COBAS[®] AmpliPrep/COBAS[®] TaqMan[®] HCV Quantitative Test, version 2.0

CORAS® AmpliPren/CORAS® TagMan® HCV



P/N: 05532264 190

FOR IN VITRO DIAGNOSTIC USE.

| Quantitative Test, v2.0 | | | |
|--|-------|------------|-------------------|
| COBAS® AmpliPrep/COBAS® TaqMan® Wash Reagent | PG WR | 5.1 Liters | P/N: 03587797 190 |
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INTENDED USE

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 is an *in vitro* nucleic acid amplification test for the quantitation of Hepatitis C Virus (HCV) RNA genotypes 1 to 6 in human EDTA plasma or serum using the COBAS® AmpliPrep Instrument for automated specimen processing and the COBAS® TaqMan® Analyzer or the COBAS® TaqMan® 48 Analyzer for automated amplification and detection. The test is intended for use in the management of patients with chronic HCV in conjunction with clinical and laboratory markers of infection. The test can be used to predict the probability of sustained virologic response (SVR) early during a course of antiviral therapy, and to assess viral response to antiviral treatment (response guided therapy) as measured by changes of HCV RNA levels in serum or EDTA plasma.

The COBAS* AmpliPrep/COBAS* TaqMan* HCV Quantitative Test, v2.0 is not intended for use as a screening test for the presence of HCV in blood or blood products or as a diagnostic test to confirm the presence of HCV infection.

SUMMARY AND EXPLANATION OF THE TEST

Hepatitis C Virus is considered to be the principal etiologic agent responsible for 90 to 95% of the cases of post-transfusion hepatitis¹⁻⁴. HCV is a single-stranded, positive sense RNA virus with a genome of approximately 9,500 nucleotides coding for 3,000 amino acids. As a blood-borne virus, HCV can be transmitted by blood and blood products. Widespread adoption of HCV blood screening measures has markedly lowered the risk of transfusion-associated hepatitis. The incidence of HCV infection is highest in association with intravenous drug abuse and to a lesser extent with other percutaneous exposures. The global prevalence of HCV infection, as determined by immunoserology, ranges from 0.6% in Canada to 1.5% in Japan³. Spontaneous viral clearance rates in exposed individuals are highly variable; between 10 and 60% have been reported as measured clinically by normalization of liver enzymes and clearance of plasma HCV RNAs².

HCV virus particles cannot be cultured from infected blood samples; hence the presence of anti-HCV antibodies in patients infected with HCV has led to the development of immunoserological assays that are specific for these antibodies. The presence of anti-HCV antibodies, however, is a measure of prior exposure to HCV infection, but cannot be considered a marker for current infection. The measurement of alanine aminotransferase levels (ALT) is considered to be a surrogate indicator of HCV infection, but is not a direct measure of viremia.

In contrast, quantitation of HCV RNA for measuring baseline viral loads and for on-treatment monitoring has been well established in demonstrating the efficacy of antiviral response to peginterferon plus ribavirin combination therapy. Our current guidelines for the management and treatment of HCV recommend quantitative testing for HCV RNA before the start of antiviral therapy, during therapy (response guided therapy), and generally 12 to 24 weeks following the end of treatment. Absence of detectable HCV RNA by a sensitive test, 24 weeks after the end of treatment, is the goal of treatment and indicates that a sustained virologic response (SVR) has been achieved. During antiviral therapy an early virologic response (EVR), defined as a two-log or greater decrease in HCV RNA after 12 weeks of therapy, is commonly observed. Failure to achieve EVR has a high negative predictive value for achieving a SVR and has been incorporated in futility (stopping) rules for pegylated interferon plus ribavirin therapies. A rapid viral response (RVR), undetectable levels of HCV RNA after 4 weeks of therapy, has a high positive predictive value for SVR. Determining the viral kinetics during therapy has more recently been used to further personalize treatment duration with the novel direct acting antiviral agents for the treatment of chronic HCV infections.

PRINCIPLES OF THE PROCEDURE

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 is a nucleic acid amplification test for the quantitation of Hepatitis C Virus (HCV) RNA in human serum or EDTA plasma. Specimen preparation is automated using the COBAS® AmpliPrep Instrument with amplification and detection automated using the COBAS® TaqMan® Analyzer or the COBAS® TaqMan® 48 Analyzer.

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 is based on three major processes: (1) specimen preparation to isolate HCV RNA; (2) reverse transcription of the target RNA to generate complementary DNA (cDNA) and (3) simultaneous PCR amplification of target cDNA and detection of cleaved dual-labeled oligonucleotide detection probes specific to the target.

Specimen Preparation

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 utilizes automated specimen preparation on the COBAS® AmpliPrep Instrument by a generic silica-based capture technique. The sample input volume is 650 µL, whereas the procedure processes 500 µL of EDTA plasma or serum. The HCV virus particles are lysed by incubation at an elevated temperature with protease and chaotropic lysis/binding buffer to release nucleic acids and protect the released HCV RNA from RNases in serum or EDTA plasma. Protease and a known number of HCV Quantitation Standard (QS) RNA molecules are introduced into each specimen along with the lysis reagent and magnetic glass particles. Subsequently, the mixture is incubated and the HCV RNA and HCV QS RNA are bound to the surface of the magnetic glass particles. Unbound substances, such as salts, proteins and other cellular impurities, are removed by washing the magnetic glass particles. After separating the beads and completing the washing steps, the adsorbed nucleic acids are eluted at elevated temperature with an aqueous solution. The processed specimen, containing the released HCV RNA and HCV QS RNA, is added to the amplification mixture and transferred to the COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer.

Reverse Transcription and PCR Amplification

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 uses reverse transcription of HCV RNA to complementary DNA (cDNA) and PCR amplification of cDNA using primers that define a sequence within the highly conserved region of the 5'-untranslated region of the HCV genome¹7. The nucleotide sequence of the primers has been optimized to yield comparable amplification of HCV genotypes 1 to 6. The reverse transcription and PCR amplification reaction is performed with an optimized blend of thermostable recombinant enzymes: Z05 and Z05D DNA polymerase. In the presence of manganese (Mn²¹) and under the appropriate buffer conditions, Z05 and Z05D have both reverse transcriptase and DNA polymerase activity. This allows both reverse transcription and PCR amplification to occur together with real-time detection of the amplicon.

Processed specimens are added to the amplification mixture in amplification tubes (K-tubes) where both reverse transcription and PCR amplification occur. The reaction mixture is heated to allow a downstream primer to anneal specifically to the HCV target RNA and to the HCV QS RNA. In the presence of Mn²* and excess deoxynucleotide triphosphates (dNTPs), including deoxyadenosine, deoxyguanosine, deoxycytidine and deoxyuridine triphosphates. Z05 and Z05D polymerases extend the annealed primers forming a DNA strand complementary to the RNA target.

Target Amplification

Following reverse transcription of the HCV target RNA and the HCV QS RNA, the Thermal Cycler in the COBAS® TaqMan® Analyzer or COBAS® TaqMan® Analyzer heats the reaction mixture to denature the RNA:cDNA hybrid and to expose the specific primer target sequences. As the mixture cools, the primers anneal to the target cDNA. The thermostable DNA polymerases (Z05 and Z05D) in the presence of Mn²* and excess deoxynucleotide triphosphates (dNTPs), extends the annealed primers along the target template to produce a double-stranded DNA molecule termed an amplicon. The COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer automatically repeats this process for a designated number of cycles, with each cycle intended to double the amount of amplicon DNA. The required number of cycles is preprogrammed into the COBAS® TaqMan® Analyzer or COBAS® TaqMan® Analyzer. Amplification occurs only in the region of the HCV genome between the primers; the entire HCV genome is not amplified.

Selective Amplification

Selective amplification of target nucleic acid from the specimen is achieved in the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 by the use of AmpErase (uracil-N-glycosylase) enzyme and deoxyuridine triphosphate (dUTP). The AmpErase enzyme recognizes and catalyzes the destruction of DNA strands containing deoxyuridine¹ but not DNA containing deoxyuridine beoxyuridine is not present in naturally occurring DNA, but is always present in amplicon due to the use of deoxyuridine triphosphate as one of the dNTPs in the Master Mix reagent; therefore, only amplicon contains deoxyuridine. Deoxyuridine renders contaminating amplicon susceptible to destruction by the AmpErase enzyme prior to amplification of the target DNA. Also, nonspecific product formed after initial activation of the Master Mix by manganese is destroyed by the AmpErase enzyme. The AmpErase enzyme, which is included in the Master Mix reagent, catalyzes the cleavage of deoxyuridine-containing DNA at the deoxyuridine residues by opening the deoxyribose chain at the C1-position. When heated in the first thermal cycling step, the amplicon DNA chain breaks at the position of the deoxyuridine, thereby rendering the DNA non-amplifiable. The AmpErase enzyme remains inactive for a prolonged period of time once exposed to temperatures above 55°C, i.e. throughout the thermal cycling steps, and therefore does not destroy target amplicon formed throughout the duration of the PCR reaction.

Detection of cleaved dual-labeled probes and HCV RNA quantitation

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 utilizes real-time ^{24,25} PCR technology. The use of dual-labeled fluorescent probes allows for real-time detection of PCR product accumulation by monitoring the emission intensity of fluorescent reporter dyes released during the amplification process. The probes consist of HCV and HCV QS-specific oligonucleotide probes with a reporter dye and a quencher dye. In the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0, the HCV and HCV QS probes are labeled with different fluorescent reporter dyes. When these probes are intact, the fluorescence of the reporter dyes is suppressed by the proximity of the quencher dye due to Förster-type energy transfer effects. During PCR, the probe hybridizes to a target sequence and is cleaved by the 5¹ → 3¹ nuclease activity of the thermostable 205 and 205D DNA polymerases. Once the reporter and quencher dyes are released and separated, quenching no longer occurs, and the fluorescent activity of the reporter dye is increased. The amplification of HCV RNA and HCV QS RNA are measured independently at different wavelengths. This process is repeated for a designated number of cycles, each cycle effectively increasing the emission intensity of the individual reporter dyes, permitting independent it dentification of HCV RNA and HCV QS RNA. The PCR cycle where a growth curve starts exponential growth is related to the amount of starting material at the beginning of the PCR.

The quantitation of HCV viral RNA is performed using the HCV QS. It compensates for effects of inhibition and controls the preparation and amplification processes, allowing a more accurate quantitation of HCV RNA in each specimen. The HCV QS is a non-infectious armored RNA (aRNA) construct that contains fragments of HCV sequences with identical primer binding sites as the HCV target RNA and a unique probe binding region that allows HCV QS amplicon to be distinguished from HCV target amplicon.

The HCV QS is added to each specimen at a known copy number and is carried through the specimen preparation, reverse transcription, PCR amplification and detection of cleaved dual-labeled oligonucleotide detection probes. The COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer calculates the HCV RNA concentration in the test specimens by comparing the HCV signal to the HCV QS signal for each specimen and control.

During the extension phase of the PCR on the COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer, the specimens are illuminated and excited by filtered light and the filtered emission fluorescence data are collected for each specimen. The readings from each specimen are then corrected for instrumental fluctuations. These fluorescence readings are sent by the instrument to the AMPLILINK software and stored in a database. Pre-Checks are used to determine if the HCV RNA and HCV QS RNA data represent sets that are valid, and flags are generated when the data lie outside the preset limits. After all Pre-Checks are completed and passed, the fluorescence readings are processed to generate Ct values for the HCV RNA and the HCV QS RNA. The lot-specific calibration constants provided with the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 are generated using calibration material and are used to calculate the titer value for the specimens and controls based upon the difference between the HCV RNA and HCV QS RNA Ct values. The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 is standardized against the WHO International Standard for Hepatritis C Virus RNA for Nucleic Acid Amplification Technology Assays (NIBSC Code 96/798)²²³ and titer results are reported in International Units per milliliter (IU/mL).

REAGENTS

COBAS® AmpliPrep/COBAS® TagMan® 72 Tests **HCVQTV2** HCV Quantitative Test, v2.0 (P/N: 05532264 190) HCV OT v2.0 CS1 1 x 72 Tests (HCV Magnetic Glass Particles Reagent Cassette) 1 x 7.0 mL Magnetic glass particles Tris buffer 0.09% Sodium azide 0.1% Methylparaben HCV QT v2.0 CS2 1 x 72 Tests (HCV Lysis Reagent Cassette) 1 x 78 ml Sodium citrate dihydrate 42.5% Guanidine thiocyanate < 6% Polydocanol 0.9% Dithiothreitol HCV QT v2.0 CS3 1 x 72 Tests HCV Multi-Reagent Cassette containing: 1 x 3.8 ml (Proteinase Solution) Tris buffer < 0.05% EDTA Calcium chloride Calcium acetate < 7.8% Proteinase Glycerol FR 1 x 8.1 mL (Flution Buffer) Tris-base buffer 0.09% Sodium azide

HCV OT v2.0 CS4 1 x 72 Tests HCV Test-Specific Reagent Cassette containing: 1 x 3.6 ml (HCV Quantitation Standard) Tris buffer **FDTA** < 0.002% Poly rA RNA (synthetic) < 0.001% Armored HCV RNA construct containing HCV primer binding sequences and a unique probe binding region (non-infectious RNA in MS2 bacteriophage) 0.05% Sodium azide MMX 1 x 3.5 mL (HCV Master Mix) Tricine buffer Potassium acetate Potassium hydroxide < 20% Dimethyl sulfoxide Glycerol < 0.004% dATP, dCTP, dGTP, dUTP < 0.002% Upstream and downstream HCV primers to the 5' UTR region of HCV < 0.001% Fluorescent-labeled oligonucleotide probes specific for HCV and the HCV Quantitation Standard < 0.001% Oligonucleotide aptamer < 0.05% Z05 and Z05D DNA polymerase (microbial) < 0.1% AmpErase (uracil-N-glycosylase) enzyme (microbial) 0.09% Sodium azide Mn²⁺ 1 x 19.8 ml (Manganese Solution) < 0.5% Manganese acetate Glacial acetic acid 0.09% Sodium azide HCV H(+)C, v2.0 6 x 0.85 ml (HCV High Positive Control) < 0.001% Armored HCV RNA construct containing HCV sequences (non-infectious RNA in MS2 bacteriophage) Negative Human Plasma, non-reactive by tests for antibody to HCV, antibody to HIV-1/2, HIV p24 antigen and HBsAg; HIV-1 RNA. HCV RNA and HBV DNA not detectable by PCR methods 0.1% ProClin® 300 preservative HCV L(+)C, v2.0 6 x 0.85 mL (HCV Low Positive Control) < 0.001% Armored HCV RNA construct containing HCV sequences (non-infectious RNA in MS2 bacteriophage) Negative Human Plasma, non-reactive by tests for antibody to HCV. antibody to HIV-1/2. HIV p24 antigen and HBsAg; HIV-1 RNA. HCV RNA and HBV DNA not detectable by PCR methods 0.1% ProClin® 300 preservative CTM (-) C 6 x 1.0 mL [COBAS® TagMan® Negative Control (Human Plasma)] Negative Human Plasma, non-reactive by tests for antibody to HCV. antibody to HIV-1/2, HIV p24 antigen and HBsAg; HIV-1 RNA, HCV RNA and HBV DNA not detectable by PCR methods 0.1% ProClin® 300 preservative

HCV H(+)C, v2.0 Clip (HCV High Positive Control Barcode Clip) 1 x 6 Clips

HCV L(+)C, v2.0 Clip

(HCV Low Positive Control Barcode Clip)

1 x 6 Clips

HCV (-) C, v2.0 Clip

(HCV Negative Control Barcode Clip)

1 x 6 Clips 1 x 5.1 L

COBAS® AmpliPrep/COBAS® TagMan® Wash Reagent (P/N: 03587797 190)

PG WR

PG WR

(COBAS® AmpliPrep/COBAS® TaqMan® Wash Reagent) Sodium citrate dihydrate < 0.1% N-Methylisothiazolone-HCI

WARNINGS AND PROCEDURAL PRECAUTIONS

As with any test procedure, good laboratory technique is essential to the proper performance of this assay. Due to the high sensitivity of this test, care should be taken to keep reagents and amplification mixtures free of contamination.

- A. FOR IN VITRO DIAGNOSTIC USF.
- B. This test is for use with human serum or plasma collected in the anticoagulant EDTA.
- C. Do not pipet by mouth.
- D. Do not eat, drink or smoke in laboratory work areas. Wear protective disposable gloves, laboratory coats and eye protection when handling specimens and kit reagents. Wash hands thoroughly after handling specimens and test reagents.
- F Avoid microbial and ribonuclease contamination of reagents when removing aliquots from control vials.
- F The use of sterile disposable pipets and RNase-free pipet tips is recommended.
- G Do not pool controls from different lots or from different vials of the same lot.
- н Do not mix reagent cassettes or controls from different kits.
- Do not open COBAS® AmpliPrep cassettes and exchange, mix, remove or add bottles. ı
- J. Dispose of unused reagents, waste and specimens in accordance with country, federal, state and local regulations.
- K. Do not use a kit after its expiration date.
- Safety Data Sheets (SDS) are available on request from your local Roche office.
- M. Specimens and controls should be handled as if infectious using safe laboratory procedures such as those outlined in Biosafety in Microbiological and Biomedical Laboratories 19 and in the CLSI Document M29-A3²⁰. Thoroughly clean and disinfect all work surfaces with a freshly prepared solution of 0.5% sodium hypochlorite in deionized or distilled water.
- CTM (-) C, HCV L(+)C, v2.0 and HCV H(+)C, v2.0 contain Human Plasma derived from human N. blood. The source material has been tested and found non-reactive for the presence of Hepatitis B Surface Antigen (HBsAg), antibodies to HIV-1/2 and HCV, and HIV p24 Antigen. Testing of Negative Human Plasma by PCR methods showed no detectable HIV-1 RNA, HCV RNA or HBV DNA. No known test methods can offer complete assurance that products derived from human blood will not transmit infectious agents. Therefore, all human sourced material, including CTM (-) C. HCV L(+)C, v2.0 and HCV H(+)C, v2.0 should be considered potentially infectious.
- MGP. EB. QS, Mn²⁺ and MMX contain sodium azide. Sodium azide may react with lead and copper 0. plumbing to form highly explosive metal azides. While disposing of sodium azide-containing solutions down laboratory sinks, flush the drains with a large volume of water to prevent azide buildup.

- P. Wear eye protection, laboratory coats and disposable gloves when handling any reagent. Avoid contact of these materials with the skin, eyes or mucous membranes. If contact does occur, immediately wash with large amounts of water. Burns can occur if left untreated. If spills of these reagents occur, dilute with water before wiping dry.
- Q. Do not allow HCV QT v2.0 CS2 and liquid waste including used COBAS® AmpliPrep Sample Processing Units (SPUs) from the COBAS® AmpliPrep Instrument, which contain guanidine thiocyanate, to contact sodium hypochlorite (bleach) solution. These mixtures can produce a highly toxic gas.

STORAGE AND HANDLING REQUIREMENTS

- A. Store HCV QT v2.0 CS1, HCV QT v2.0 CS2, HCV QT v2.0 CS3 and HCV QT v2.0 CS4 at 2-8°C. Unused, these reagents are stable until the expiration date indicated. Once used, these reagents are stable for 70 days at 2-8°C or until the expiration date, whichever comes first. HCV QT v2.0 CS1, HCV QT v2.0 CS3 and HCV QT v2.0 CS4 can be used up to a maximum of 96 hours cumulative on board the COBAS[®] AmpliPrep Instrument. Reagents must be stored at 2-8°C between instrument cycles.
- B. Store HCV H(+)C, v2.0, HCV L(+)C, v2.0 and CTM (-) C at 2-8°C. The controls are stable until the expiration date indicated. Once opened, any unused portion must be discarded.
- C. Store Barcode clips [HCV H(+)C, v2.0 Clip, HCV L(+)C, v2.0 Clip and HCV (-) C, v2.0 Clip] at 2-30°C.
- D. Store PG WR at 2-30°C. Unused PG WR is stable until the expiration date indicated. Once opened, this reagent is stable for 28 days at 2-30°C or until the expiration date, whichever comes first.

MATERIALS PROVIDED

COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0

HCVQTV2

HCV QT v2.0 CS1

(HCV Magnetic Glass Particles Reagent Cassette)

HCV OT v2.0 CS2

(HCV Lysis Reagent Cassette)

HCV QT v2.0 CS3

(HCV Multi-Reagent Cassette)

HCV QT v2.0 CS4

(HCV Test-Specific Reagent Cassette)

HCV H(+)C, v2.0

(HCV High Positive Control)

HCV L(+)C, v2.0

(HCV Low Positive Control)

CTM (-) C

[COBAS® TaqMan® Negative Control (Human Plasma)]

HCV H(+)C, v2.0 Clip

(HCV High Positive Control Barcode Clip)

HCV L(+)C, v2.0 Clip

(HCV Low Positive Control Barcode Clip)

HCV (-) C, v2.0 Clip

(HCV Negative Control Barcode Clip)

COBAS® AmpliPrep/COBAS® TagMan® Wash Reagent

PG WR

PG WR

(COBAS® AmpliPrep/COBAS® TaqMan® Wash Reagent)

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MATERIALS REQUIRED BUT NOT PROVIDED

Instrumentation and Software

- COBAS[®] AmpliPrep Instrument
- COBAS[®] TaqMan[®] Analyzer or COBAS[®] TaqMan[®] 48 Analyzer
- · Docking Station (optional)
- cobas p 630 Instrument (optional)
- AMPLILINK Software Version 3.3 or Version 3.4 Series
- · Control Unit for the AMPLILINK Software, with printer
- Instrument and Software Manuals:
 - COBAS® AmpliPrep Instrument Manual for use with the AMPLILINK Software Version 3.3 and 3.4 Series
 - COBAS® TaqMan® Analyzer Instrument Manual for use with AMPLILINK Software Version 3.3 and 3.4 Series
 - COBAS® TaqMan® 48 Analyzer Instrument Manual for use with the AMPLILINK Software Version 3.3 and 3.4 Series
 - AMPLILINK Software Version 3.3 Series Application Manual for use with COBAS[®] AmpliPrep Instrument, COBAS[®] TaqMan[®] Analyzer, COBAS[®] TaqMan[®] 48 Analyzer, COBAS[®] AMPLICOR Analyzer, and cobas p 630 Instrument

OI

- AMPLILINK Software Version 3.4 Series Application Manual
- Optional: cobas p 630 Instrument Operator's Manual Software Version 2.2
- Test Definition File (TDF). See Product Information Card, provided with the kit, for name and current version of the TDF.

Other Materials

- Sample Rack (SK 24 rack)
- Reagent Rack
- SPU rack
- K-carrier
- K-carrier Transporter
- K-carrier rack
- Pipettors with aerosol barrier or positive displacement RNase-free tips (capacity 1,000 µL); Pipettors should be accurate within 3% of stated volume. Aerosol barrier or positive displacement RNase-free tips must be used to prevent specimen and amplicon cross-contamination.

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- · Disposable gloves, powderless
- Vortex mixer

Disposables

- Sample Processing units (SPUs)
- · Sample input tube (S-tubes) with barcode clips
- Rack of K-tips
- K-tube Box of 12 x 96

SPECIMEN COLLECTION, TRANSPORT AND STORAGE

NOTE: Handle all specimens and controls as if they are capable of transmitting infectious agents.

Specimen Collection and Storage

The CDBAS® AmpliPrep/CDBAS® TaqMan® HCV Quantitative Test. v.20 is for use with serum or EDTA plasma specimens. Blood should be collected in SST® Serum Separation Tubes, BD Vacutaine® PPT™ Plasma Preparation Tubes for Molecular Diagnostic Test Methods or in sterile tubes using EDTA (lavender top) as the anticoagulant. Follow the manufacturer's instructions for handling of collection tubes. Freshly drawn specimens (whole blood) may be stored at 2-25°C for up to 24 hours prior to centifugation. After carrifugation, transfer serum or EDTA plasma to a sterile polypropylene tube. It is recommended that specimens be stored in approximately 1,000 µL aliquots in sterile, 2.0 mL polypropylene screw-cap tubes (such as 2 mL screw cap micro tube from Sarstedt). Serum or EDTA plasma specimens may be stored:

- At 2-8°C for up to 72 hours
- At -20°C to -80°C for up to 6 weeks

Serum and EDTA plasma specimens may be frozen and thawed up to five times without loss of HCV RNA.

Specimen Transport

Transportation of whole blood, serum or EDTA plasma must comply with country, federal, state and local regulations for the transport of etiologic agents²¹. Whole blood must be transported at 2-25°C and centrifuged within 24 hours of collection. EDTA plasma or serum may be transported at 2-8°C or frozen at -20°C to -80°C.

INSTRUCTIONS FOR USE

For detailed operating instructions, a description of the possible configurations, printing results and interpreting flags, comments and error messages, refer to AMPLILINK Software Version 3.3 or Version 3.4 Series manuals, as listed in section Instrumentation and Software.

Batch Size and Workflow

Each kit contains reagents sufficient for 72 tests, which may be performed in batches of 12 to 24 tests. At least one of each control [CTM (-) C, HCV L(+)C, v2.0 and HCV H(+)C, v2.0] must be included in each batch (see "Quality Control" section). The COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer run must be started within 120 minutes following completion of specimen and control preparation. DO NOT FREEZE or STORE processed specimens and controls at 2-8°C.

Specimen and Control Preparation

If using frozen specimens, place the specimens at room temperature until completely thawed and vortex for 3-5 seconds before use. Controls should be removed from 2-8°C storage, equilibrated to ambient temperature and vortexed for 3-5 seconds before use.

COBAS® AmpliPrep Instrument Set-up

Part A. Maintenance and Priming

- A1. The COBAS® AmpliPrep Instrument is ready for operation in stand-by mode.
- A2. Turn the Control Unit for the AMPLILINK software ON. Prepare the Control Unit as follows:
 - 1. Log onto Microsoft Windows Operating System.
 - Double click the AMPLILINK software icon.
 - 3. Log onto AMPLILINK software by entering the assigned User ID and password.
- A3. Check the supply of **PG WR** using the **Status** Screen and replace if necessary.
- A4. Perform all Maintenance that is listed in the **Due** Tab. The COBAS® AmpliPrep Instrument will automatically prime the system.

Part B. Loading of Reagent Cassettes

- NOTE: All reagent cassettes should be removed from 2-8°C storage, immediately loaded onto the COBAS® AmpliPrep Instrument and allowed to equilibrate to ambient temperature on the instrument for at least 30 minutes before the first specimen is to be processed. Do not let reagent cassettes come to ambient temperature outside the instrument as condensation may form on the barcode labels. Do not wine off condensation if it appears on the barcode labels.
- B1. Place HCV QT v2.0 CS1 onto a reagent rack. Place HCV QT v2.0 CS2, HCV QT v2.0 CS3 and HCV QT v2.0 CS4 onto a separate reagent rack.
- B2. Load the reagent rack containing HCV QT v2.0 CS1 onto rack position A of the COBAS® AmpliPrep Instrument.
- B3. Load the reagent rack containing HCV QT v2.0 CS2, HCV QT v2.0 CS3 and HCV QT v2.0 CS4 onto rack position B, C, D or E of the COBAS[®] AmpliPrey Instrument (please refer to the appropriate Instrument Manuals for additional and detailed information).

Part C. Loading of Disposables

NOTE: Determine the number of COBAS® AmpliPrep reagent cassettes, Sample Processing Units (SPUs), Input Sample tubes (S-tubes), K-tips and K-tubes needed. One SPU, one Input S-tube, one K-tip and one K-tube are needed for each specimen or control.

Multiple configurations for use of the COBAS® AmpliPrep Instrument with the COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer are possible. Depending on the configuration used, load the appropriate number of reagent cassette racks, sample racks with Input S-tubes, SPU racks, K-tip racks, K-tube racks and K-carriers on K-carrier racks onto the respective rack positions of the COBAS® AmpliPrep Instrument.

- C1. Place the SPUs in the SPU rack(s) and load the rack(s) onto rack position J, K or L of the COBAS® AmpliPrep Instrument.
- C2. Depending on the configuration used, load full K-tube rack(s) onto rack position **M, N, 0** or **P** of the COBAS® AmpliPrep Instrument.
- C3. Load full K-tip rack(s) onto rack position M, N, O or P of the COBAS® AmpliPrep Instrument.
- C4. Depending on the configuration used, load K-carriers on K-carrier rack(s) onto rack position **M, N, 0** or **P** of the COBAS® AmpliPrep Instrument.

Part D. Ordering and Loading of Specimens

- D1. Prepare sample racks as follows: attach a barcode label clip to each sample rack position where a specimen (S-tube) is to be placed. Attach one of the specific barcode label clips for the controls (CTM (-) C, HCV (1-)C, v2.0 and HCV H(+)C, v2.0] to each sample rack position where the controls (S-tube) are to be placed. The barcode label clips for controls should have the same control lot number as the lot number on the control vials in the kit. Take care in assigning the right control to the position with the appropriate control barcode clip. Place one Input S-tube into each position containing a barcode label clip.
- D2. Using the AMPLILINK software, create specimen orders for each specimen and control in the **Orders** window **Sample** folder. Select the appropriate test file and complete by saving.
- D3. Assign specimen and control orders to sample rack positions in the **Orders** window **Sample Rack** folder. The sample rack number must be for the rack prepared in Step D1.
- D4. Print the Sample Rack Order report to use as a worksheet.
- D5. Prepare specimen and control racks in the designated area for specimen and control addition as follows: Ontrex each specimen and control [CTM (-) C, HCV L(+)C, v2.0 and HCV H(+)C, v2.0] for 3 to 5 seconds. Avoid contaminating gloves when manipulating the specimens and controls.

- D6. Transfer 650 μL of each specimen and control [CTM (-) C, HCV L(+)C, v2.0 and HCV H(+)C, v2.0] to the appropriate barcode labeled Input S-tube using a micropipettor with an aerosol barrier or positive displacement RNase-free tip. Avoid transferring particulates and/or fibrin clots from the original specimen to the Input S-tube. Specimens and controls should be transferred to tube positions as assigned and recorded on the worksheet in step D4. The barcode label plips for controls should have the same control lot number as the lot number on the control vials in the kit. Assign the right control to the position with the appropriate control barcode clip. Avoid contaminating the upper part of the S-tubes with specimens or controls.
- D7. If using the **cobas p** 630 Instrument for preparation of specimens, refer to the **cobas p** 630 Instrument Operators Manual.
- D8. Depending on the configuration used, load the sample rack(s) filled with Input S-tubes onto rack positions **F. G** or **H** of the COBAS® AmpliPrep Instrument.
- D9. Depending on the configuration used, load sample rack(s) with Input S-tubes and K-tubes (one for each Input S-tube, loaded in the right position adjacent to Input S-tubes) onto rack position F, G or H of the COBAS® AnniProp Instrument.

Part E. Start of COBAS® AmpliPrep Instrument Run

E1. Start the COBAS® AmpliPrep Instrument using the AMPLILINK software.

Part F. End of COBAS* AmpliPrep Instrument Run and Transfer to COBAS* TaqMan* Analyzer or COBAS* TaqMan* 48 Analyzer (only for manual transfer)

- F1. Check for flags or error messages.
- F2. Remove processed specimens and controls from the COBAS® AmpliPrep Instrument on either sample racks (for COBAS® TagMan® Analyzer without Docking Station) or K-carrier racks (for COBAS® TagMan® 48 Analyzer), depending on the configuration.
- F3. Remove waste from the COBAS® AmpliPrep Instrument.

NOTE: All processed specimens and controls should not be exposed to light after completion of specimen and control preparation.

Amplification and Detection

COBAS® TagMan® Analyzer or COBAS® TagMan® 48 Analyzer Set-up

The COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer run must be started within 120 minutes following completion of specimen and control preparation. DO NOT FREEZE or STORE processed specimens and controls at 2-8°C.

Part G. Loading Processed Specimens

G1. Depending on the instrument configuration, perform the appropriate steps to transfer the K-tubes to the COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer:

Part H. Start of COBAS® TagMan® Analyzer or COBAS® TagMan® 48 Analyzer Run

H1. Start the COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer depending on the configuration used.

Part I. End of COBAS® TagMan® Analyzer or COBAS® TagMan® 48 Analyzer Run

- 11. At the completion of the COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer run, print Results Report. Check for flags or error messages in the Result report. Specimens with flags and comments are interpreted as described in the Results section. After acceptance, store data in archive.
- 12. Remove used K-tubes from the COBAS® TaqMan® Analyzer or COBAS® TaqMan® 48 Analyzer.

QUALITY CONTROL

One COBAS® TaqMan® Negative Control, one HCV Low Positive Control and one HCV High Positive Control must be included in each test batch. The batch is valid if no flags appear for any of the controls [HCV LC+]C, v2.0, HCV H(+-)C, v2.0 and CTM (--) Ci.

There are no requirements regarding the position of the controls on the sample rack.

Check the batch printout for flags and comments to ensure that the batch is valid.

Negative Control

The CTM (-) C must yield a "Target Not Detected" result. If the CTM (-) C is flagged as invalid, then the entire batch is invalid. Repeat the entire process (specimen and control preparation, amplification and detection). If CTM (-) C is consistently invalid in multiple batches, contact your local Roche office for technical assistance.

Positive Controls

The assigned range for **HCV L(+)C, v2.0** and **HCV H(+)C, v2.0** is specific for each reagent, and is provided on the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 reagent cassette barcodes.

The HCV RNA IU/mL for **HCV L(+)C, v2.0** and **HCV H(+)C, v2.0** should fall within their assigned ranges. If one or both of the positive controls are flagged as invalid, then the entire batch is invalid. Repeat the entire process (specimen and control) preparation, amplification and detection). If the HCV RNA titer of one or both of the positive controls is consistently outside the assigned ranges in multiple batches, contact your local Roche office for technical assistance.

RESULTS

The COBAS* TaqMan* Analyzer or the COBAS* TaqMan* 48 Analyzer automatically determines the HCV RNA concentration for the specimens and controls. The HCV RNA concentration is expressed in International Units (IUI)/mL

AMPLILINK Software:

- . Determines the Ct for the HCV RNA and the HCV QS RNA.
- Determines the HCV RNA concentration based upon the Ct values for the HCV RNA and HCV QS RNA and the lot-specific calibration coefficients provided on the cassette barcodes.
- Determines that the calculated IU/mL for HCV L(+)C, v2.0 and HCV H(+)C, v2.0 fall within the assigned ranges.

Batch Validation:

Check AMPLILINK software results window or printout for flags and comments to ensure that the batch is valid.

For control orders, a check is made to determine if the IU/mL value for the control is within its specified range. If the IU/mL value for the control lies outside of its range, a FLAG is generated to show the control has failed.

The batch is valid if no flags appear for any of the controls [HCV L(+)C, v2.0, HCV H(+)C, v2.0 and CTM (-) C].

The batch is not valid if any of the following flags appear for the HCV Controls:

Negative Control:

| Flag | Result | Interpretation |
|------------|---------|--|
| NC_INVALID | Invalid | An invalid result or the calculated titer result for the negative control is not negative, i.e. the result Target Not Detected is not generated. |

HCV Low Positive Control:

| Flag | Result | Interpretation |
|------------|---------|--|
| LPCINVALID | Invalid | An invalid result or the calculated titer result for the low positive control is not within the assigned range. |

HCV High Positive Control:

| Flag | Result | Interpretation |
|------------|---------|---|
| HPCINVALID | Invalid | An invalid result or the calculated titer result for the high positive control is not within the assigned range. |

If the batch is invalid, repeat the entire batch including specimen and control preparation, reverse transcription, amplification and detection.

Interpretation of Results:

For a valid batch, check each individual specimen for flags or comments on the result printout.

A <u>valid</u> batch may include both valid and invalid specimen results depending on whether flags and/or comments are obtained for the individual specimens.

Specimen results are interpreted as follows:

| Result | Interpretation |
|--|---|
| Target Not Detected | Ct value for HCV is above the limit for the assay or no Ct value for HCV is obtained. Report results as "HCV RNA not detected". |
| < 1.50E+01 IU/mL | Calculated IU/mL is below the Lower Limit of Quantitation (LLOQ) of the assay. Report results as "HCV RNA detected, less than 15 IU/mL HCV RNA". |
| ≥ 1.50E+01 IU/mL and ≤ 1.00E+08 IU/mL | Calculated results greater than or equal to 15 IU/mL and less than or equal to 1.00E+08 IU/mL are within the Linear Range of the assay. Report results as "XX IU/mL HCV RNA detected". |
| > 1.00E+08 IU/mL | Calculated results are above the Linear Range of the assay. Report results as "greater than 1.00E+08 IU/mL HCV RNA". If quantitative results are desired, the original specimen should be diluted with HCV-negative human serum or EDTA plasma, depending on the matrix of the original specimen, and the test repeated. Multiply the reported result by the dilution factor. |

If specimen result display element is "Failed", "Invalid" or "Aborted" please refer to the AMPLILINK software Version 3.3 or Version 3.4 Series Application Manual as listed in section "Materials required but not provided".

NOTE: Specimens above the range of the assay may also produce an invalid result with a flag "QS_INVALID". If quantitative results are desired, the original specimen should be diluted with HCV-negative human serum or EDTA plasma, depending on the matrix of the original specimen, and the test repeated. Multiply the reported result by the dilution factor.

PROCEDURAL LIMITATIONS

- This test has only been validated for use with human serum or plasma collected in EDTA anticoagulant.
 Testing of other specimen types may result in inaccurate results.
- Though rare, mutations within the highly conserved regions of the viral genome covered by the test's primers and/or probes may result in the under-quantitation of or failure to detect the virus.
- Quantitation of HCV RNA is dependent on the number of virus particles present in the specimen and may be affected by specimen collection methods, patient factors (e.g. age, presence of symptoms) and/or stage of infection.
- Reliable results are dependent on adequate specimen collection, transport, storage and processing procedures.
- 5. The presence of AmpErase enzyme in the COBAS® AmpliPrep/COBAS® TaqMan® HCV Master Mix reduces the risk of amplicon contamination. However, contamination from HCV positive controls and clinical specimens can be avoided only by good laboratory practices and careful adherence to the procedures specified in this Package Insert.
- 6. Use of this product should be limited to personnel trained to operate the cobas p 630 Instrument (optional), the COBAS® AmpliPrep Instrument and the COBAS® TaqMan® Analyzer or the COBAS® TaqMan® 48 Analyzer. The operator should have a thorough knowledge of the applications run on the instruments and should follow good laboratory practices.
- This product can only be used with the cobas p 630 Instrument (optional), the COBAS® AmpliPrep Instrument and the COBAS® TaoMan® Analyzer or the COBAS® TaoMan® 48 Analyzer.
- Due to inherent differences between technologies, it is recommended that, prior to switching from one technology to the next users perform method correlation studies in their laboratory to quantify technology differences.

INTERFERING SUBSTANCES

Elevated levels of triglycerides (3,300 mg/dL), conjugated bilirubin (25 mg/dL) and unconjugated bilirubin (20 mg/dL), albumin (6,000 mg/dL), hemoglobin (200 mg/dL) and human DNA (40 mg/dL) in specimens as well as the presence of autoimmune diseases such as Systemic Lupus Erythematosus (SLE), Rheumatoid Arthritis (RA), and Antinuclear Antibody (ANA) did not interfere with the quantitation of HCV RNA by the COBAS[®] AmpliPrep/COBAS[®] TaoMan[®] HCV Quantitative Test. v2.0.

The following drug compounds tested at the Peak Plasma Level (C_{max}) and at 3 times the C_{max} did not interfere with the quantitation of HCV RNA by the COBAS[®] AmpliPrep/COBAS[®] TaqMan[®] HCV Quantitative Test, v2.0:

| Nucleotide Reverse Transcriptase and DNA Polymerase Inhibitors Tenofovir Adefovir dipivoxil | Non-nucleoside Reverse Transcriptase Inhibitors Efavirenz Nevirapine |
|---|---|
| HIV Protease Inhibitors Atazanavir Saquinavir Ritonavir Lopinavir/Ritonavir Nelfinavir Darunavir Tipranavir Fosamprenavir | Nucleoside Reverse Transcriptase Inhibitors Lamivudine Zidovudine Stavudine Abacavir Didanosine Emtricitabine Entecavir Telbivudine |
| HIV Fusion Inhibitor Enfuvirtide | HIV Entry Inhibitor Maraviroc |
| Compounds for the Treatment of Herpes Viruses Ganciclovir Valganciclovir Acyclovir | Immune Modulator Peginterferon alfa-2b Ribavirin Peginterferon alfa-2a |
| HIV Integrase Inhibitor Raltegravir | |

NON-CLINICAL PERFORMANCE EVALUATION

A. Limit of Detection

The limit of detection of the COBAS* AmpliPrep/COBAS* TaqMan* HCV Quantitative Test, v2.0 was determined by analysis of serial dilutions of the WHO International Standard for Hepatitis C Virus RNA for Nucleic Acid Amplification Technology Assays, genotype 1a, obtained from NIBSC, in HCV negative human EDTA plasma or serum. Three independent dilution series were analyzed for each matrix. A total of up to 252 replicates per concentration level were tested for each matrix type. The study was performed with three lots of COBAS* AmpliPrep/COBAS* TaqMan* HCV Quantitative Test, v2.0 reagents.

The results for EDTA plasma and serum are shown in Tables 1 and 2 and demonstrate that the COBAS $^{\infty}$ AmpliPrep/CDBAS $^{\infty}$ TaqNMan HCV Quantitative Test, v2.0 detected HCV RNA at concentrations of 15 IU/mL or qreater with a hit rate of > 99%. The difference between serum and EDTA plasma was not statistically significant.

Table 1 Limit of Detection in EDTA plasma determined with the WHO International Standard for Henatitis C Virus RNA for Nucleic Acid Amplification Technology Assays

| • | | | | | |
|--------------------------------|---|---------------------|---------------|--|--|
| Input Titer (HCV RNA IU/mL) | Number of Valid Replicates | Number of Positives | Hit Rate in % | | |
| 50 | 251 | 251 | 100 | | |
| 25 | 251 | 250 | 100 | | |
| 15 | 251 | 246 | 98 | | |
| 10 | 252 | 236 | 94 | | |
| 5 | 252 | 180 | 71 | | |
| 2.5 | 251 | 121 | 48 | | |
| 0 | 250 0 | | 0 | | |
| LOD by PROBIT at 95 % Hit Rate | 11 IU/mL 95% confidence range: 10 – 13 IU/mL | | | | |
| LOD by Hit Rate | 15 IU/mL | | | | |

Table 2 Limit of Detection in serum determined with the WHO International Standard for Hepatitis C Virus RNA for Nucleic Acid Amplification Technology Assays

| Input Titer (HCV RNA IU/mL) | Number of Valid Replicates | Number of Positives | Hit Rate in % | | |
|--------------------------------|---|---------------------|---------------|--|--|
| 50 | 188 | 188 | 100 | | |
| 25 | 189 | 188 | 99 | | |
| 15 | 189 | 185 | 98 | | |
| 10 | 189 | 172 | 91 | | |
| 5 | 189 | 140 | 74 | | |
| 2.5 | 189 | 92 | 49 | | |
| 0 | 189 0 | | 0 | | |
| LOD by PROBIT at 95 % Hit Rate | 12 IU/mL 95% confidence range: 10 – 14 IU/mL | | | | |
| LOD by Hit Rate | 15 IU/mL | | | | |

B. Precision

Precision of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 was determined by analysis of serial dilutions of clinical HCV specimens (genotype 1a) or of armored HCV RNA (aRNA) in HCV negative human EDTA plasma or in serum.

Six dilution levels were tested in 3 replicates per level in 12 runs on 4 days. Each sample was carried through the entire COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 procedure, including specimen preparation, amplification, and detection. The study was performed with three lots of COBAS® AmpliPrev/COBAS® TaqMan® HCV Quantitative Test, v2.0 reagents, and the results are shown in Table 3.

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 shows good precision for three lots of reagents across a concentration range of 3.0E+02 IU/mL to 1.0E+08 IU/mL.

Table 3
Precision of the COBAS* AmpliPrep/CoBAS* TaqMan* HCV Quantitative Test, v2.0
(EDTA plasma and serum Samples)*

| Nominal | Precision as total SD [log ₁₀] | | | | | | | |
|---------------|--|------------|-------|-------|-------|-------|--|--|
| Concentration | | EDTA Plasm | a | Serum | Serum | | | |
| [IU/mL] | Lot 1 | Lot 2 | Lot 3 | Lot 1 | Lot 2 | Lot 3 | | |
| 3.0E+02 | 0.22 | 0.07 | 0.09 | 0.07 | 0.05 | 0.09 | | |
| 3.0E+03 | 0.15 | 0.07 | 0.07 | 0.06 | 0.06 | 0.06 | | |
| 3.0E+04 | 0.06 | 0.05 | 0.07 | 0.05 | 0.07 | 0.08 | | |
| 3.0E+05 | 80.0 | 0.07 | 80.0 | 0.05 | 0.05 | 0.04 | | |
| 3.0E+06 | 0.14 | 0.04 | 0.07 | 0.11 | 0.06 | 0.07 | | |
| 1.0E+08 | 0.07 | 0.05 | 0.11 | 0.07 | 0.06 | 0.08 | | |

[•] Titer data are considered to be log-normally distributed and are analyzed following log₁₀ transformation. Columns 2-7 present the total standard deviation (SD) of the log-transformed titer for each of the three reagent lots.

C. Linear Range

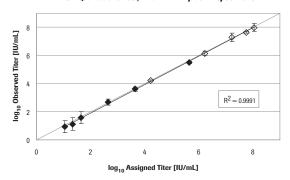
Two linearity panels were used to evaluate the linear range of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0. These panels consisted of dilutions of a HCV RNA positive clinical specimen for the lower and middle part of the dynamic range (up to 3.0E+05 IU/mL) and aRNA for the high end of the dynamic range (up to 2.0E+08 IU/mL) in either EDTA plasma or in serum The study was performed with two lots of COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 reagents in accordance with methods defined in CLSI EP6-A²². All 11 panel members for EDTA plasma and all 14 panel members for serum were tested in up to 16 replicates per concentration level, matrix and reagent lot.

The COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 is linear from 15 HCV RNA IU/mL to at least 1.0E+08 HCV RNA IU/mL using an acceptable absolute deviation from Linearity of +/- 0.2 log₁₀ (see Figures 1 and 2 for representative results). Across the linear range, the accuracy of the test is within +/- 0.2 log₁₀.

Figure 1

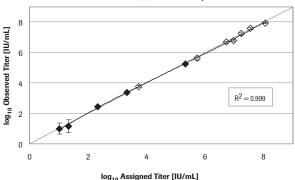
Linear Range Determination for the COBAS* AmpliPrep/COBAS* TaqMan*

HCV Quantitative Test. v2.0 in EDTA plasma Specimens



The regression plot is showing the mean observed sample results for clinical samples (filled diamond) and aRNA samples (open diamond) plotted against the assigned \log_{10} titer. The regression line (bold; from 11 to 1.1E+08 IU/mL) is shown together with the line of unity (grey) in order to visualize the linear behavior of the test. Standard deviation of \log_{10} titer is shown as error bars, the R^2 is presented.

Figure 2 Linear Range Determination for the COBAS* AmpliPrep/COBAS* TaqMan* HCV Quantitative Test, v2.0 in serum Specimens



The regression plot is showing the mean observed sample results for clinical samples (filled diamond) and aRNA samples (open diamond) plotted against the assigned log₁₀ titer. The regression line (black; from 11 to 1.2E+08 IU/mL) is shown together with the line of unity (grey) in order to visualize the linear behavior of the test. Standard deviation of log₁₀ titers is shown as error bars, the R² is presented.

D. Inclusivity

The performance of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 on HCV genotypes was evaluated by (i) verifying the Limit of Detection for genotypes 1 to 6, and (ii) verifying of the Linear Range for genotypes 1 to 6.

Verification of Limit of Detection for genotypes 1 to 6

HCV RNA clinical specimens for 8 different genotypes/subtypes (1a, 1b, 2a, 2b, 3, 4, 5 and 6) were diluted to three different concentration levels in EDTA plasma or serum and a Hit Rate determination was performed for each level with up to 70 replicates. The study was conducted with one lot of COBAS[®] AmpliPrep/COBAS[®] TaoMan[®] HCV Quantitative Test. v2.0 reagents.

The results for EDTA plasma and serum are shown in Tables 4 and 5 and verify that the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 detected HCV RNA for 8 different genotypes/subtypes at concentrations of 15 IU/mL or greater with a hit rate of \geq 95%. The difference between serum and EDTA plasma was not statistically significant.

Table 4
HCV RNA Genotype Verification of Limit of Detection in EDTA plasma

| | 5 IU/mL | | | 15 IU/mL | | | 45 IU/mL | | |
|----------|----------------------------------|------------------------|---------------------|----------------------------------|---------------------------|---------------------|----------------------------------|------------------------|---------------------|
| Genotype | Number of Valid Replicates | Number of Positives | Hit Rate in % | Number of Valid Replicates | Number of Positives | Hit Rate in % | Number of Valid Replicates | Number of Positives | Hit Rate in % |
| 1a | 63 | 44 | 70 | 63 | 63 | 100 | 63 | 63 | 100 |
| 1b | 63 | 47 | 75 | 63 | 62 | 98 | 63 | 63 | 100 |
| 2a | 63 | 43 | 68 | 63 | 61 | 97 | 62 | 61 | 98 |
| 2b | 62 | 57 | 92 | 62 | 62 | 100 | 62 | 62 | 100 |
| 3 | 62 | 58 | 94 | 63 | 63 | 100 | 62 | 62 | 100 |
| 4 | 63 | 43 | 68 | 63 | 62 | 98 | 63 | 63 | 100 |
| 5 | 63 | 47 | 75 | 62 | 62 | 100 | 62 | 62 | 100 |
| 6 | 63 | 55 | 87 | 63 | 62 | 98 | 63 | 63 | 100 |

Table 5
HCV RNA Genotype Verification of Limit of Detection in serum

| | 5 IU/mL | | | 15 IU/mL | | | 45 IU/mL | | |
|----------|----------------------------------|-----------|---------------------|----------------------------------|---------------------------|---------------------|----------------------------------|----|---------------------|
| Genotype | Number of Valid Replicates | Docitivos | Hit Rate in % | Number of Valid Replicates | Number of Positives | Hit Rate in % | Number of Valid Replicates | | Hit Rate in % |
| 1a | 63 | 45 | 71 | 62 | 62 | 100 | 63 | 63 | 100 |
| 1b | 62 | 48 | 77 | 63 | 63 | 100 | 63 | 63 | 100 |
| 2a | 63 | 47 | 75 | 61 | 60 | 98 | 63 | 63 | 100 |
| 2b | 63 | 42 | 67 | 63 | 61 | 97 | 63 | 63 | 100 |
| 3 | 63 | 58 | 92 | 63 | 63 | 100 | 63 | 63 | 100 |
| 4 | 63 | 41 | 65 | 63 | 62 | 98 | 63 | 63 | 100 |
| 5 | 62 | 46 | 74 | 61 | 60 | 98 | 62 | 62 | 100 |
| 6 | 70 | 58 | 83 | 70 | 69 | 99 | 69 | 69 | 100 |

Verification of Linear Range for Genotypes 1 to 6

HCV clinical specimens for 8 different genotypes/subtypes (1a, 1b, 2a, 2b, 3, 4, 5 and 6) were tested in up to 22 concentration levels. These panels consisted of dilutions of HCV RNA positive clinical genotype specimens for the lower and middle part of the dynamic range and genotype specific aRNA for the high end of the dynamic range (genotypes 1a, 1b, 3 and 4 up to the upper limit of quantitation) or across the complete dynamic range (genotypes 2a, 2b, 5 and 6) in EDTA plasma. The study was performed with one lot of COBAS* AmpliPrep/COBAS* TaqMan* HCV Quantitative Test, v2.0 reagents. All 22 panel members were tested in up to 15 replicates.

The Linear Range of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 was verified with HCV genotypes 1 to 6 from 13 HCV RNA IU/mL to at least 1.4E+08 HCV RNA IU/mL using an acceptable absolute deviation from Linearity of +/- 0.2 log₁₀-

E. Diagnostic Sensitivity

The diagnostic sensitivity of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 was determined by analyzing individual HCV RNA positive EDTA plasma or serum samples (488 total results) with two lots of COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 reagents. All specimens tested positive for HCV RNA. In this panel, the diagnostic sensitivity of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 is 100% (one sided lower 95% confidence limit: > 99.4%).

F. Specificity

The specificity of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 was determined by analyzing HCV RNA- and sero-negative EDTA plasma or serum samples from blood donors. Individual EDTA plasma and serum specimens (600 total results) were tested with two lots of COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 reagents. All specimens tested negative for HCV RNA. In this panel, the specificity of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 is 100% (one sided lower 95% confidence limit: > 99.5%).

G. Analytical Specificity

The analytical specificity of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 was evaluated by diluting high titer stocks of different pathogens (see Table 6) with HCV RNA positive and HCV RNA negative clinical EDTA plasma specimens. None of the non-HCV pathogens interfered with test performance, or showed a false positive result in the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0.

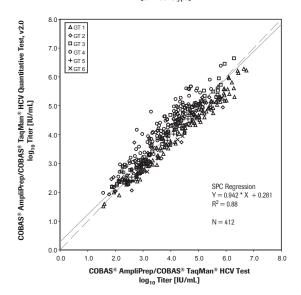
Table 6 Analytical Specificity Specimens

| Non-HCV Flaviviruses West Nile Virus St. Louis Encephalitis Virus Murray Valley Encephalitis Virus Dengue Virus types 1, 2, 3 and 4 Yellow Fever Virus Zika Virus FSME Virus (strain HYPR) | Viruses Adenovirus Type 5 Cytomegalovirus Epstein-Barr Virus Hepatitis B Virus Hepatitis A Virus HIV-1 Human T-Cell Lymphotropic Virus types 1 and 2 |
|--|--|
| Bacteria Propionibacterium acnes Staphylococcus aureus Yeast Candida albicans | Human Herpes Virus type 6 Herpes Simplex Virus types 1 and 2 Influenza A Human Papillomavirus Varicella Zoster Virus |

H. Performance Compared to COBAS® AmpliPrep / COBAS® TaqMan® HCV Test

The performance of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 and the COBAS® AmpliPrep/COBAS® TaqMan® HCV Test were compared by analysis of serum and EDTA plasma specimens from HCV infected patients (diluted and undiluted). A total of 412 EDTA plasma and serum specimens across all genotypes, analyzed in duplicate, were valid and within the quantitation range of both tests. Deming regression and Bland Altman analysis was performed. The results for Deming Regression are shown in Figure 3.

Figure 3
Correlation of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0
and the COBAS® AmpliPrep/COBAS® TaqMan® HCV Test
(GT=Genotype)



The Deming Regression analysis was performed. The R-squared value was 0.88 for all samples and 0.94, if samples for genotype 4 were excluded from the analysis. After Bland-Altman analysis, the correlation showed a mean log₁₀ titer difference of 0.1 (all samples analyzed) or -0.1 (samples for genotype 4 excluded), respectively.

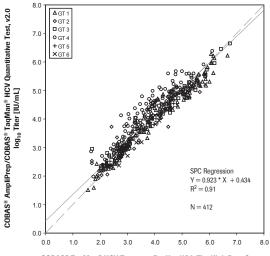
I. Performance Compared to COBAS® TaqMan® HCV Test v2.0 for Use With High Pure System

The performance of the COBAS® AmpliPrep/COBAS® TaqMan® HCV Quantitative Test, v2.0 and the COBAS® TaqMan® HCV Test v2.0 for Use With High Pure System were compared by analysis of serum and EDTA plasma specimens from HCV infected patients. A total of 412 EDTA plasma and serum specimens across all genotypes, analyzed in duplicate, were valid and within the quantitation range of both tests. Deming regression and Bland Altman analysis was performed. The results for Deming Regression are shown in Figure 4.

Figure 4

Correlation of the COBAS* AmpliPrep/COBAS* TaqMan* HCV Quantitative Test, v2.0 and the COBAS* TaqMan* HCV Test, v2.0 For Use With The High Pure System

(GT=Genotype)



COBAS* TaqMan* HCV Test, v2.0 For Use With The High Pure System \log_{10} Titer [IU/mL]

The Deming Regression analysis was performed and the R-squared value was 0.91. After Bland-Altman analysis, the correlation showed a mean \log_{10} titer difference of 0.1.

REFERENCES

- Choo Q-L, Kuo G, Weiner AJ, Overby LR., Bradley DW and Houghton M. 1989. Isolation of a cDNA clone derived from a blood-borne non-A, non-B viral hepatitis viral genome. Science 244:359-362.
- Armstrong GL, Wasley A, Simard EP et al. 2006. The prevalence of hepatitis C virus infection in the United States, 1999 through 2002. Ann Intern Med 144:705-714.
- Rustgi VK. 2007. The epidemiology of hepatitis C infection in the United States. J Gastroenterol 42:513-521.
- Lauer GM, Walker BD. 2001. Hepatitis C virus infection. N Engl J Med 345:41-52.
- Caruntu FA, Benea L. 2006. Acute hepatitis C virus infection: Diagnosis pathogenesis, treatment. JGLD 15:249-256.
- Mc Hutchison JG, Gordon SC, Schiff ER et al. 1998. Interferon alfa-2b alone or in combination with ribavirin as initial treatment for chronic hepatitis C. N Engl J Med 339:1485-1492.
- Davis GL, Esteban-Mur R, Rustgi V et al. 1998. Interferon alfa-2b alone or in combination with ribavirin for the treatment of relapse of chronic hepatitis C. N Engl J Med 339:1493-1499.
- Manns MP, McHutchinson JG, Gordon SC et al. 2001. Peginterferon alfa-2b plus ribavirin compared with interferon alfa-2b plus ribavirin for initial treatment of chronic hepatitis C: a randomized trial. Lancet 358:958-965.
- Fried MW, Shiffman ML, Reddy KR et al. 2002. Peginterferon alfa-2a plus ribavirin for chronic hepatitis C virus infection. N Engl J Med 347:975-982.
- Hadziyannis SJ, Sette H Jr., Morgan TR et al. 2004. Peginterferon-[alpha] 2a and ribavirin combination therapy in chronic hepatitis C: a randomized study of treatment duration and ribavirin dose. *Ann Intern* Med 140:346-355.
- Ghany MG, Strader DB, Thomas DL et al. 2009. Diagnosis management and treatment of hepatitis C: an update. Hepatology 49:1335-1374.
- 12. NIH Consensus and State-of-the-Science Statements. Management of Hepatitis C. 2002. 19:1-46.
- EASL International Consensus Conference on Hepatitis C. Consensus Statement. 1999. Hepatology 30:956-961.
- Jensen DM, Morgan TR, Marcellin P et al. 2006. Early identification of HCV genotype 1 patients responding to 24 weeks peginterferon alpha-2a (40 kd)/ribavirin therapy. Hepatology 43:954-960.
- Poordad F, McCone J Jr., Bacon BR et al. 2011. Boceprevir for untreated chronic HCV genotype 1 infection. N Engl J Med 364:1195-1206.
- Jacobson IM, McHutchison JG, Dusheiko G et al. 2011. Telaprevir for previously untreated chronic hepatitis C virus infection. N Engl J Med 364:2405-2416.
- Bukh J, Purcell RH and Miller RH. 1992. Sequence analysis of the 5' noncoding region of hepatitis C virus. Proc Natl Acad Sci USA 89:4942-4946.
- Longo MC, Berninger MS and Hartley JL. 1990. Use of uracil DNA glycosylase to control carry-over contamination in polymerase chain reactions. Gene 93:125-128.
- U.S. Department of Health and Human Services. Biosafety in Microbiological and Biomedical Laboratories. 5th Edition, HHS Publication No. (CDC) 21-1112; December 2009.
- Clinical and Laboratory Standards Institute. Protection of Laboratory Workers from Occupationally Acquired Infections: Approved Guideline – 3rd Edition. CLSI Document M29-A3. CLSI: Wayne, PA 2005.

- 21. International Air Transport Association. Dangerous Goods Regulations, 49th Edition. 2008.
- Clinical and Laboratory Standards Institute. Evaluation of the Linearity of Quantitative Measurement Procedures: A Statistical Approach; Approved Guideline. CLSI Document EP6-A. CLSI: Wayne, PA 2002.
- Saldanha, J., Heath, A., Aberham, C., Albrech, J., Gentili, G., Gessner, M. and Pisani, G. 2005. World Health Organization collaborative study to establish a replacement WHO international standard for hepatitis C virus RNA nucleic acid amplification technology assays. Vox Sanguinis 88:202-204.
- Higuchi, R., Dollinger, G., Walsh, P.S., and Griffith, R. 1992. Simultaneous amplification and detection of specific DNA sequences. Bio-Technology 10:413-417.
- Heid, C.A., Stevens, J., Livak, J.K., and Williams, P.M. 1996. Real time quantitative PCR. Genome Research 6:986-994.

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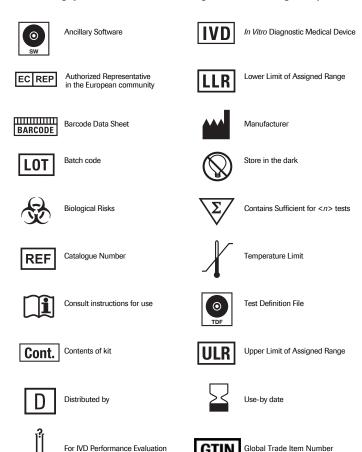
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