

Primerdesign™ Ltd

# Human Rhinovirus 16

Polyprotein gene

genesig® Advanced Kit

150 tests

GENESIG

Kits by Primerdesign

For general laboratory and research use only

# Introduction to Human Rhinovirus 16

Rhinovirus is a genus of the Picornaviridae family of viruses. Rhinoviruses are the most common viral infective agents in humans and are a causative agent of the common cold, being responsible for approximately 50% of all cases. Rhinoviruses have linear, single-stranded, positive-sense RNA genomes of between 7.2 and 8.5 kb in length. At the 5' end of the genome is a virus-encoded protein, and like mammalian mRNA, there is a 3' poly-A tail. Structural proteins are encoded in the 5' region of the genome and non structural at the 3' end. The viral particles themselves are not enveloped and are icosahedral in structure with a diameter of approximately 30nm.

Rhinoviruses are composed of a capsid that contains four viral proteins VP1, VP2, VP3 and VP4. VP1, VP2, and VP3 form the major part of the protein capsid. The much smaller VP4 protein has a more extended structure and lies at interface between the capsid and the RNA genome. There are 60 copies of each of these proteins assembled as an icosahedron. Antibodies are a major defense against infection with the epitopes lying on the exterior regions of VP1-VP3.

Rhinoviruses have two main modes of transmission: direct transmission via inhalation of aerosolised respiratory droplets and indirect transmission via contact with surfaces contaminated with respiratory droplets. The viral capsid proteins bind to specific nasal cell receptors mediating entry into the host cell. Intracellular enzymes then digest the viral capsid leaving only the genome which functions as a template for the synthesis of the complementary strand. This encodes the viral capsid proteins for new viral particles as well as being packaged into these. The newly synthesised virus buds off from the host cell membrane facilitating infection of other cells.

Rhinoviruses occur worldwide causing disease with symptoms such as fever, cough, and nasal congestion which are the result of the immune system's response to the virus. The frequency of colds is high in childhood and decreases during adulthood most probably because of the possession of immunity.

There are many HRV serotypes which, based on differences in their surface proteins and genome sequences have been segregated into two different groups: Human Rhinovirus A and B although some serotypes remain unclassified. HRV16 belongs to the HRVA species.

# Specificity

The Primerdesign genesig Kit for Human Rhinovirus 16 (HRV16) genomes is designed for the in vitro quantification of HRV16 genomes. The kit is designed to have the broadest detection profile possible whilst remaining specific to the HRV16 genome.

The primers and probe sequences in this kit have 100% homology with a broad range of HRV16 sequences based on a comprehensive bioinformatics analysis.

Our kit for human rhinovirus 16 has been designed for the specific and exclusive in vitro quantification of this subtype and does not detect other human rhinovirus strains. The primers and probe sequences in this kit have 100% homology with a broad range of clinically relevant reference sequences based on a comprehensive bioinformatics analysis.

If you require further information, or have a specific question about the detection profile of this kit then please send an e.mail to [enquiry@primerdesign.co.uk](mailto:enquiry@primerdesign.co.uk) and our bioinformatics team will answer your question.

# Kit contents

- HRV16 specific primer/probe mix (150 reactions **BROWN**)  
FAM labelled
- HRV16 positive control template (for Standard curve **RED**)
- Internal extraction control primer/probe mix (150 reactions **BROWN**)  
VIC labelled as standard
- Internal extraction control RNA (150 reactions **BLUE**)
- Endogenous control primer/probe mix (150 reactions **BROWN**)  
FAM labelled
- HRV16/Internal extraction control/endogenous control RT primer mix (150 reactions **GREEN**)  
Required for two step protocol only
- RNase/DNase free water (**WHITE**)  
for resuspension of primer/probe mixes
- Template preparation buffer (**YELLOW**)  
for resuspension of internal control template, positive control template and standard curve preparation

## Reagents and equipment to be supplied by the user

### Real-time PCR Instrument

#### RNA extraction kit

This kit is recommended for use with genesig Easy. DNA/RNA Extraction kit. However, it is designed to work well with all processes that yield high quality RNA with minimal PCR inhibitors.

#### oasig™ lyophilised OneStep or Precision®PLUS OneStep 2X RT-qPCR Master Mix

Contains complete OneStep RT-qPCR master mix

#### Pipettors and Tips

#### Vortex and centrifuge

#### Thin walled 1.5 ml PCR reaction tubes

## Kit storage and stability

This kit is stable at room temperature but should be stored at -20°C on arrival. Once the lyophilised components have been resuspended they should not be exposed to temperatures above -20°C for longer than 30 minutes at a time and unnecessary repeated freeze/thawing should be avoided. The kit is stable for six months from the date of resuspension under these circumstances.

If a standard curve dilution series is prepared this can be stored frozen for an extended period. If you see any degradation in this serial dilution a fresh standard curve can be prepared from the positive control.

Primerdesign does not recommend using the kit after the expiry date stated on the pack.

## Suitable sample material

All kinds of sample material suited for PCR amplification can be used. Please ensure the samples are suitable in terms of purity, concentration, and RNA/DNA integrity (An internal PCR control is supplied to test for non specific PCR inhibitors). Always run at least one negative control with the samples. To prepare a negative-control, replace the template RNA sample with RNase/DNase free water.

## Dynamic range of test

Under optimal PCR conditions genesig HRV16 detection kits have very high priming efficiencies of >95% and can detect less than 100 copies of target template.

## Notices and disclaimers

This product is developed, designed and sold for research purposes only. It is not intended for human diagnostic or drug purposes or to be administered to humans unless clearly expressed for that purpose by the Food and Drug Administration in the USA or the appropriate regulatory authorities in the country of use. During the warranty period Primerdesign genesig detection kits allow precise and reproducible data recovery combined with excellent sensitivity. For data obtained by violation to the general GLP guidelines and the manufacturer's recommendations the right to claim under guarantee is expired. PCR is a proprietary technology covered by several US and foreign patents. These patents are owned by Roche Molecular Systems Inc. and have been sub-licensed by PE Corporation in certain fields. Depending on your specific application you may need a license from Roche or PE to practice PCR. Additional information on purchasing licenses to practice the PCR process may be obtained by contacting the Director of Licensing at Roche Molecular Systems, 1145 Atlantic Avenue, Alameda, CA 94501 or Applied Biosystems business group of the Applied Biosystems Corporation, 850 Lincoln Centre Drive, Foster City, CA 94404. In addition, the 5' nuclease assay and other homogeneous amplification methods used in connection with the PCR process may be covered by U.S. Patents 5,210,015 and 5,487,972, owned by Roche Molecular Systems, Inc. and by U.S. Patent 5,538,848, owned by The Perkin-Elmer Corporation.

## Trademarks

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The PCR process is covered by US Patents 4,683,195, and 4,683,202 and foreign equivalents owned by Hoffmann-La Roche AG. BI, ABI PRISM® GeneAmp® and MicroAmp® are registered trademarks of the Applied Biosystems (Applied Biosystems Corporation). BIOMEK® is a registered trademark of Beckman Instruments, Inc.; iCycler™ is a registered trademark of Bio-Rad Laboratories, Rotor-Gene is a trademark of Corbett Research. LightCycler™ is a registered trademark of the Idaho Technology Inc. GeneAmp®, TaqMan® and AmpliTaqGold® are registered trademarks of Roche Molecular Systems, Inc., The purchase of the Primerdesign™ reagents cannot be construed as an authorization or implicit license to practice PCR under any patents held by Hoffmann-La Roche Inc.

# Principles of the test

## Real-time PCR

A HRV16 specific primer and probe mix is provided and this can be detected through the FAM channel.

The primer and probe mix provided exploits the so-called TaqMan® principle. During PCR amplification, forward and reverse primers hybridize to the HRV16 cDNA. A fluorogenic probe is included in the same reaction mixture which consists of a DNA probe labeled with a 5`-dye and a 3`-quencher. During PCR amplification, the probe is cleaved and the reporter dye and quencher are separated. The resulting increase in fluorescence can be detected on a range of qPCR platforms.

## OneStep vs. Two step real-time PCR

When detecting/quantifying the presence of a target with an RNA genome Primerdesign recommend the use of a OneStep RT-qPCR protocol. OneStep RT-qPCR combines the reverse transcription and qPCR reaction in a simple closed tube protocol. This saves significant bench time but also reduces errors. The sensitivity of a OneStep protocol is also greater than a two step because the entire biological sample is available to the PCR without dilution. This kit will also work well with a two step approach (Precision nanoScript2 reverse transcription kit and PrecisionPLUS Master Mix) if required but the use of oasig OneStep or PrecisionPLUS OneStep Master Mix is the preferred method.

## Positive control

For copy number determination and as a positive control for the PCR set up, the kit contains a positive control template.

This can be used to generate a standard curve of HRV16 copy number / Cq value. Alternatively the positive control can be used at a single dilution where full quantitative analysis of the samples is not required. Each time the kit is used, at least one positive control reaction must be included in the run. A positive result indicates that the primers and probes for detecting the target HRV16 gene worked properly in that particular experimental scenario. If a negative result is obtained the test results are invalid and must be repeated. Care should be taken to ensure that the positive control does not contaminate any other kit component which would lead to false-positive results. This can be achieved by handling this component in a Post PCR environment. Care should also be taken to avoid cross-contamination of other samples when adding the positive control to the run. This can be avoided by sealing all other samples and negative controls before pipetting the positive control into the positive control well.

## Negative control

To validate any positive findings a negative control reaction should be included every time the kit is used. For this reaction the RNase/DNase free water should be used instead of template. A negative result indicates that the reagents have not become contaminated while setting up the run.

### **Internal RNA extraction control**

When performing RNA extraction, it is often advantageous to have an exogenous source of RNA template that is spiked into the lysis buffer. This control RNA is then co-purified with the sample RNA and can be detected as a positive control for the extraction process. Successful co-purification and qPCR for the control RNA also indicates that PCR inhibitors are not present at a high concentration.

A separate RT primer mix and a qPCR primer/probe mix are supplied with this kit to detect the exogenous RNA using qPCR. The PCR primers are present at PCR limiting concentrations which allows multiplexing with the target sequence primers. Amplification of the control cDNA does not interfere with detection of the HRV16 target cDNA even when present at low copy number. The Internal control is detected through the VIC channel and gives a Cq value of 28+/-3 depending on the level of sample dilution.

### **Endogenous control**

To confirm extraction of a valid biological template, a primer and probe mix is included to detect an endogenous gene. Detection of the endogenous control is through the FAM channel and it is NOT therefore possible to perform a multiplex with the HRV16 primers. A poor endogenous control signal may indicate that the sample did not contain sufficient biological material.

## Resuspension protocol

To minimize the risk of contamination with foreign DNA, we recommend that all pipetting be performed in a PCR clean environment. Ideally this would be a designated PCR lab or PCR cabinet. Filter tips are recommended for all pipetting steps.

- 1. Pulse-spin each tube in a centrifuge before opening.**  
This will ensure lyophilised primer and probe mix is in the base of the tube and is not spilt upon opening the tube.
- 2. Resuspend the primer/probe mixes in the RNase/DNase free water supplied, according to the table below:**  
To ensure complete resuspension, vortex each tube thoroughly.

Component - resuspend in water	Volume
<b>Pre-PCR pack</b>	
HRV16 primer/probe mix (BROWN)	165 µl
Internal extraction control primer/probe mix (BROWN)	165 µl
HRV16 RT primer mix (GREEN)	165 µl
Endogenous control primer/probe mix (BROWN)	165 µl

- 3. Resuspend the internal control template and positive control template in the template preparation buffer supplied, according to the table below:**  
To ensure complete resuspension, vortex each tube thoroughly.

Component - resuspend in template preparation buffer	Volume
<b>Pre-PCR heat-sealed foil</b>	
Internal extraction control RNA (BLUE)	600 µl
<b>Post-PCR heat-sealed foil</b>	
HRV16 Positive Control Template (RED) *	500 µl

\* This component contains high copy number template and is a VERY significant contamination risk. It must be opened and handled in a separate laboratory environment, away from the other components.

## RNA extraction

The internal extraction control RNA can be added either to the RNA lysis/extraction buffer or to the RNA sample once it has been resuspended in lysis buffer.

**DO NOT add the internal extraction control RNA directly to the unprocessed biological sample as this will lead to degradation and a loss in signal.**

- 1. Add 4µl of the Internal extraction control RNA (BLUE) to each sample in RNA lysis/extraction buffer per sample.**
- 2. Complete RNA extraction according to the manufacturer's protocols.**



# OneStep RT-qPCR detection protocol

A OneStep approach combining the reverse transcription and amplification in a single closed tube is the preferred method. If however, a two step approach is required see page 11.

## For optimum performance and sensitivity.

All pipetting steps and experimental plate set up should be performed on ice. After the plate is poured proceed immediately to the OneStep amplification protocol. Prolonged incubation of reaction mixes at room temperature can lead to PCR artifacts that reduce the sensitivity of detection.

1. **For each RNA sample prepare a reaction mix according to the table below: Include sufficient reactions for positive and negative controls.**

Component	Volume
oasig OneStep or PrecisionPLUS OneStep 2X RT-qPCR Master Mix	10 µl
HRV16 primer/probe mix (BROWN)	1 µl
Internal extraction control primer/probe mix (BROWN)	1 µl
RNase/DNase free water (WHITE)	3 µl
<b>Final Volume</b>	<b>15 µl</b>

2. **For each RNA sample prepare an endogenous control reaction according to the table below (optional):**  
This control reaction will provide crucial information regarding the quality of the biological sample.

Component	Volume
oasig OneStep or PrecisionPLUS OneStep 2X RT-qPCR Master Mix	10 µl
Endogenous control primer/probe mix (BROWN)	1 µl
RNase/DNase free water (WHITE)	4 µl
<b>Final Volume</b>	<b>15 µl</b>

3. **Pipette 15µl of these mixes into each well according to your qPCR experimental plate set up.**
4. **Pipette 5µl of RNA template into each well, according to your experimental plate set up.**  
For negative control wells use 5µl of RNase/DNase free water. The final volume in each well is 20µl.

5. If a standard curve is included for quantitative analysis prepare a reaction mix according to the table below:

Component	Volume
oasig OneStep or PrecisionPLUS OneStep 2X RT-qPCR Master Mix	10 µl
HRV16 primer/probe mix (BROWN)	1 µl
RNase/DNase free water (WHITE)	4 µl
<b>Final Volume</b>	<b>15 µl</b>

6. Preparation of standard curve dilution series.

- 1) Pipette 90µl of template preparation buffer into 5 tubes and label 2-6
- 2) Pipette 10µl of Positive Control Template (RED) into tube 2
- 3) Vortex thoroughly
- 4) Change pipette tip and pipette 10 µl from tube 2 into tube 3
- 5) Vortex thoroughly

Repeat steps 4 and 5 to complete the dilution series

Standard Curve	Copy Number
Tube 1 Positive control (RED)	$2 \times 10^5$ per µl
Tube 2	$2 \times 10^4$ per µl
Tube 3	$2 \times 10^3$ per µl
Tube 4	$2 \times 10^2$ per µl
Tube 5	20 per µl
Tube 6	2 per µl

7. Pipette 5µl of standard template into each well for the standard curve according to your plate set-up

The final volume in each well is 20µl.

## OneStep RT-qPCR Amplification Protocol

Amplification conditions using oasig OneStep or PrecisionPLUS OneStep 2X RT-qPCR Master Mix.

	Step	Time	Temp
	Reverse Transcription	10 min	55 °C
	Enzyme activation	2 min	95 °C
Cycling x50	Denaturation	10 s	95 °C
	<b>DATA COLLECTION *</b>	60 s	60 °C

\* Fluorogenic data should be collected during this step through the FAM and VIC channels

# Alternative two step qPCR detection protocol

## Reverse Transcription

If you need to perform separate reverse transcription and amplification (two step real time PCR) then we recommend the Primerdesign Precision nanoScript2 Reverse Transcription kit. A reverse transcription primer (GREEN) is included and is designed for use with the Precision nanoScript2 reverse transcription kit. A protocol for this product is available at [www.primerdesign.co.uk](http://www.primerdesign.co.uk)

1. After reverse transcription, prepare a reaction mix according to the table below for each cDNA sample

Component	Volume
PrecisionPLUS 2X qPCR Master Mix	10 µl
HRV16 primer/probe mix (BROWN)	1 µl
Internal extraction control primer/probe mix (BROWN)	1 µl
RNase/DNase free water (WHITE)	3 µl
<b>Final Volume</b>	<b>15 µl</b>

2. Pipette 15µl of this mix into each well according to your qPCR experimental plate set up.
3. Prepare sample cDNA templates for each of your samples by diluting the RT reaction mix 1:5 in RNase/DNase free water.
4. Pipette 5µl of cDNA template into each well, according to your experimental plate setup.  
The final volume in each well is 20µl. For negative control wells use 5µl of RNase/DNase free water.

# Alternative two step amplification protocol

Amplification conditions using PrecisionPLUS 2X qPCR Master Mix.

	Step	Time	Temp
	Enzyme activation	2 mins	95 °C
Cycling x50	Denaturation	10 secs	95 °C
	DATA COLLECTION *	60 secs	60 °C

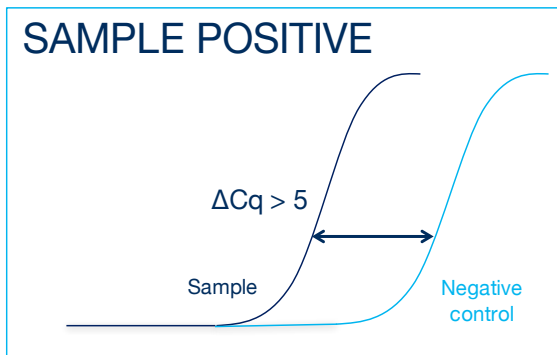
\* Fluorogenic data should be collected during this step through the FAM and VIC channels

# Interpretation of results

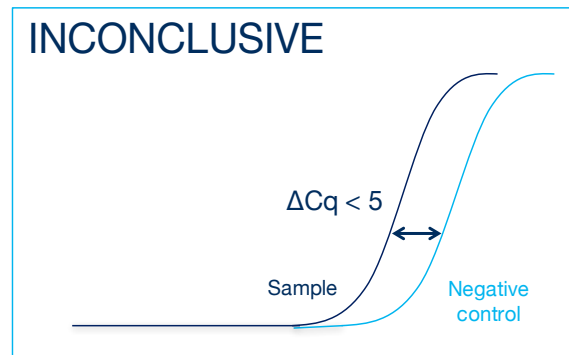
Target (FAM)	Internal control (VIC)	Positive control	Negative control	Interpretation
$\leq 30$	+ / -	+	-	<b>POSITIVE QUANTITATIVE RESULT</b> calculate copy number
$> 30$	+	+	-	<b>POSITIVE QUANTITATIVE RESULT</b> calculate copy number
$> 30$	-	+	-	<b>POSITIVE QUALITATIVE RESULT</b> do not report copy number as this may be due to poor sample extraction
-	+	+	-	<b>NEGATIVE RESULT</b>
+ / -	+ / -	+	$\leq 35$	<b>EXPERIMENT FAILED</b> due to test contamination
+ / -	+ / -	+	$> 35$	*
-	-	+	-	<b>SAMPLE PREPARATION FAILED</b>
+ / -	+ / -	-	+ / -	<b>EXPERIMENT FAILED</b>

Positive control template (**RED**) is expected to amplify between Cq 16 and 23. Failure to satisfy this quality control criterion is a strong indication that the experiment has been compromised.

\*Where the test sample is positive and the negative control is positive with a Cq  $> 35$ , the sample must be reinterpreted based on the relative signal strength of the two results:



If the sample amplifies  $> 5$  Cq earlier than the negative control then the sample should be reinterpreted (via the table above) with the negative control verified as negative.



If the sample amplifies  $< 5$  Cq earlier than the negative control then the positive sample result is invalidated and the result should be determined inconclusive due to test contamination. The test for this sample should be repeated.

**Internal PCR control**

The Cq value obtained with the internal control will vary significantly depending on the extraction efficiency, the quantity of RNA added to the RT and PCR reaction and the individual machine settings. Cq values of  $28 \pm 3$  are within the normal range. When amplifying a HRV16 sample with a high genome copy number, the internal extraction control may not produce an amplification plot. This does not invalidate the test and should be interpreted as a positive experimental result.

**Endogenous control**

The signal obtained from the endogenous control primer and probe set will vary according to the amount of biological material present in a given sample. An early signal indicates the presence of a good yield of biological material. A late signal suggests that little biological material is present in the sample.