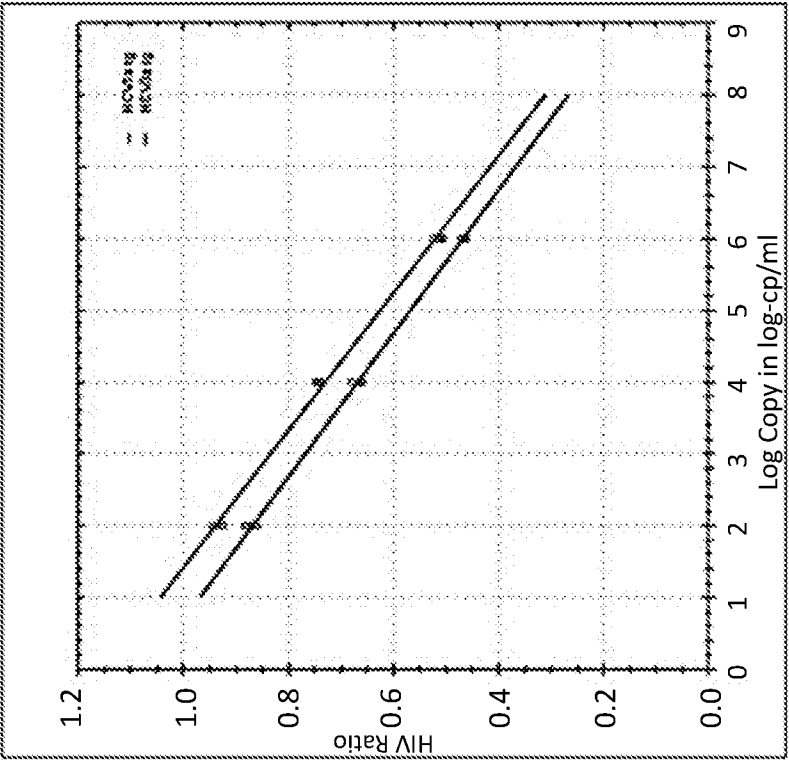


Fig. 4B

1a Match NT7 52-78

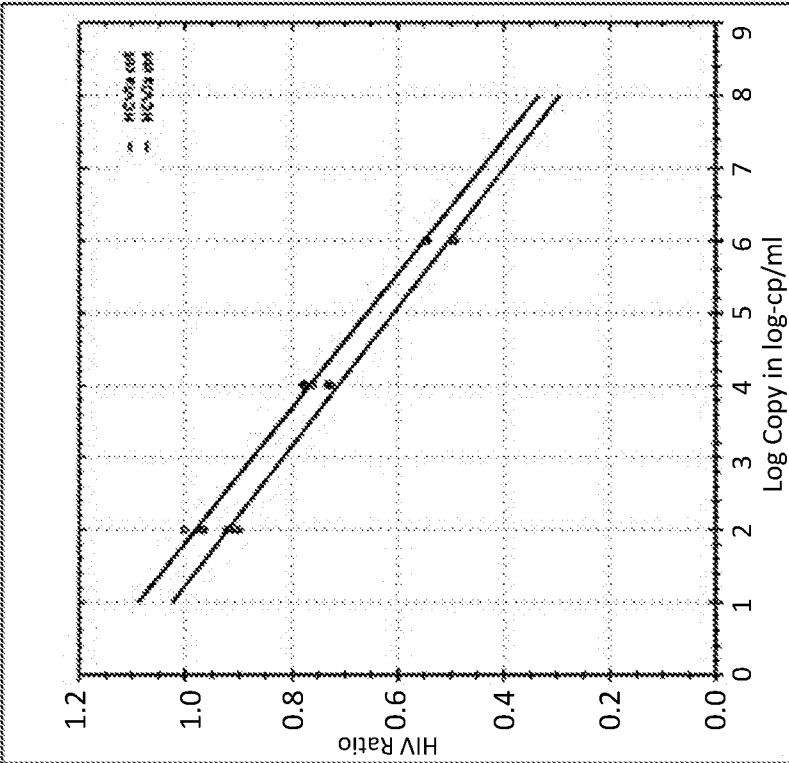


Fig. 4A

1a Match NT7 52-78 &
3a Match NT7 52-78tg

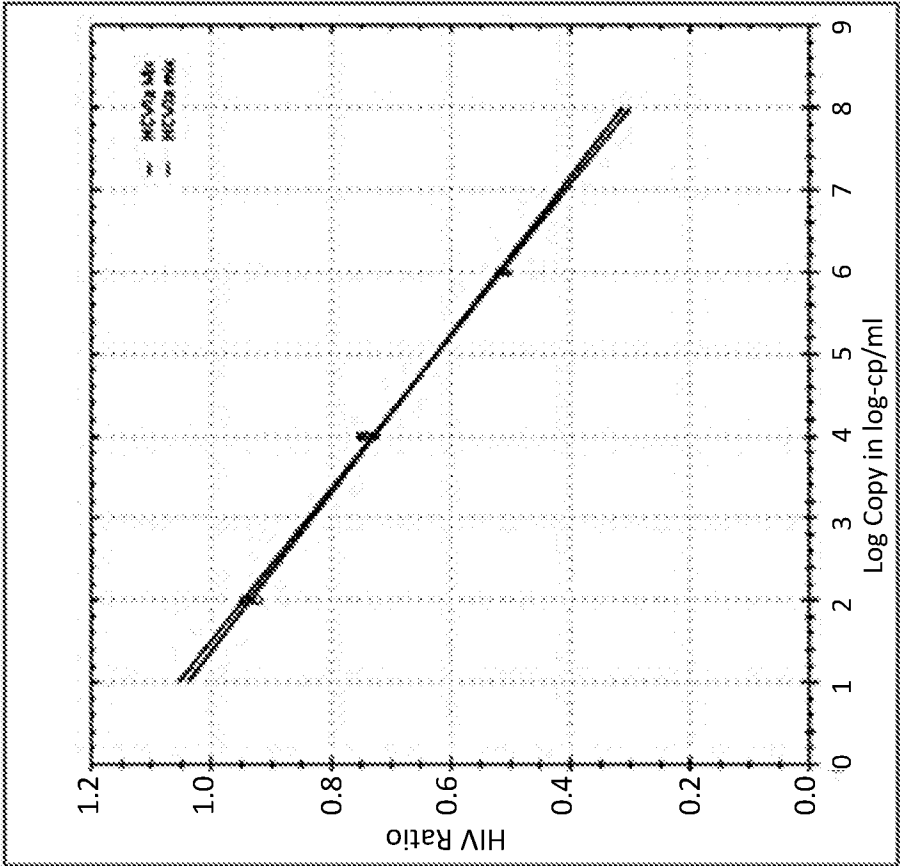


Fig. 4C

HCV nonT7 52-78 t
Only

HCV nonT7 52-78 tg
Only

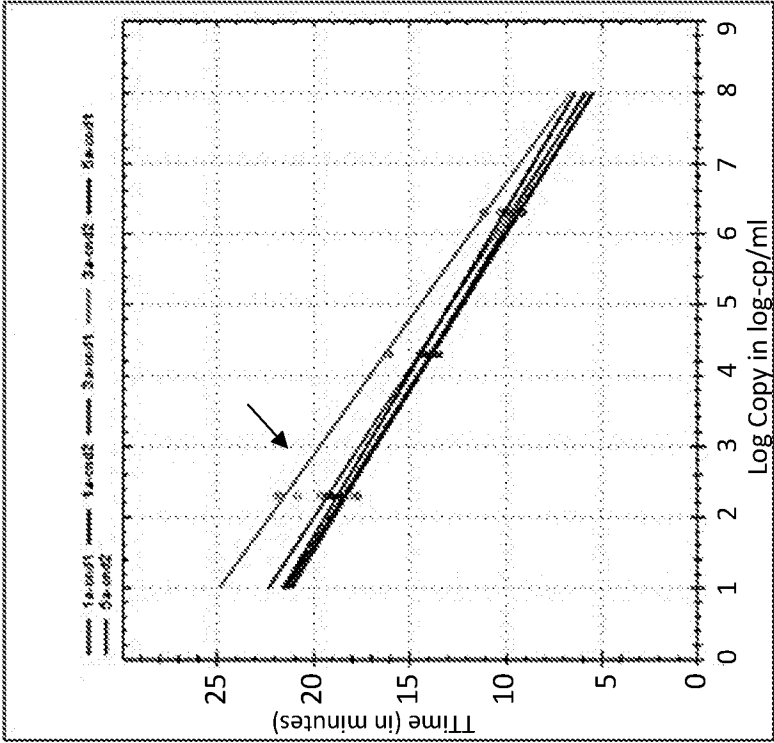


Fig. 5A

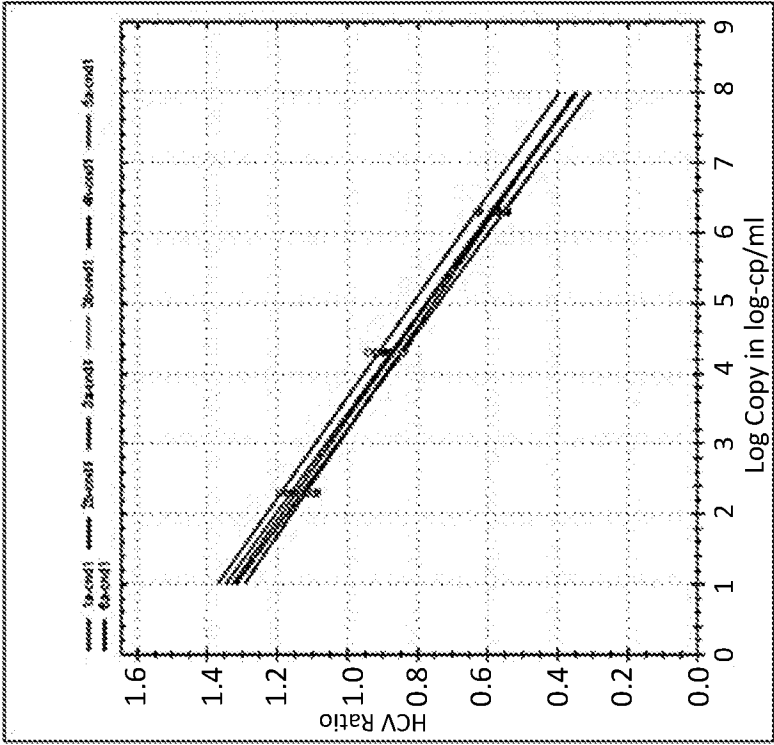


Fig. 5B

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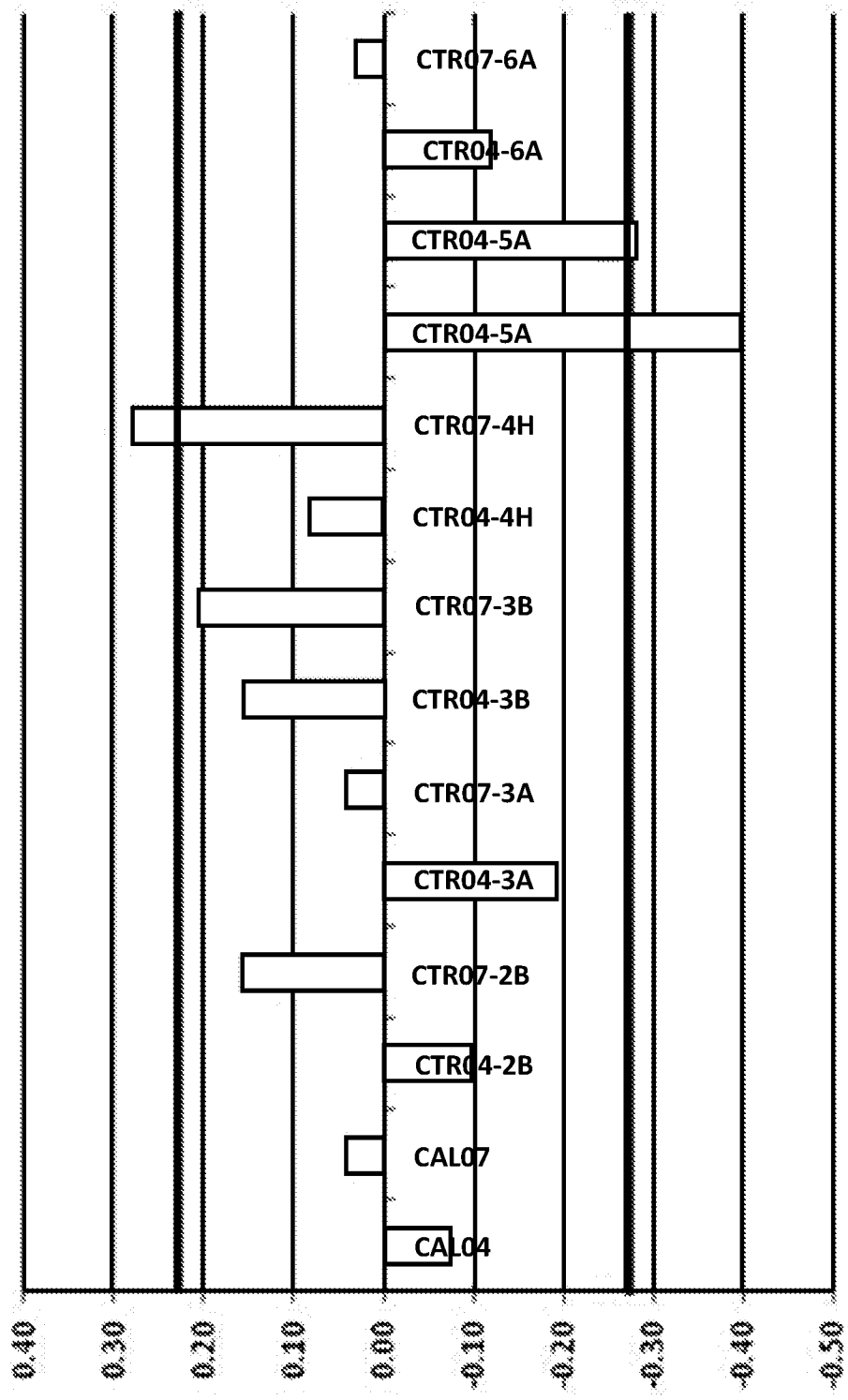


Fig. 6

HCV Torch
68-86 (+)
Two 3a Mismatches

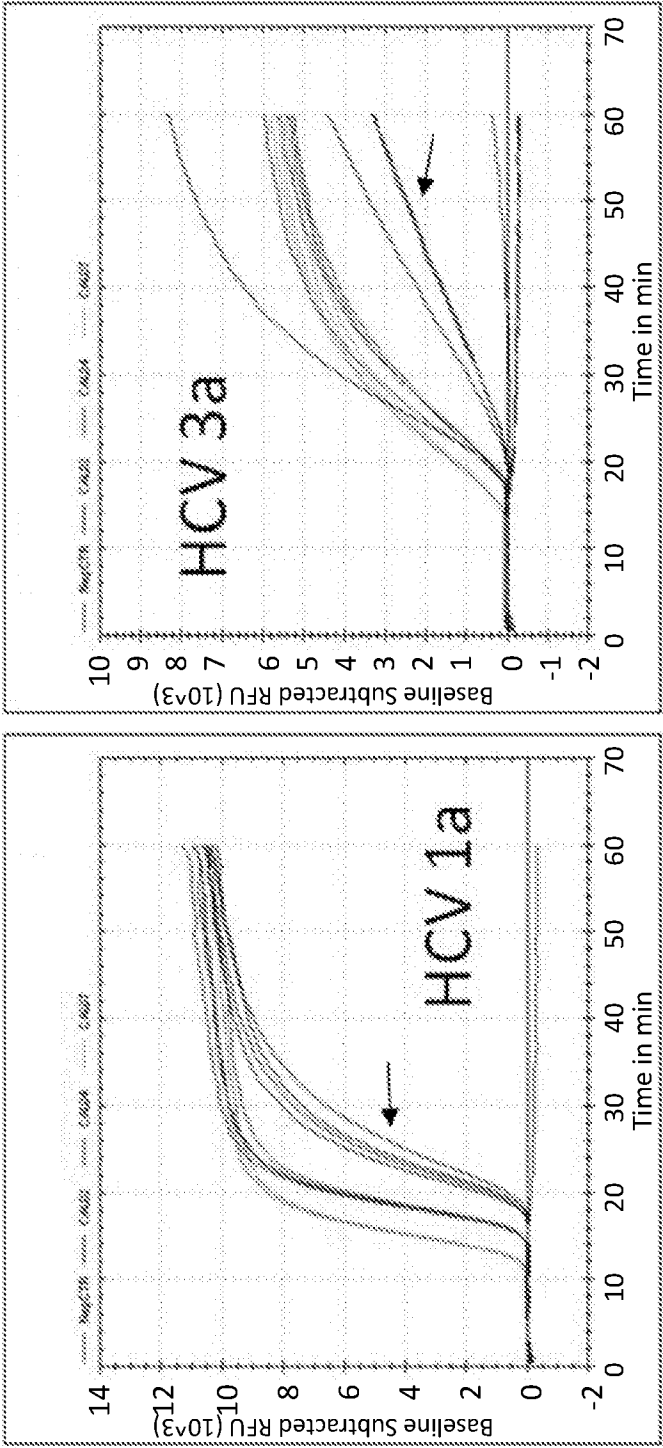


Fig. 7-1

HCV Torch
80-98 5st a (+)
No Mismatches

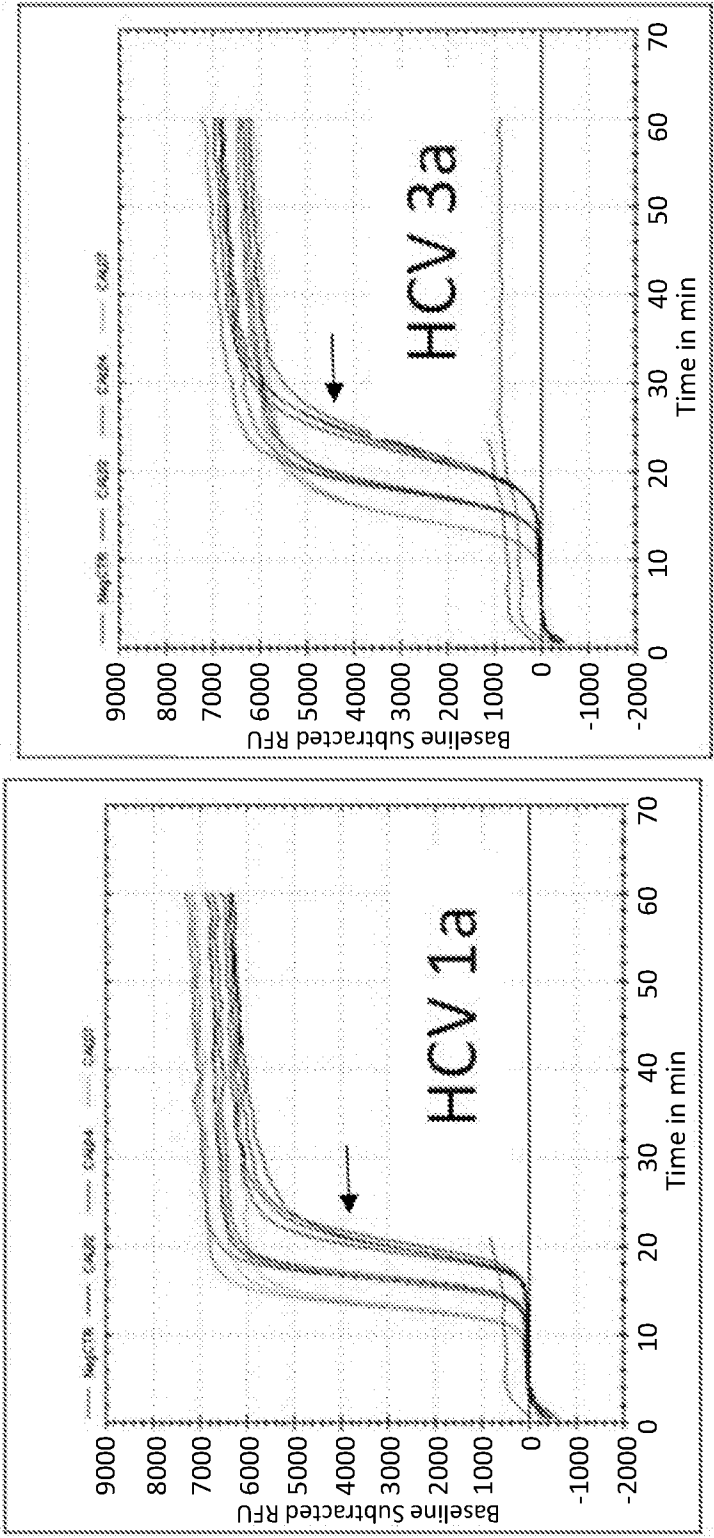


Fig. 7-2

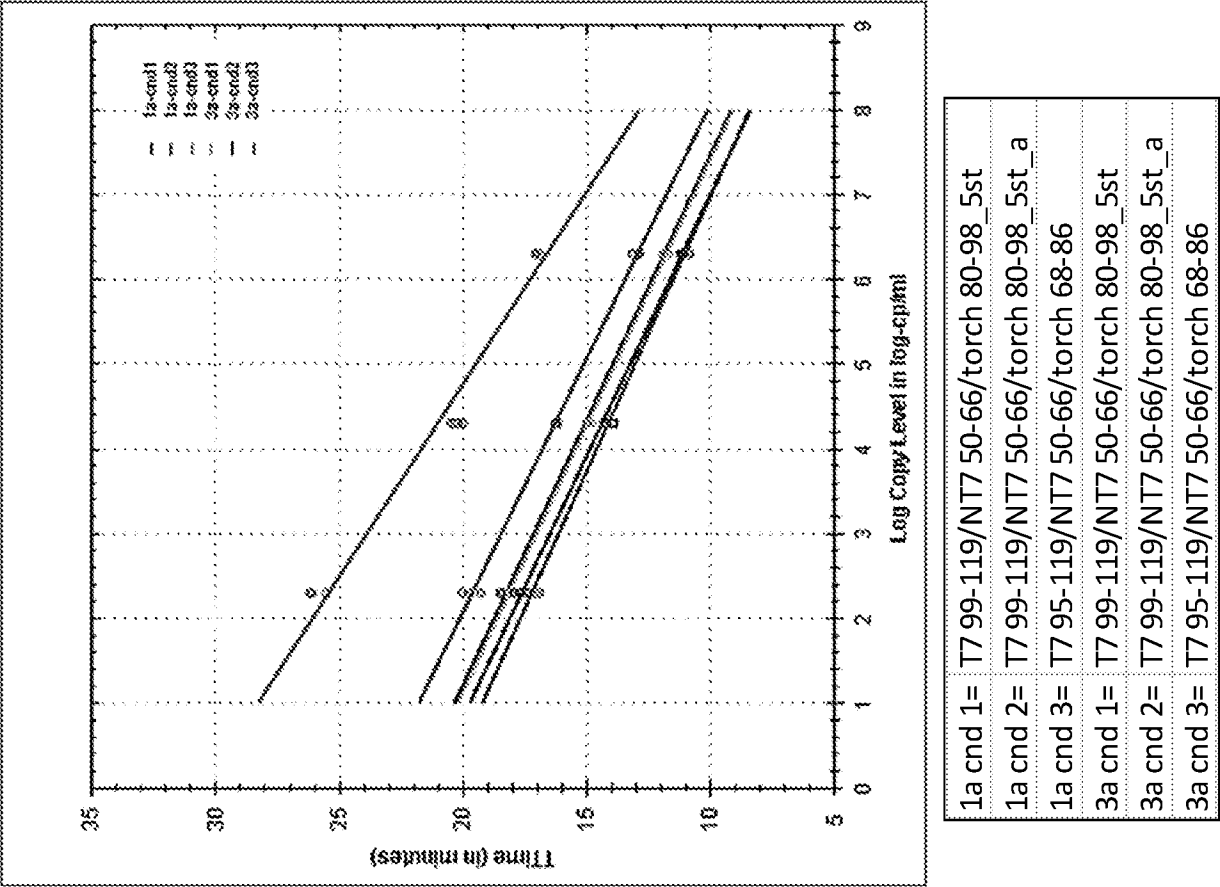


Fig. 8

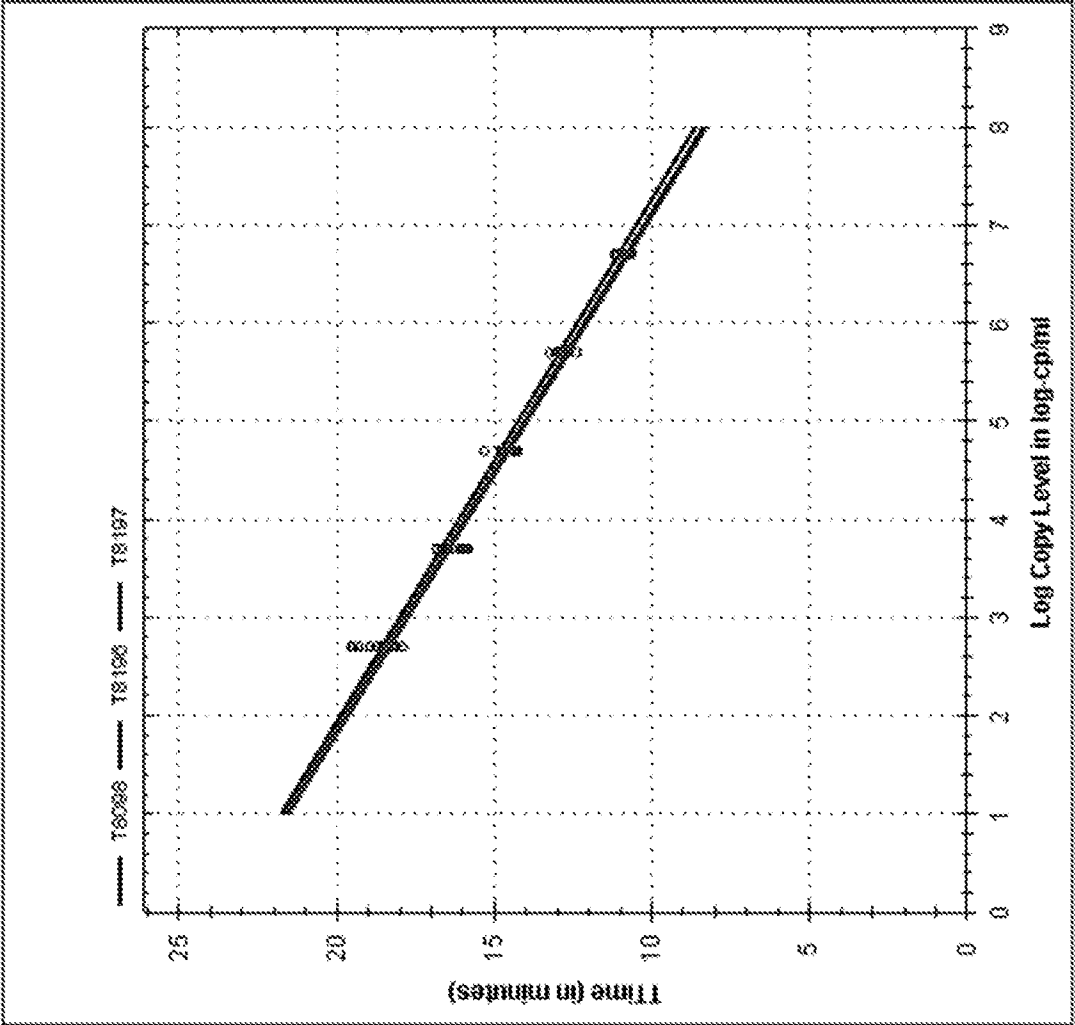


Fig. 9

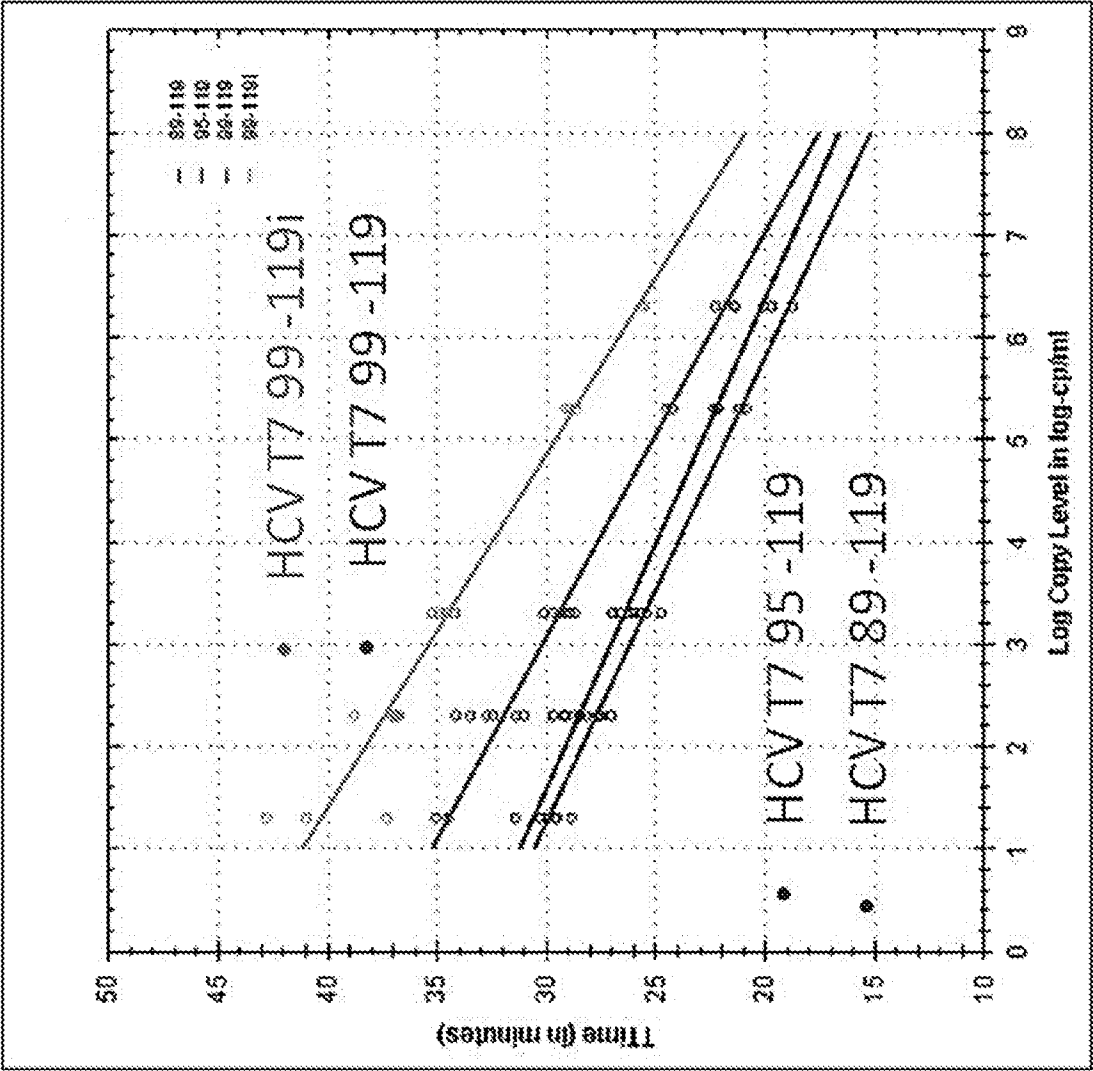


Fig. 10

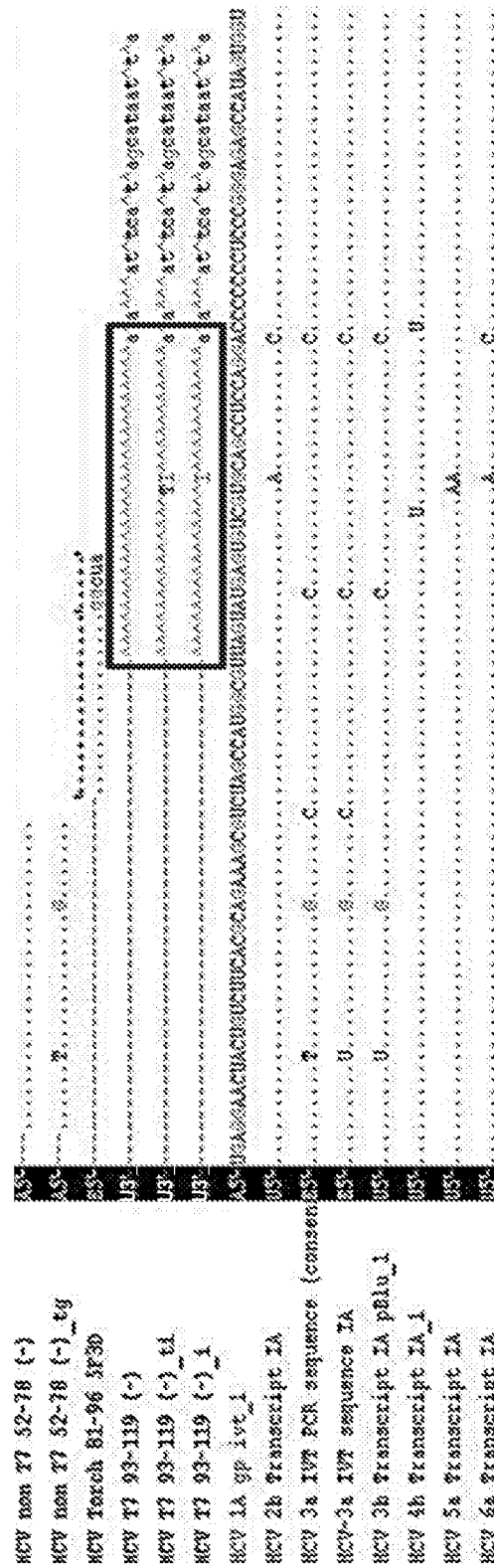


Fig. 11

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T7 93-119

HCV 1a

HCV 2b

1a Match

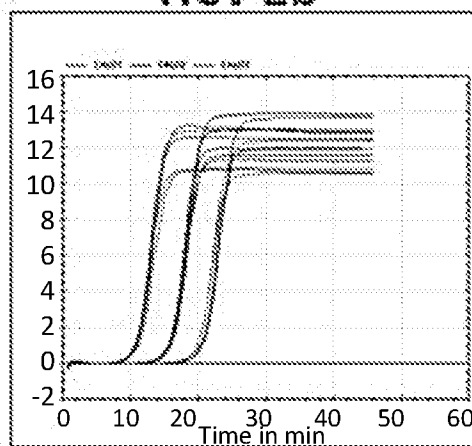
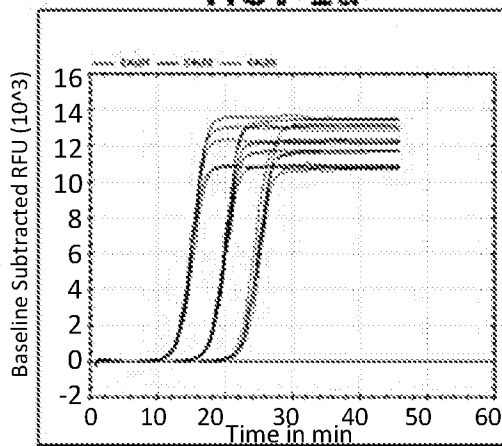
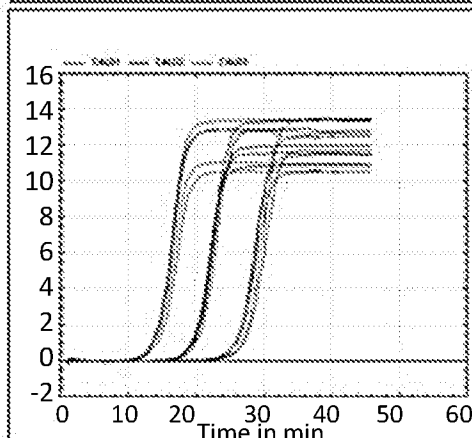
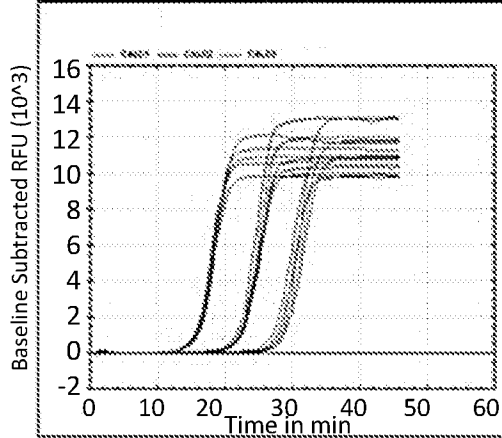
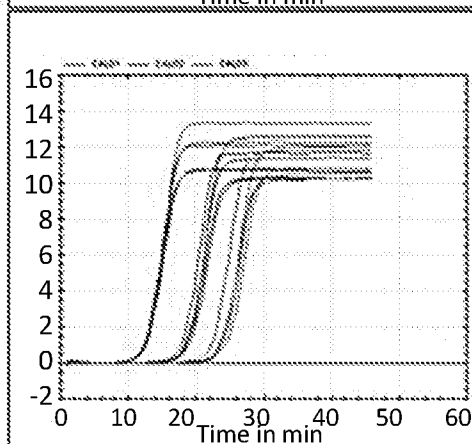
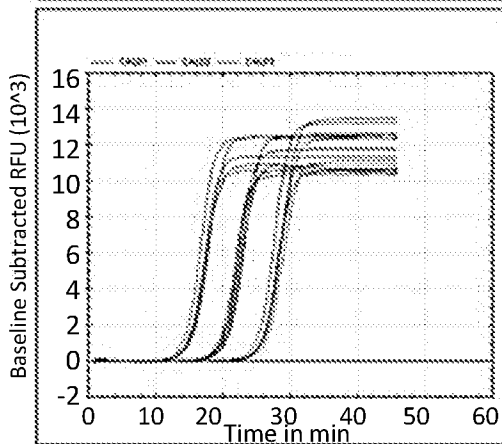
2b/5a Part
TI2b/5a Part
AI

Fig. 12A

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T7 93-119

HCV 3a

HCV 3b

1a Match

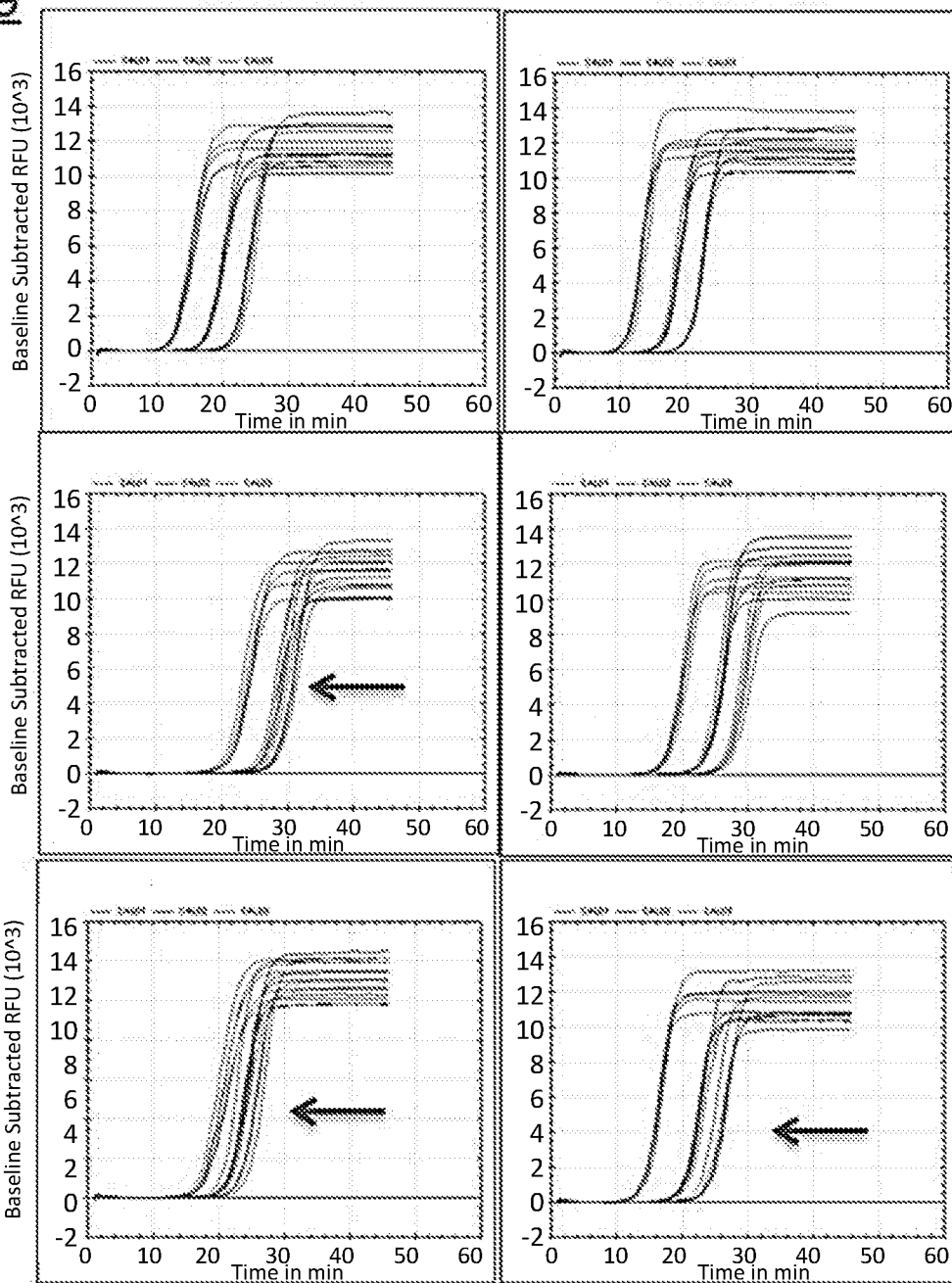


Fig. 12B

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T7 93-119

HCV 4h

HCV 5a

1a Match

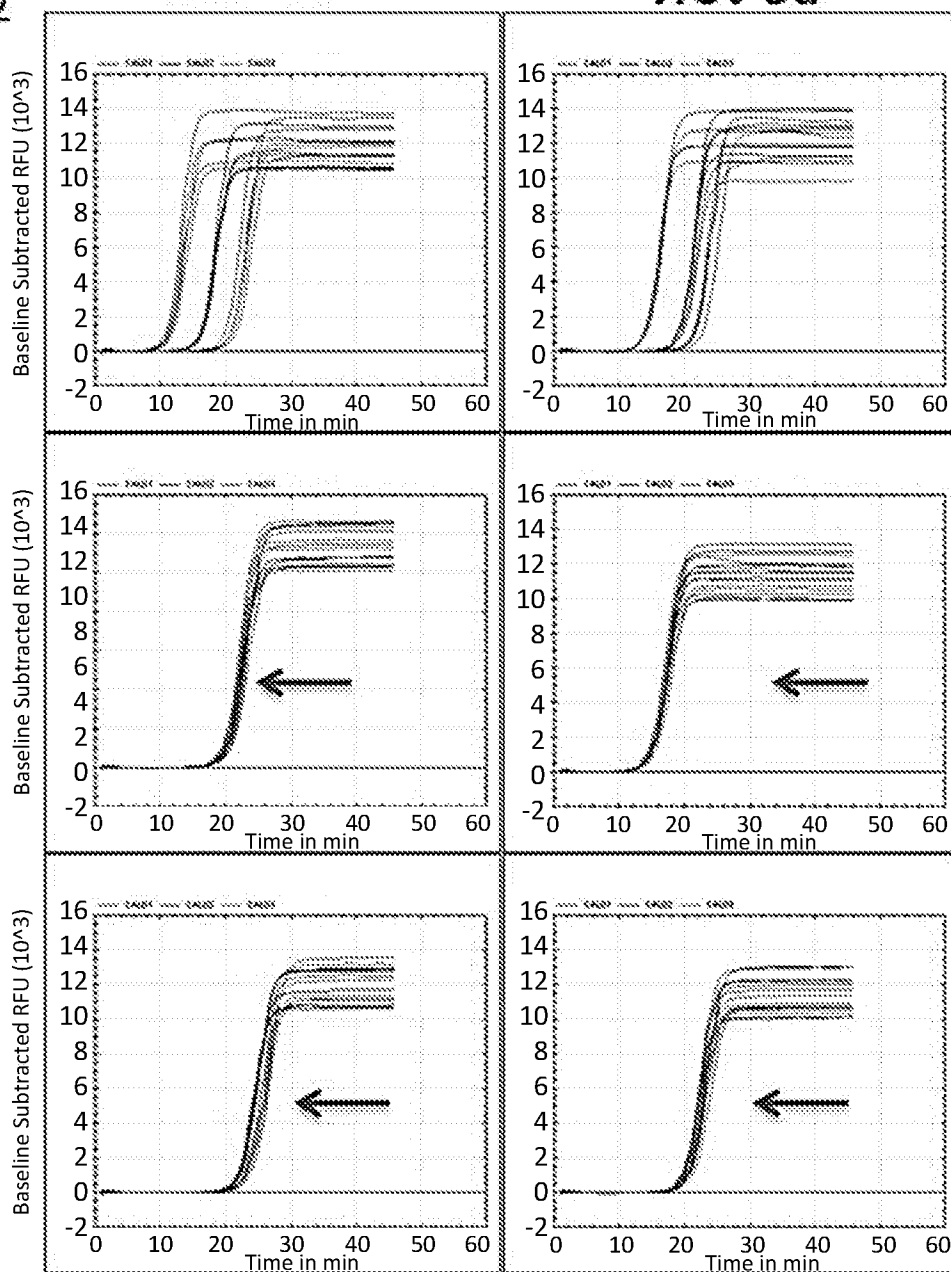


Fig. 12C

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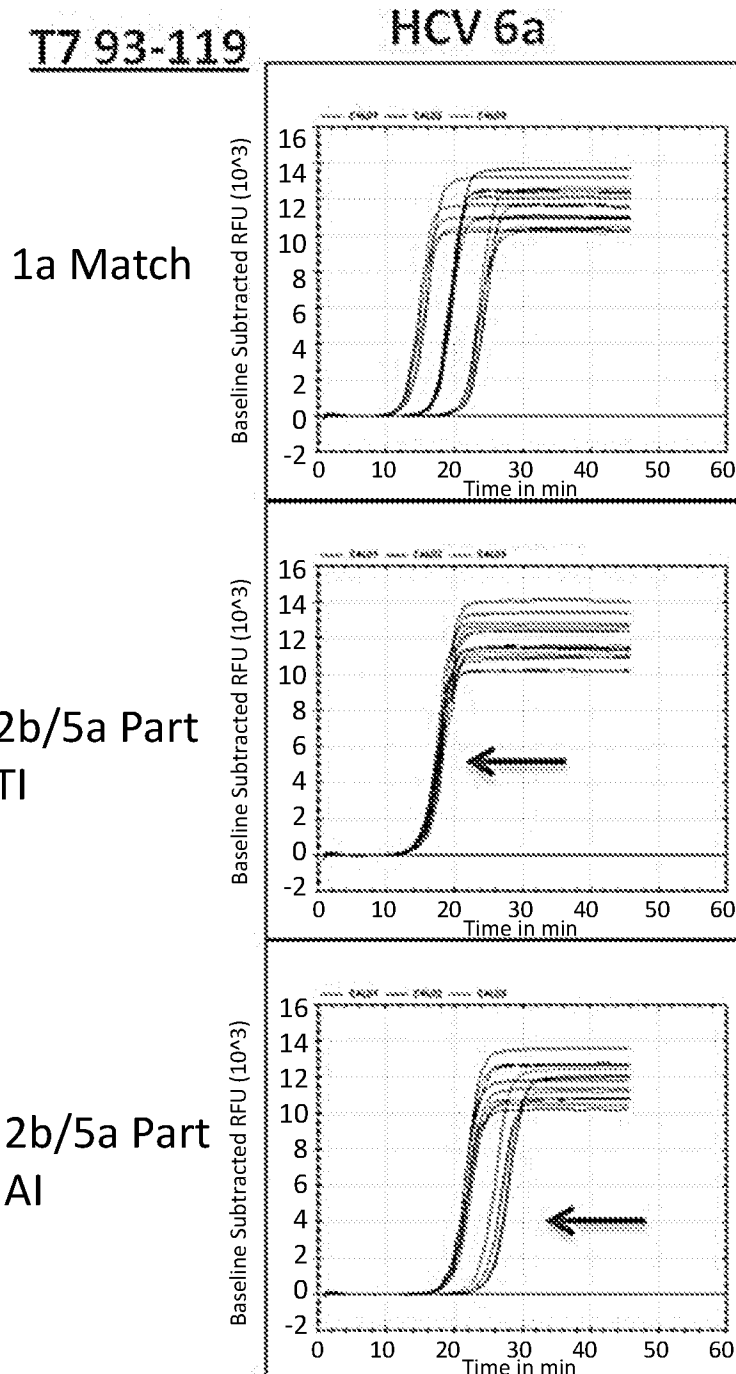


Fig. 12D

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Control T7 93-119

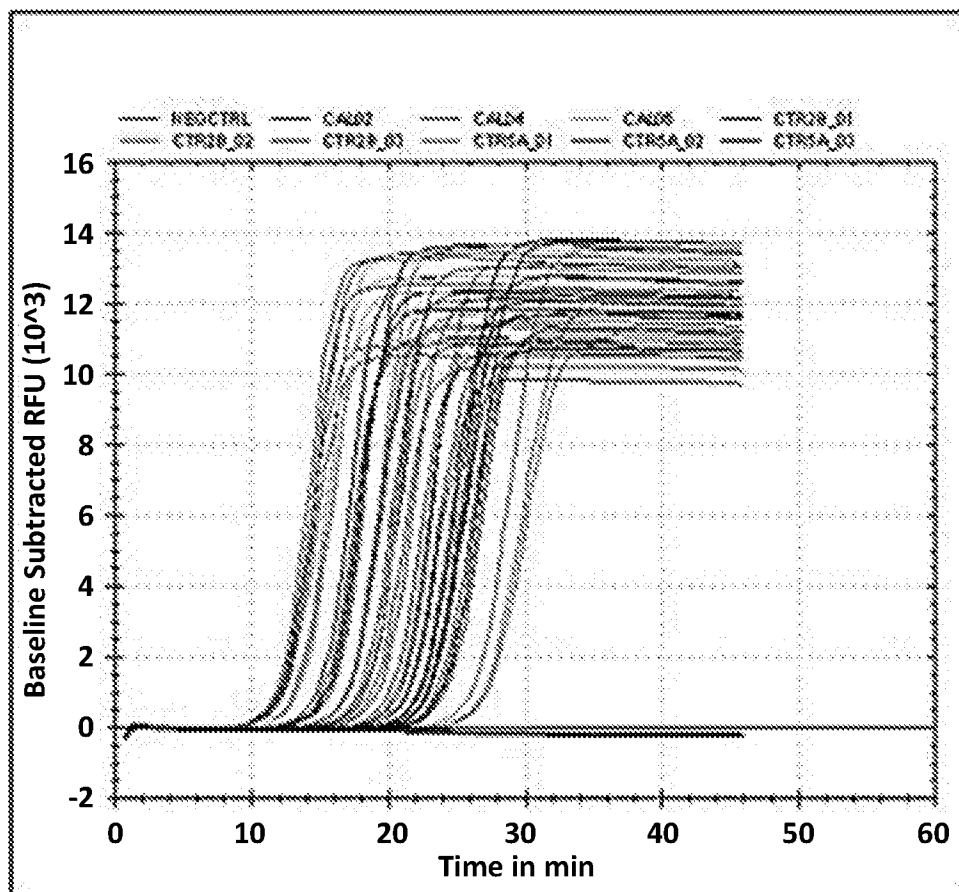


Fig. 13A

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T7 89-119

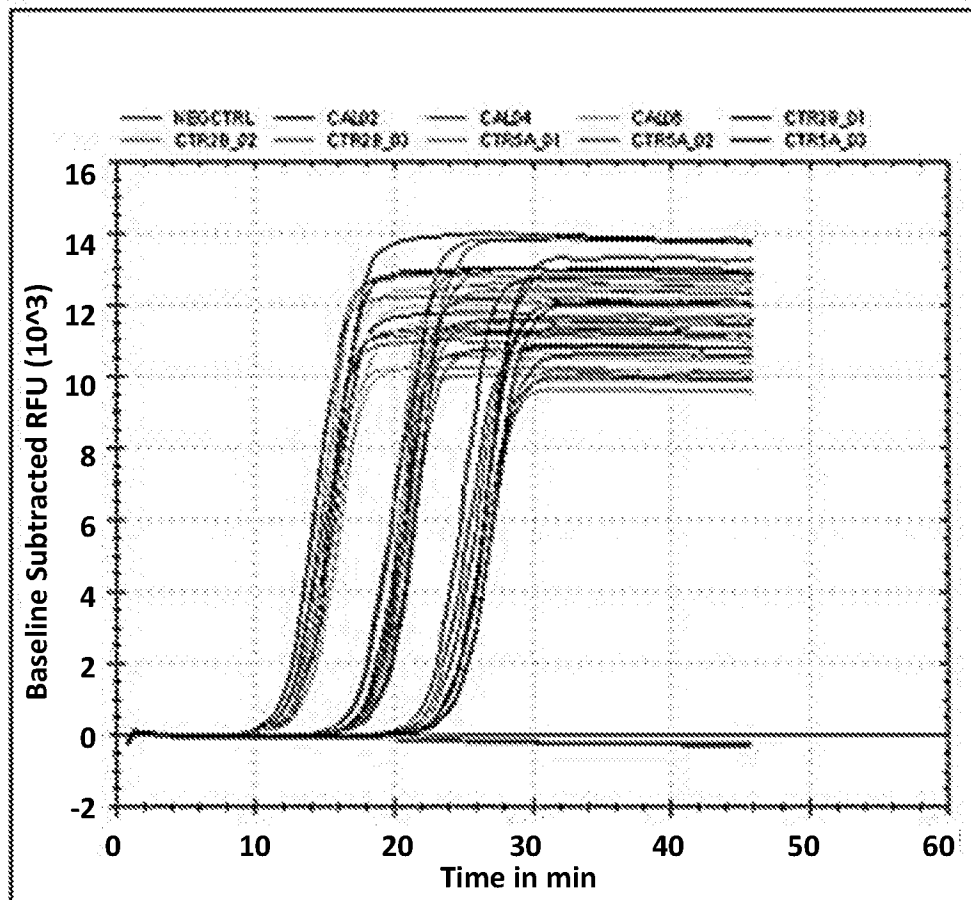


Fig. 13B

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T7 80-119

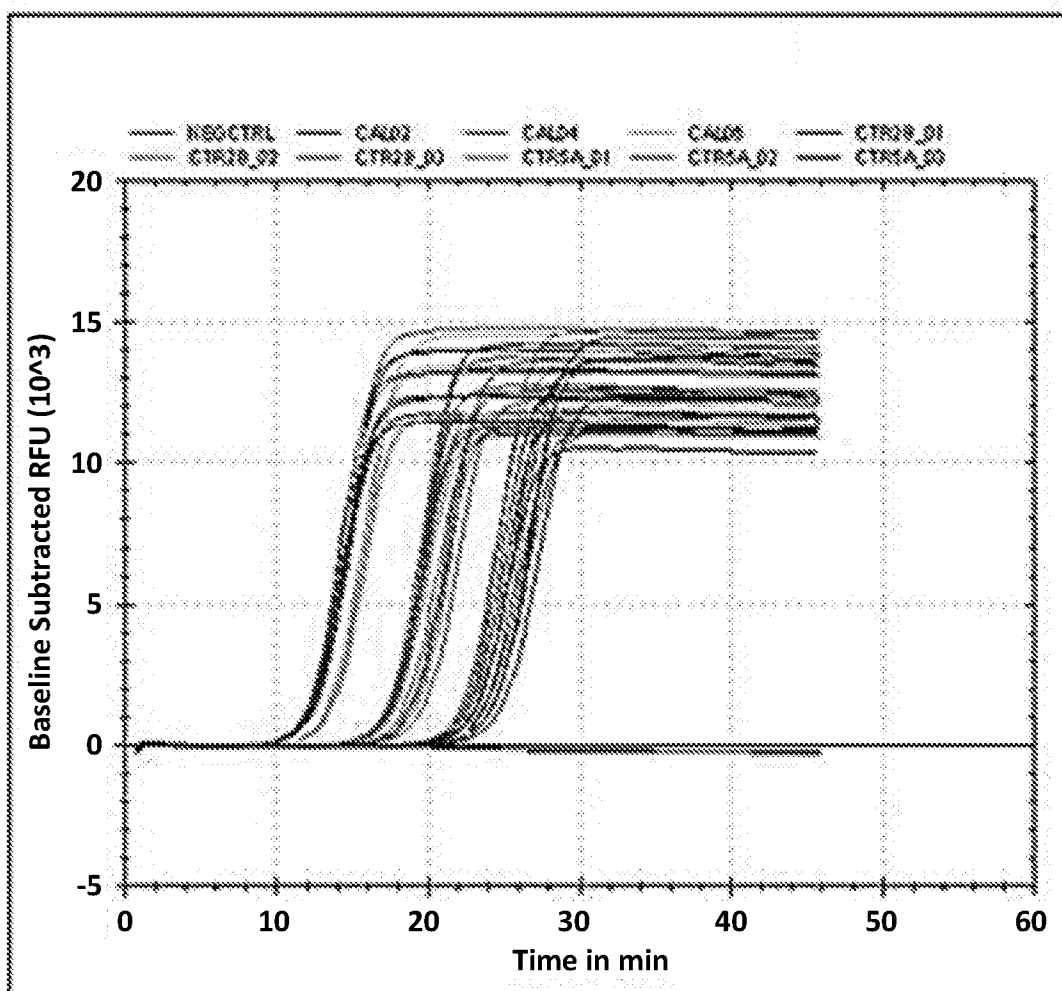


Fig. 13C

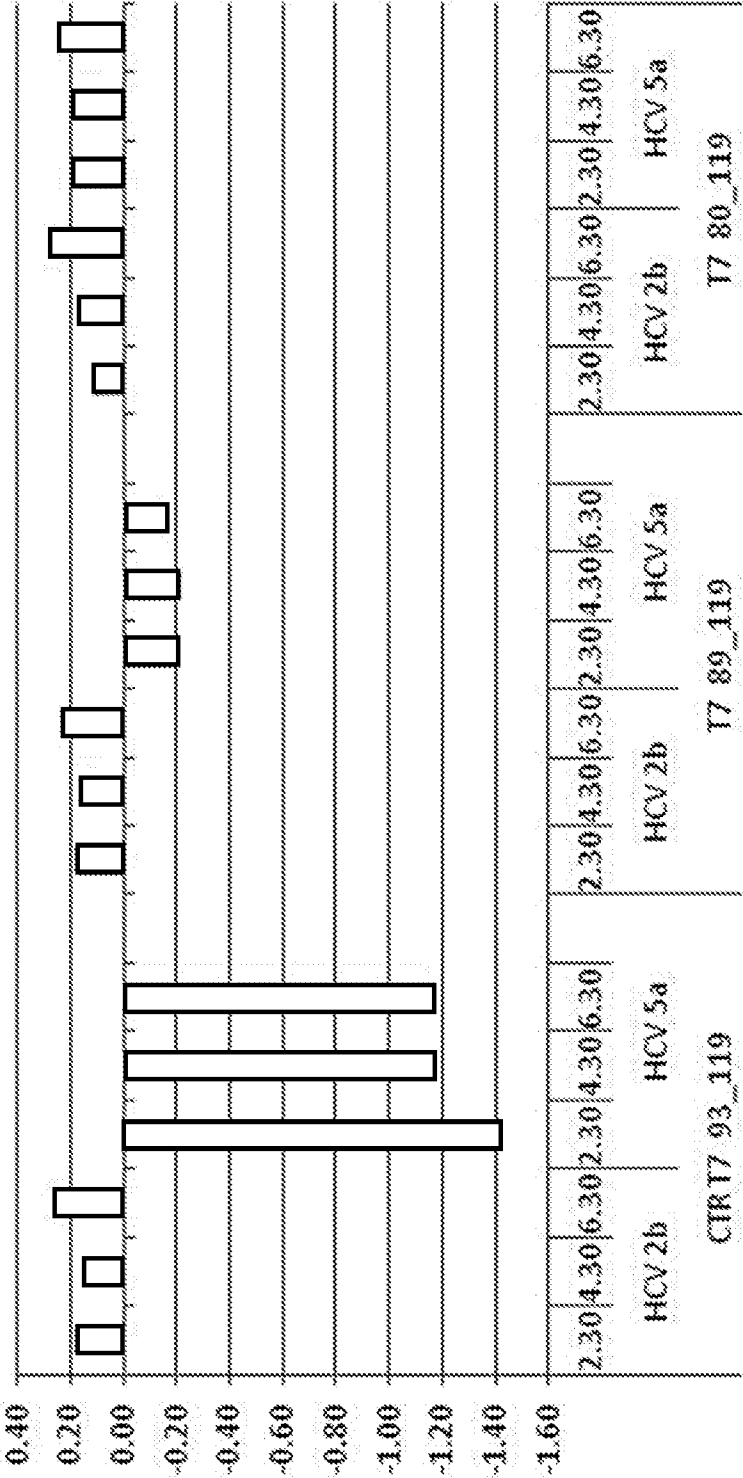


Fig. 14

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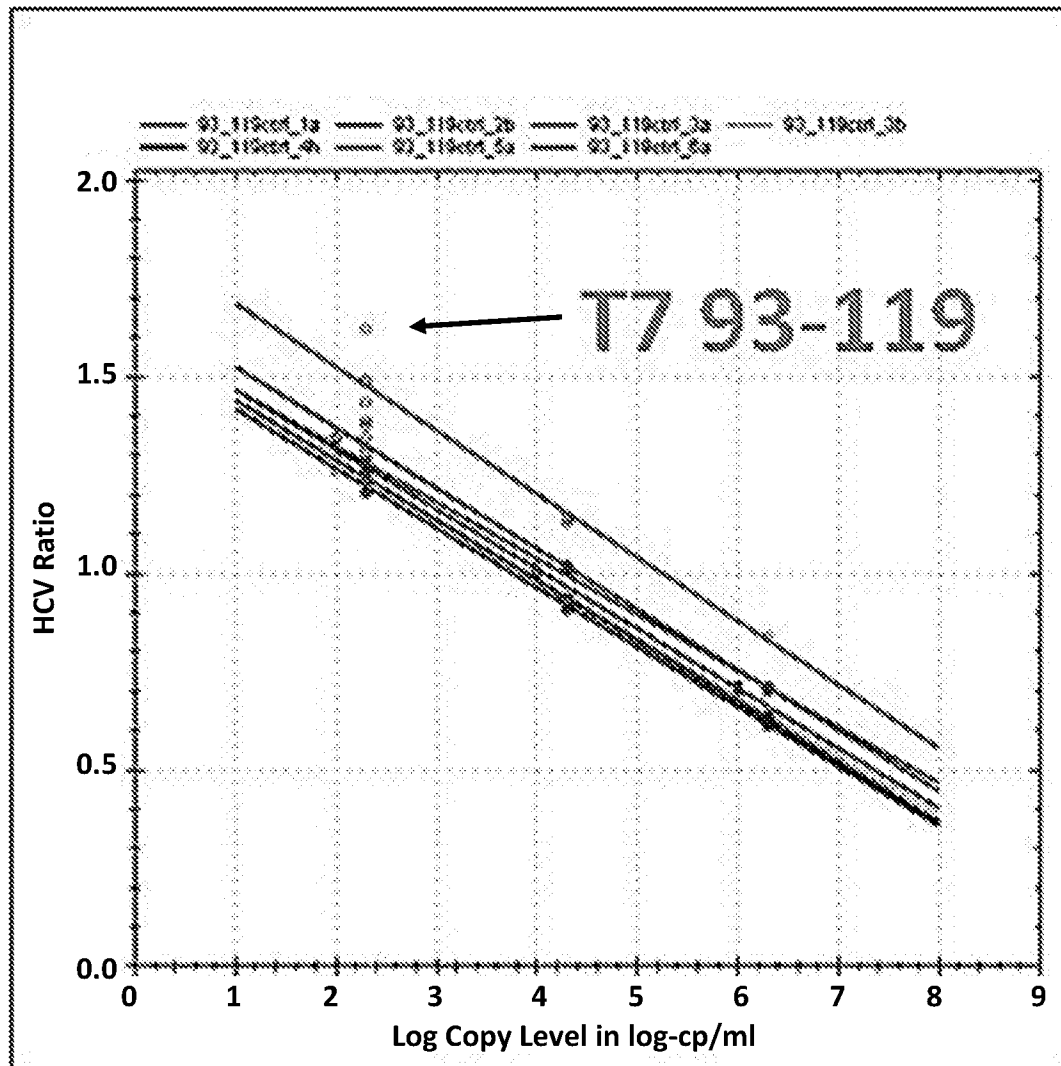


Fig. 15A

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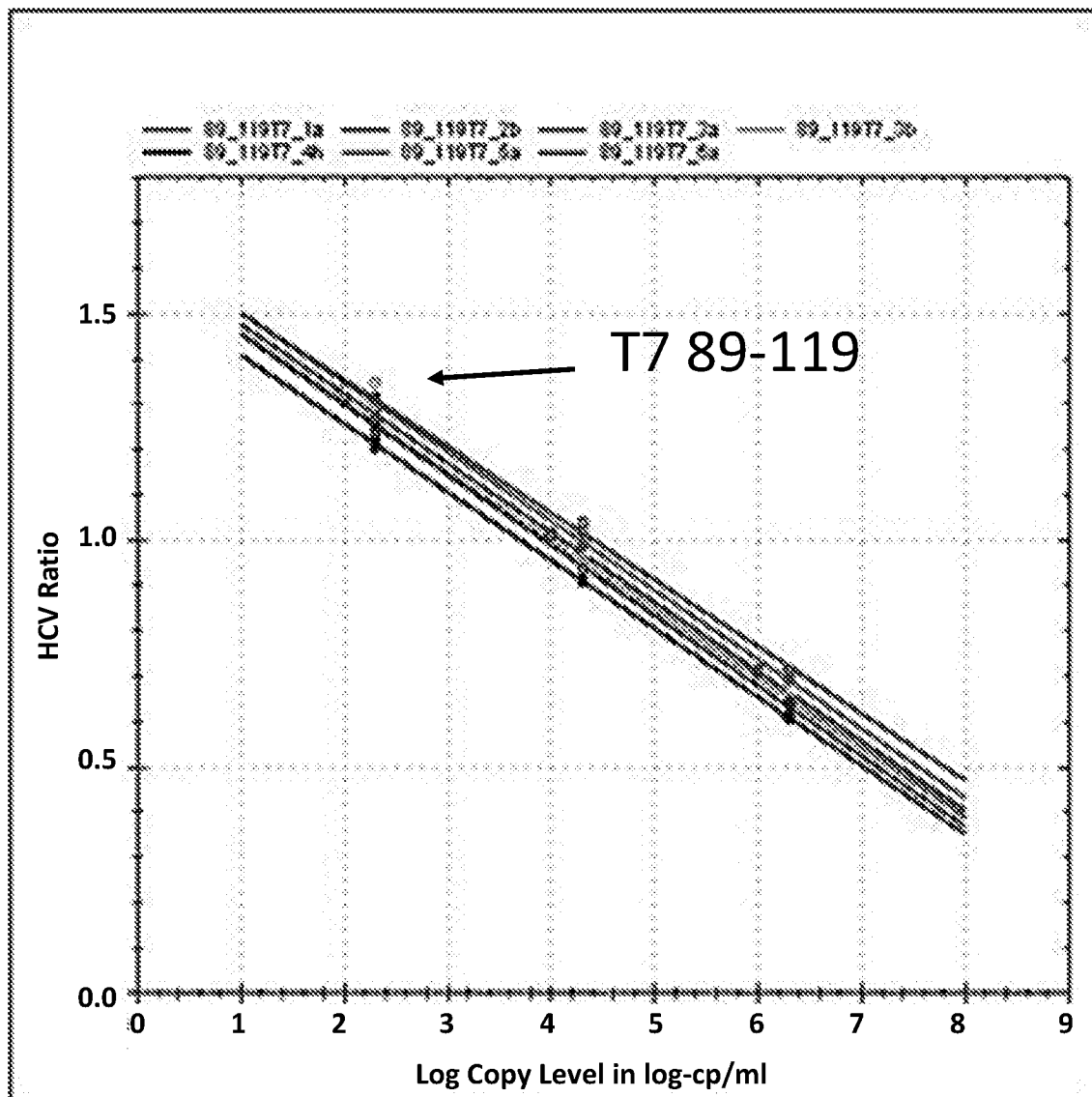


Fig. 15B

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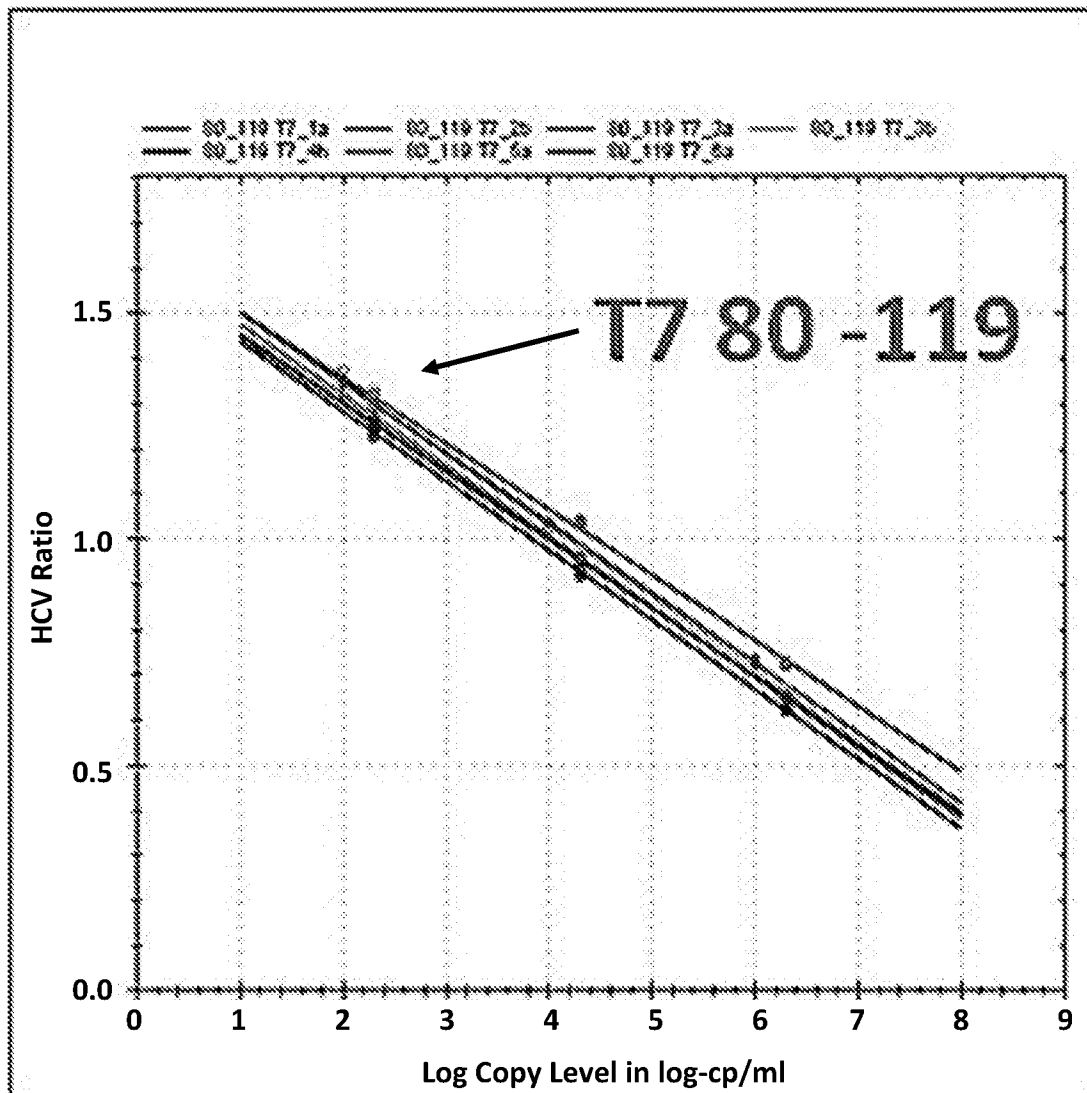


Fig. 15C

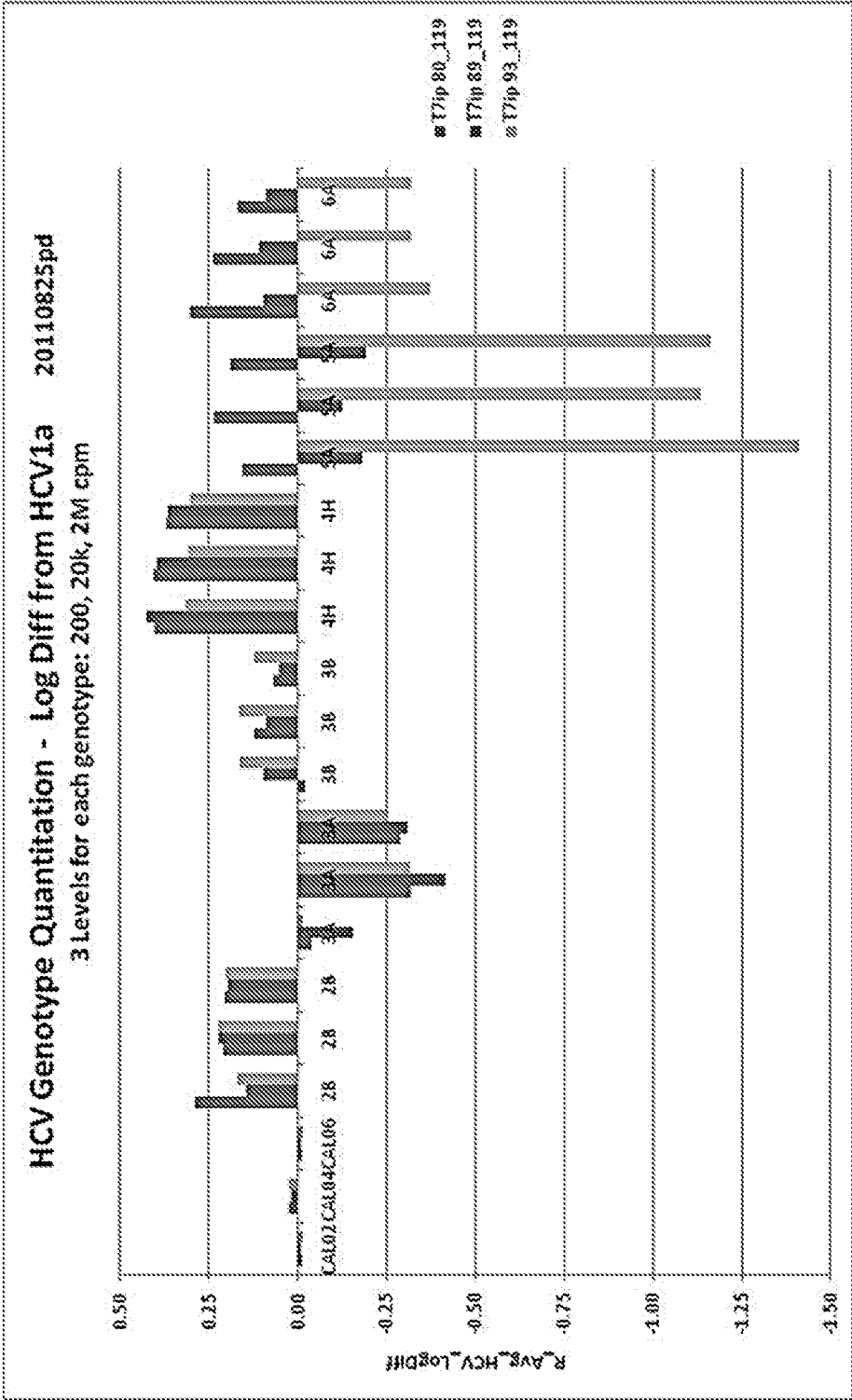


Fig. 16

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NCV non T7 52-78 (-) tg	G.....	G.....	G.....
NCV Torch 81-96 3r30	G.....	G.....	G.....
NCV 1A gp 1vt_1	G.....	G.....	G.....
NCV 2B gp 1vt_1	G.....	G.....	G.....
NCV 3A gp 1vt	G.....	G.....	G.....
NCV 3b Transcript 1A pelu	G.....	G.....	G.....
NCV 4b gp 1vt	G.....	G.....	G.....
PRW201_88_fed (5a subtype) 1 vt	G.....	G.....	G.....
NCV 5a gp 1vt	G.....	G.....	G.....
NCV T7 78-119 (-)	G.....	G.....	G.....
NCV T7 80-119 (-)	G.....	G.....	G.....
NCV T7 81-119 (-)	G.....	G.....	G.....
NCV T7 83-119 (-)	G.....	G.....	G.....
NCV T7 85-119 (-)	G.....	G.....	G.....
NCV T7 87-119 (-)	G.....	G.....	G.....
NCV T7 89-119 (-) 1	G.....	G.....	G.....
NCV T7 93-119 (-)	G.....	G.....	G.....

Fig. 17

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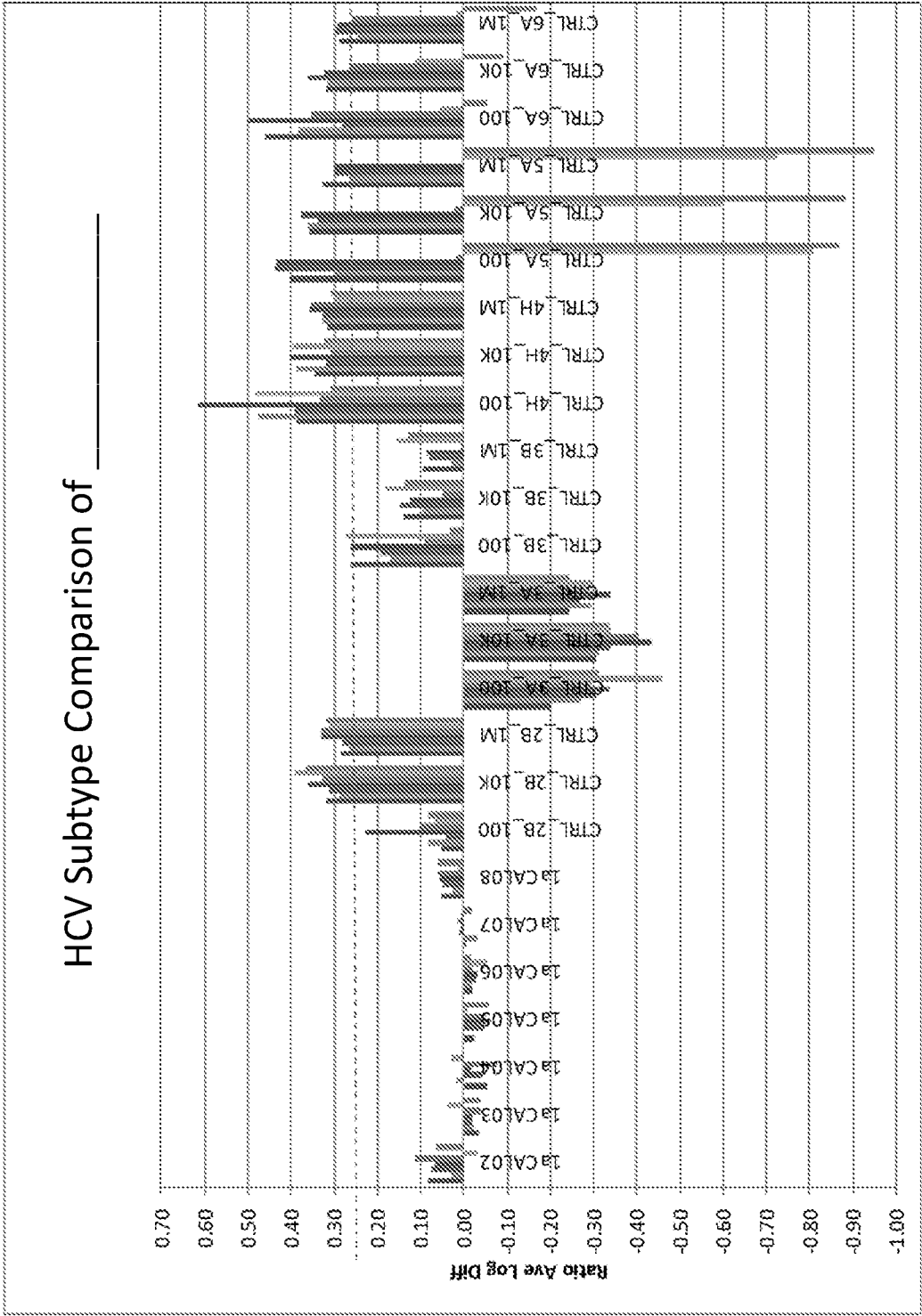


Fig. 18

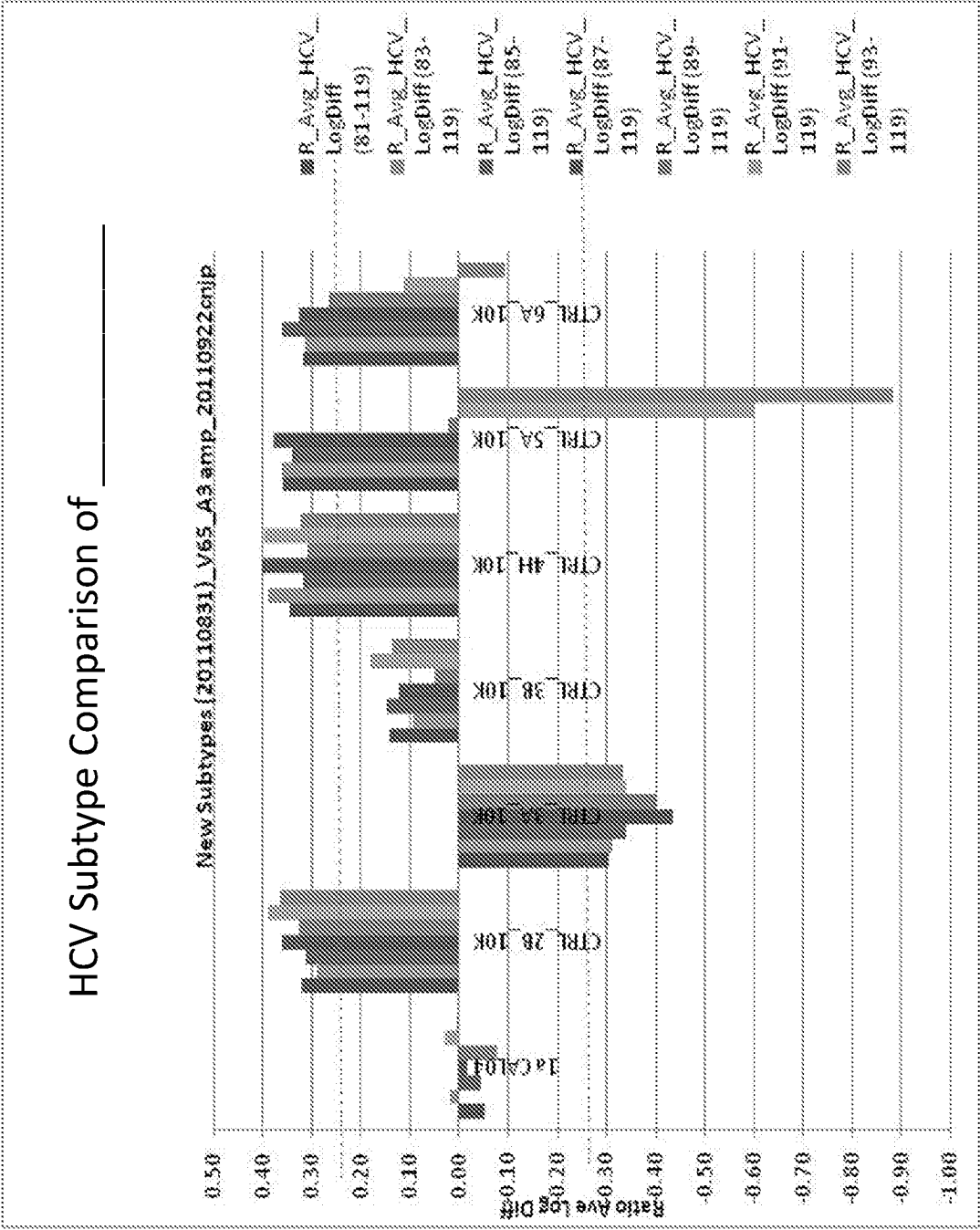


Fig. 19

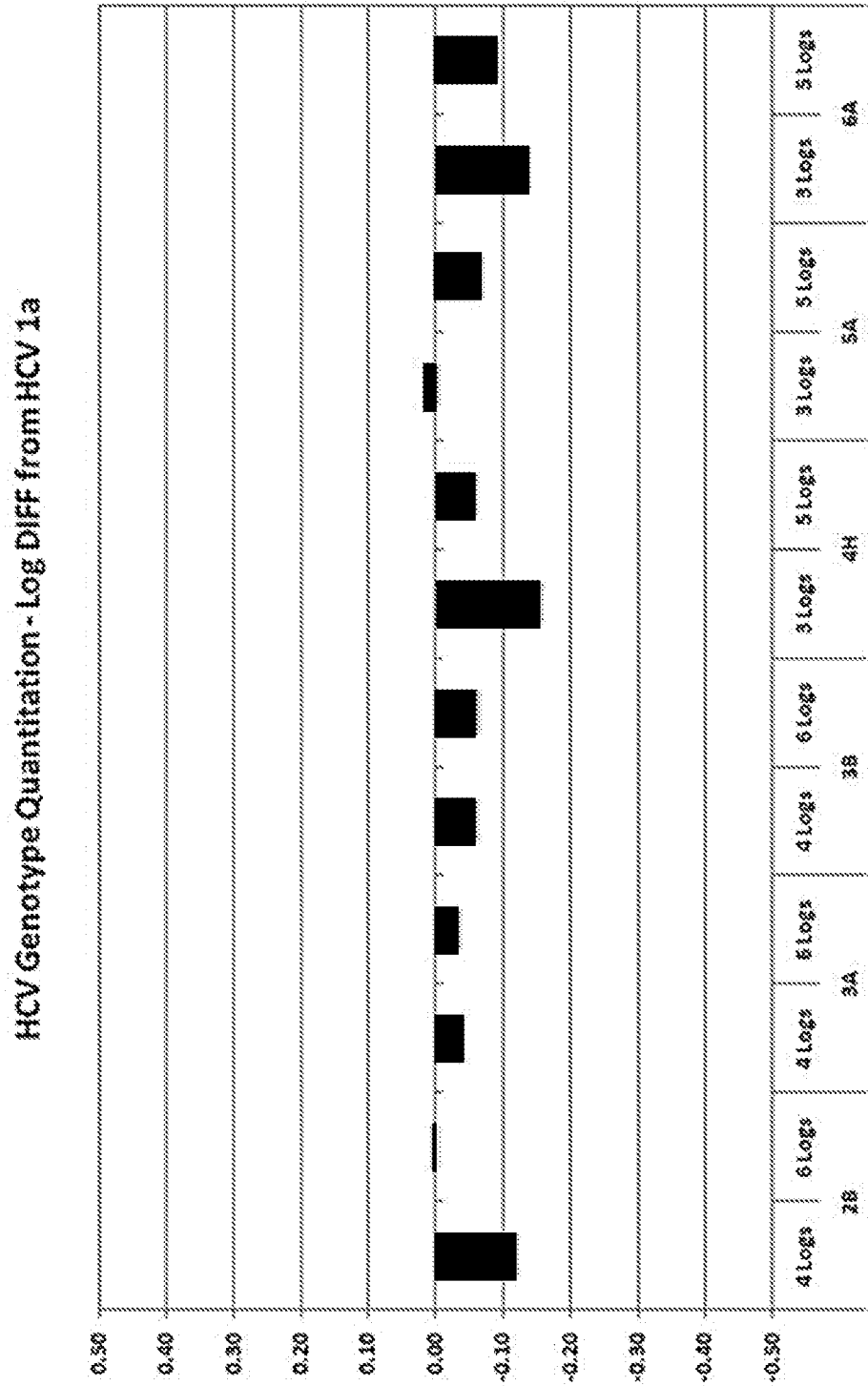


Fig. 20

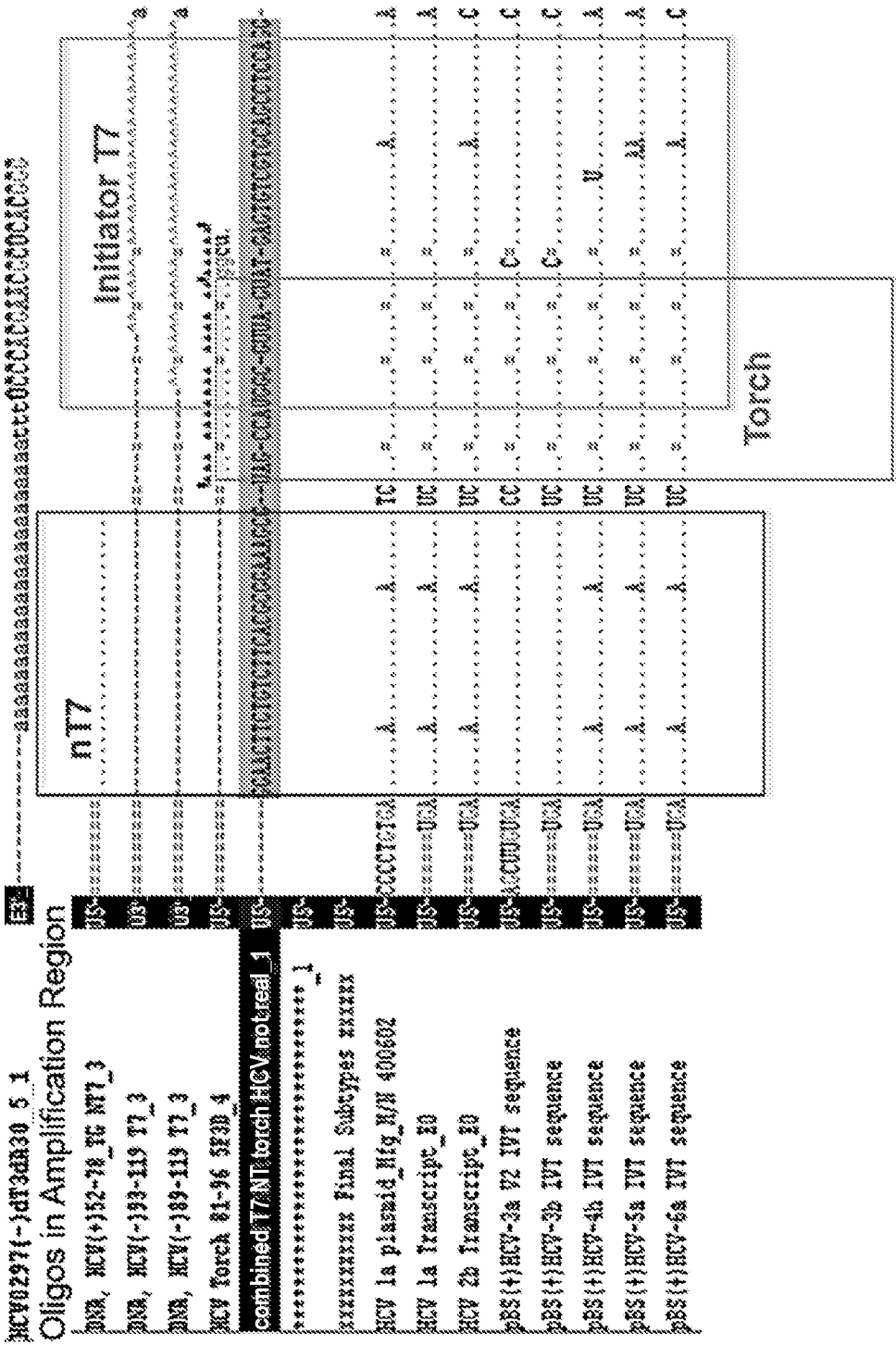


Fig. 21

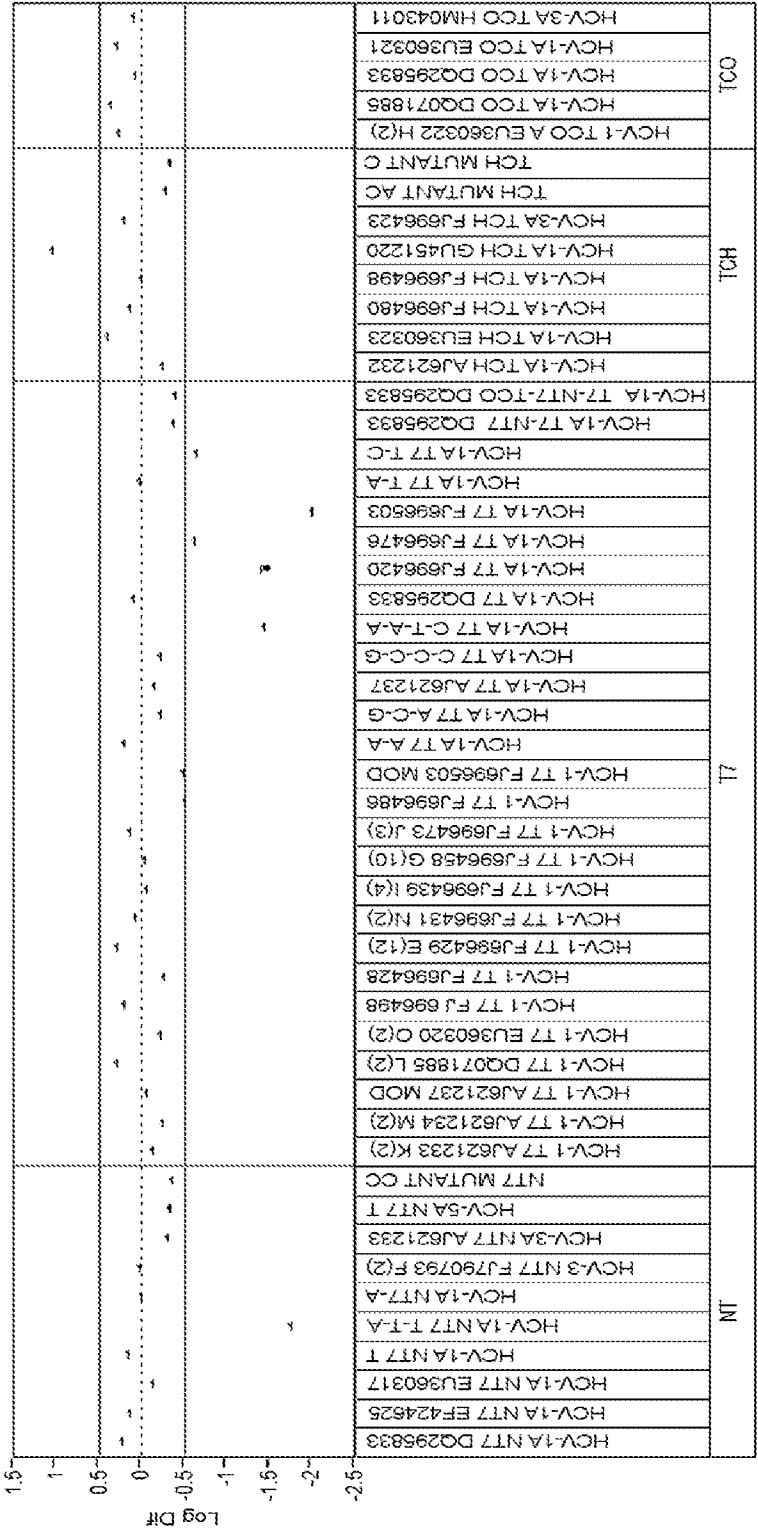


Fig. 22A

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subtype	mutate in what location(s)	frequency	# of mutations	IVT name	Accession ref	HCV ave log diff c/ml
1b	NT7	1	5	HCV-1a NT7 T-T-A	AF165050	-1.84
5	NT7	1	3	HCV-5a NT7 T	AM502711	-0.49
3a	NT7	2	4	HCV-3a NT7 TTCA AJ621233	AJ621233	-0.44
7a	NT7	1	4	HCV-5a NT7 C-C	EF108306	-0.43
1	T7/torch	1	4	HCV-1a T7 CTTC FJ696503	FJ696503	-2.06
3	T7	1	3	HCV-1a T7 CCT FJ696420	FJ696420	-1.62
6q	T7	1	4	HCV-1a T7 C-T-A-A	EF424625	-1.18
1	T7/torch	1	4	HCV-1a T7 CTTG FJ696476	FJ696476	-0.60
2a	T7	1	3	HCV-1a T7 T-C	D31604	-0.55
3a	torch	1	2	HCV-1a tch CC AJ621232	AJ621232	-0.43
3	Torch	1	1	HCV-1a Tch C	AJ621232	-0.42
1b	torch	1	3	HCV-1a tch TGC GU451220	GU451220	1.45
4a	T7/NT7/TCO	1	9	T7aT7TCO DQ295833	DQ295833	-0.51

Note: IVT mutants were tested at 1e4 c/ml.

Fig. 22B

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	n17	Torch	T7
****Original Oligo Seq****			
30A, HCV(+152-78 TC NT7			
30A, HCV(-189-119 T7			
HCV0297(-)dt34330			
HCV Torch 81-96 583B			
combined T7 NT torch HCV/not real			
****Subseqs****			
HCV 1a plasmid Hg N/N 400602	TC		
HCV 1a Transcript_E0	TC		
HCV 2b Transcript_E0	TC		
pS1{HCV-3a V2 IVT sequence	TC		
pS1{HCV-3b IVT sequence	TC		
pS1{HCV-4b IVT sequence	TC		
pS1{HCV-5a IVT sequence	TC		
pS1{HCV-5a IVT sequence	TC		
****Gorsta Mutants****			
HCV-1a T7 C11 F3696420	TC		
HCV-1a T7 C11C F3696503	TC		
HCV-5a NT7 C-C IVT sequence	TC		
HCV-3a NT T1CA A3621233	TC		
HCV-5a NT7 T IVT sequence	TC		
HCV-1a NT7 T-1-A IVT sequence	TC		
HCV 1a T7 C-1-A-A IVT sequence	TC		
HCV-1a T7 C11C F3696476	TC		
HCV 1a T7 T-C IVT sequence	TC		
HCV-1a tch CC A3621232	TC		
HCV 1a Tch C IVT sequence	TC		
HCV-1a tch TCC C0451220	TC		
HCV-1a T74HTATC0 AAA B0295833	TC		

Fig. 23

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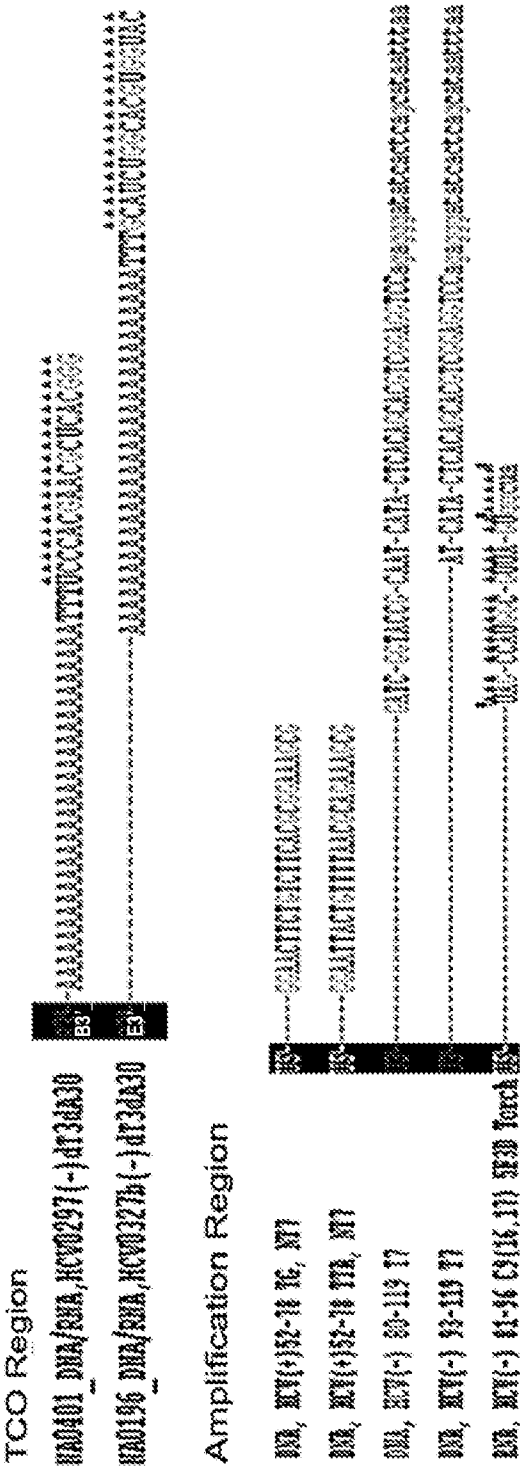


Fig. 24

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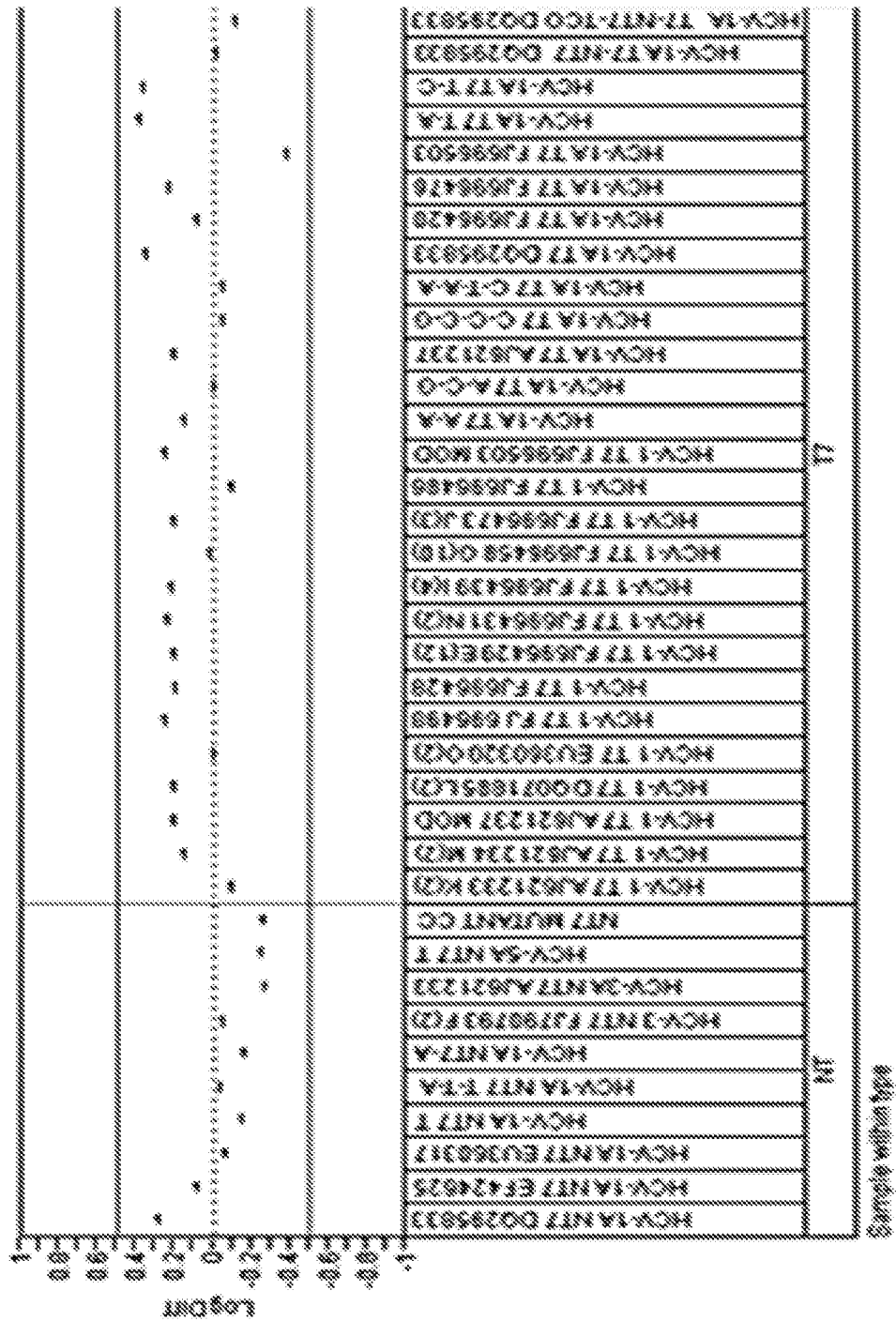


Fig. 25A-1

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[illegible]

Fig. 25A-2

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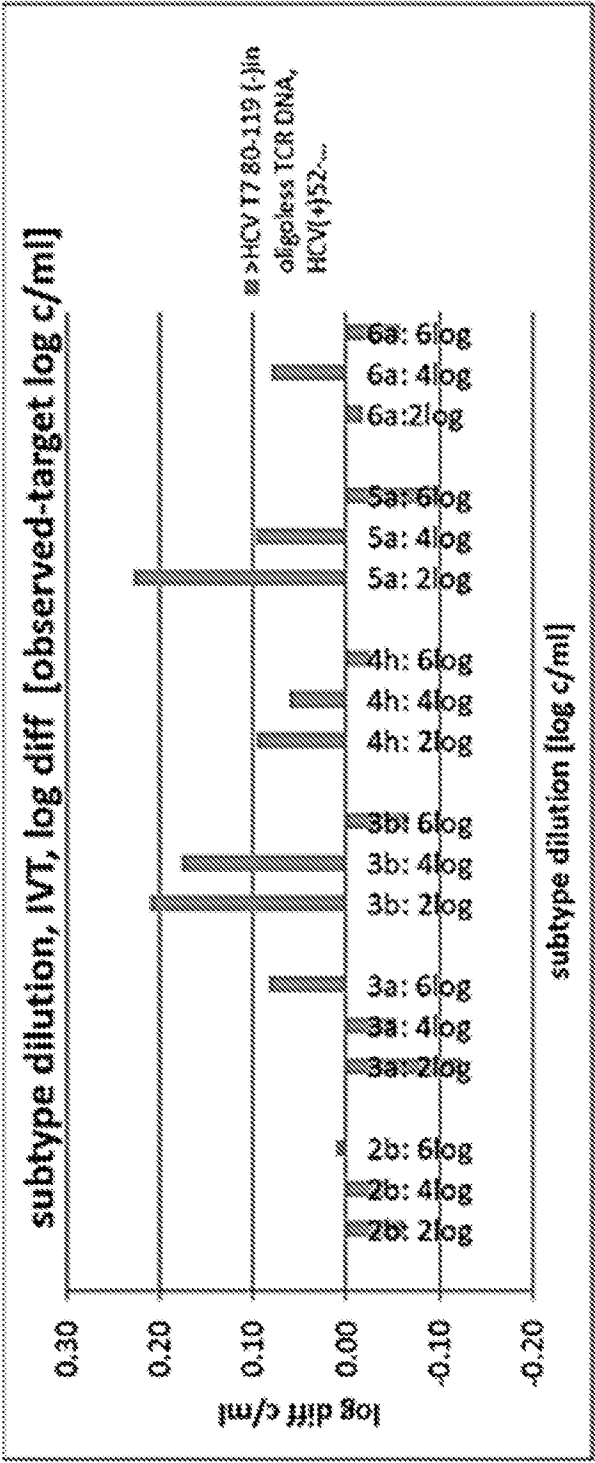


Fig. 25B

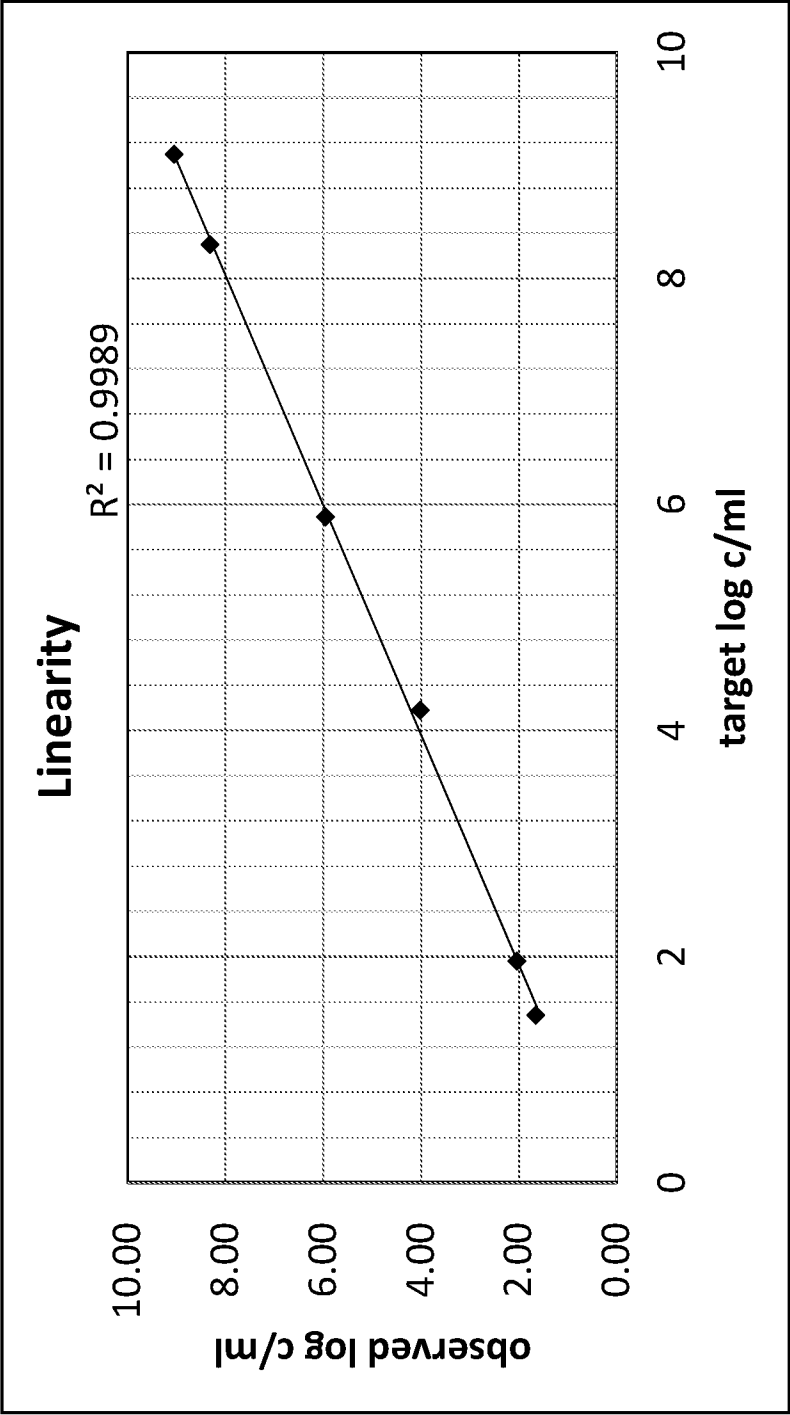


Fig. 26

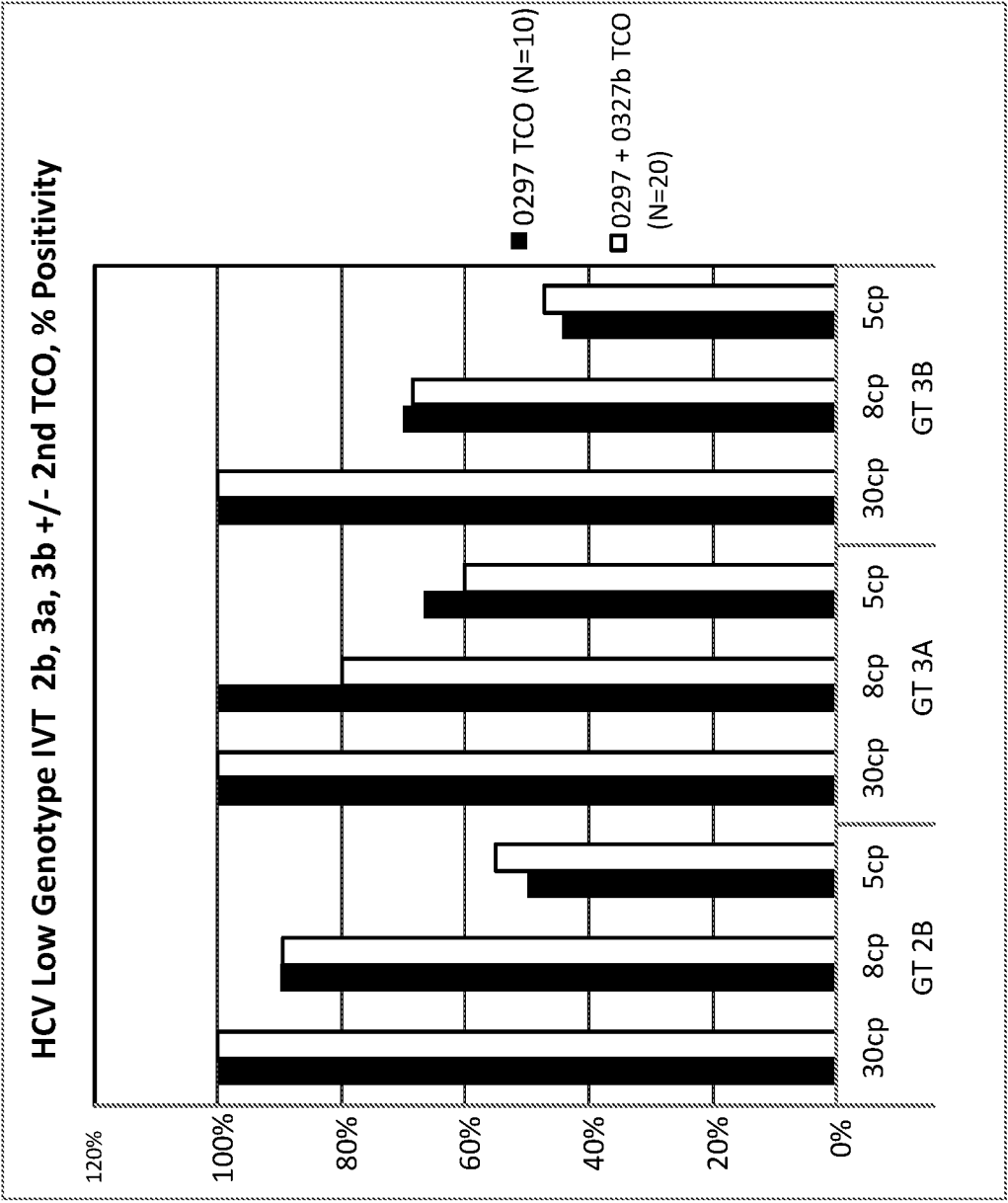


Fig. 27A

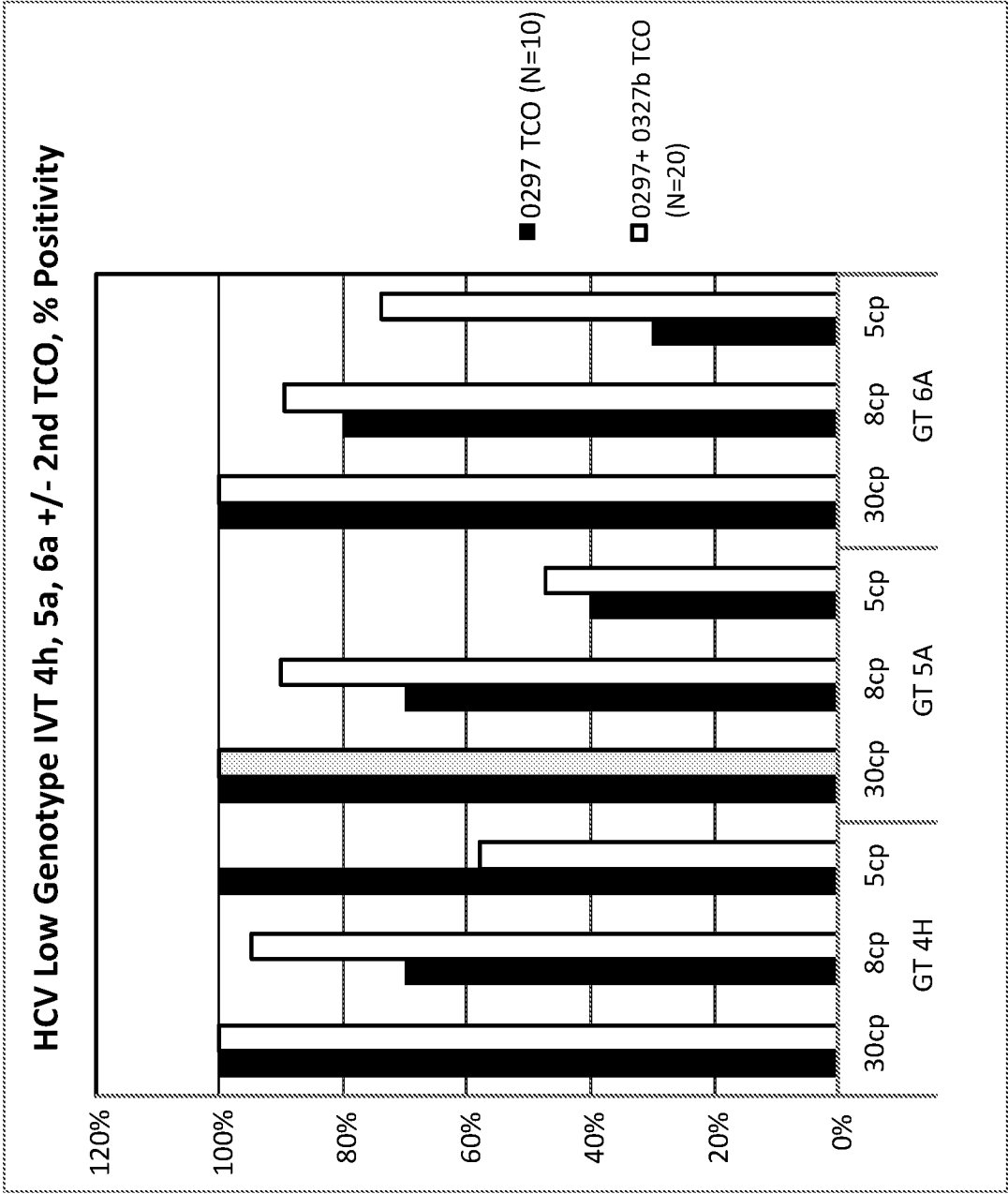


Fig. 27B