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For Professional Use Only

GUIDELINES
to AmpliSens[®] *HHV7*-screen/monitor-FRT PCR kit
using the PCR instruments with real-time
hybridization-fluorescence detection

AmpliSens[®]



Federal Budget Institute of
Science "Central Research
Institute for Epidemiology"
3A Novogireevskaya Street
Moscow 111123 Russia

Not for use in the Russian Federation
For research use only. Not for diagnostic procedures

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INTENDED USE

The guidelines describe the procedure of using **AmpliSens® HHV7-screen/monitor-FRT** PCR kit using the following PCR instruments with real-time hybridization-fluorescence detection:

- Rotor-Gene 3000, Rotor-Gene 6000 (Corbett Research, Australia);
- Rotor-Gene Q (QIAGEN, Germany);
- CFX96 (Bio-Rad, USA);
- iCycler iQ5 (Bio-Rad, USA).

Nucleic acid extraction kits recommended for DNA extraction

The Federal Budget Institute of Science “Central Research Institute for Epidemiology” recommends the following nucleic acid extraction kits for DNA extraction and further PCR analysis with the use of **AmpliSens® HHV7-screen/monitor-FRT** PCR kit:

- **RIBO-prep** for DNA/RNA extraction from biological material (blood plasma, whole blood, saliva) in accordance with the Instruction manual for the nucleic acid extraction kit.

Correspondence of targets and detection channels

Fluorophore	FAM	JOE	ROX
Detection channel name for different instrument models¹	FAM/Green	JOE/HEX/R6G/ Yellow/Cy3	ROX/Orange/ TxR
DNA target	human DNA (IC Glob)	<i>HHV7</i> DNA	Internal Control-FL (IC) DNA
Target gene	β-globin gene	<i>MCP</i> -gene	artificially synthesized sequence

¹ The detection channels names in each section of the guidelines are specified in accordance with the described instrument.

AMPLIFICATION AND DATA ANALYSIS USING Rotor-Gene 3000/6000 (Corbett Research, Australia) AND Rotor-Gene Q (QIAGEN, Germany) INSTRUMENTS

When working with Rotor-Gene 3000 one should use the Rotor-Gene version 6.1 and higher software and the Rotor-Gene 6000 versions 1.7 (build 67) software or higher for Rotor-Gene 6000 and Rotor-Gene Q instruments.

Hereinafter, all the terms corresponding to different instruments and software are indicated in the following order: for Rotor-Gene 3000 / for Rotor-Gene 6000/Q.

Carry out the sample pretreatment and reaction mixture preparation stages according to the PCR kit *Instruction Manual*. When carrying out the amplification it is recommended to use thin-walled PCR tubes (0.2 ml) with flat caps (e.g. Axygen, USA), or PCR tubes (0.1 ml) with caps from the four-pieces-strips (e.g. Corbett Research, Australia; QIAGEN, Germany) (detection through the bottom of the tube).

Programming the thermocycler

1. Turn on the instrument, run the Rotor-Gene software.
2. Insert the tubes or strips into the rotor of the Rotor-Gene 3000/6000/Q instrument beginning from the first well (the rotor wells are numbered, the numbers are used for the further programming of the samples' order in the thermocycler). Insert the rotor into the instrument, close the lid.

NOTE: Well 1 must be filled with any test tube except for an empty one.

3. Program the instrument according to the *Instruction Manual* given by the manufacturer of the instrument.

Creating the template for the run

1. Click the **New** button in the software main menu. To create the template select the **Advanced** tab in the opened window **New run**.
2. Select the **TwoStep/Hidrolysis Probes** template in the tab for edition and click the **New** button.
3. In the opened window select the **36-Well Rotor (or 72-Well Rotor)** and tick the **No Domed 0,2ml Tubes / Locking Ring Attached** option. Click the **Next** button.
4. In the opened window enter the operator name, select the reaction volume – 25 µl. Tick the **15 µl oil layer volume** option. Click the **Next** button.
5. In the **New Run Wizard** window set the temperature profile of the experiment. To do this click the **Edit profile** button and set the amplification program:

AmpliSens unified amplification program

Step	Temperature, °C	Time	Fluorescence detection	Number of cycles
Hold	50	15 min	–	1
Hold	95	15 min	–	1
Cycling	95	10 s	–	45
	60	20 s	FAM/Green, JOE/Yellow, ROX/Orange	

NOTE: Any combination of the tests can be performed in one instrument simultaneously with the use of the unified amplification program. If only the tests for pathogen agent DNA detection are performed in one instrument then the first step of reverse transcription (50 °C – 15 minutes) can be deleted from the program for time saving.

Note – The Cy5/Red and Cy5.5/Crimson channels are enabled when required if the “multiprime” format tests are performed.

6. After setting up the temperature profile click the **OK** button.
7. Click the **Calibrate/Gain Optimisation...** button in the **New Run Wizard** window. In the opened window:
 - a) for signal measurement optimisation for the selected channels set calibration from **5FI to 10FI** for all the channels (FAM/Green, JOE/Yellow, ROX/Orange).
To do this, click the **Calibrate Acquiring/Optimise Acquiring** button. In the opened window for first channel (**Auto Gain Optimisation Channel Settings/Auto Gain Calibration Channel Settings**) indicate the values of minimum and maximum signal in the **Target Sample Range** line. Click the **OK** button. The window for the next channel will open automatically. The selected values for all the channels can be checked in the **Min Reading, Max Reading** boxes.
 - b) perform the calibration in the selected channels before the first detection (tick the **Perform Calibration Before 1st Acquisition/ Perform Optimisation Before 1st Acquisition** option). Click the **Close** button.
8. Click the **Next** button. For saving the programmed template it is necessary to click the **Save Template** button and enter the template file name, corresponding to the amplification program – **AmpliSens**. Save the file into a proposed folder: **Templates\Quick Start Templates**; close the **New Run Wizard window**. After that the programmed template will appear in the template list in the **New Run** window.

Using the ready template for the run

1. Click the **New** button in the software main menu. In the opened **New Run** window select the **Advanced** tab. Then select the **AmpliSens** template (which is programmed as described in the “Creating the template for the run” section) in the template list.
2. In the opened window select the **36-Well Rotor (or 72-Well Rotor)** and tick the **No**

- Domed 0,2ml Tubes / Locking Ring Attached** option. Click the **Next** button.
3. In the opened window check that the reaction volume is 25 µl and the **15 µl oil layer volume** option is activated. Click the **Next** button.
 4. In the next window the correctness of the amplification program and signal level auto-optimisation parameters can be checked. Go to the next window clicking the **Next** button. Start the amplification by the **Start run** button. Herewith, the rotor with the samples should be already fixed and the lid should be closed. Name the experiment and save it to the disc (the results of the experiment will be automatically saved in this file).
 5. Enter the data into the grid of the samples (it opens automatically after the amplification has been started). Enter the names/numbers of the test samples in the **Name** column. Define the Negative control of amplification as NCA. Set the type **Unknown** opposite all the test samples, the type **Negative control** – for the Negative control of amplification. Set the type **Standard** for DNA-calibrators C1 and C2 and enter the values from the *Important product information bulletin* enclosed to the given lot of the PCR kit into the **Given conc.** column. Set the type **None** for the cells matching with the corresponding empty tubes. Click the **Finish/OK** button.

NOTE: Samples indicated as **None** won't be analysed.

Note – To edit the table of samples before the start it is needed previously to select the **Edit Samples Before Run Started** option in the **User preferences** submenu of the **File** menu.

Data analysis:

The obtained results are analyzed by the Rotor-Gene software. The results are interpreted according to the crossing (or not-crossing) of the S-shaped (sigmoid) fluorescence curve with the threshold line set at the specific level, that corresponds to the presence (or absence) of the *Ct* (threshold cycle) value of the DNA sample in the corresponding column of the results table. The calibration curve plotting and calculation of the *HHV7* DNA concentration are performed automatically in accordance with the *Ct* values.

Amplification data analysis in the FAM/Green channel:

1. Activate the button **Analysis** in the menu, select the mode of the analysis **Quantitation**, activate the **Cycling A. FAM/Cycling A. Green, Show** buttons.
2. Cancel the automatic choice of the threshold line level **Threshold**.
3. Select the **Linear scale**.

4. Activate the **Dynamic tube** and **Slope Correct** buttons in the menu of main window (**Quantitation analysis**).
5. In the **Calculation** menu (in the right part of the window) indicate the threshold line level **0.03** in the **Threshold** box.
6. Choose the parameter **More settings/Outlier Removal** and set **10 %** for the value of negative samples threshold (**NTC/Threshold**).
7. Set **5** in the **Eliminate cycles before:** menu (in the right part of the window).
8. In the results grid (the **Quantitation Results** window) one will be able to see the *Ct* values and DNA concentration values (**Calc Conc (copies/reaction)**).

Results analysis in the JOE/Yellow, ROX/Orange is carried out similarly to results analysis in the FAM/Green channel in accordance with the settings in the table below.

Channel	Threshold	Dynamic tube	Slope Correct	More Settings/ Outlier Removal	Eliminate cycles before:
FAM/Green	0.03	on	on	10%	5
JOE/Yellow	0.03	on	on	10%	5
ROX/Orange	0.03	on	on	10%	5

NOTE: If the fluorescence curves in the FAM/Green, JOE/Yellow, ROX/Orange channels do not correspond to the exponential growth, then **NTC threshold** value can be increased up to 20 %.

Results interpretation

The result of the PCR analysis is considered reliable only if the results for the controls of the amplification and the extraction are correct in accordance with the table of assessment of results for controls (see the *Instruction manual*) and boundary values specified in the *Important Product Information Bulletin* enclosed to the PCR kit.

The interpretation of the test samples is to be carried out in accordance with the *Instruction Manual* and the *Important Product Information Bulletin* enclosed to the PCR kit.

Possible problems and special aspects of results analysis with the use of Rotor-Gene 3000/6000/Q software

Possible problems	Reason	Characters	Ways to eliminate
Negative samples are analyzed as positive by Rotor-Gene software	Incorrect mathematical processing of negative samples in the presence of the fluorescence decrease section at the initial cycles	A typical positive sample has a characteristic S-shaped curve of fluorescence accumulation. Incorrectly processed negative samples are viewed as quite straight bottom-up lines	One must use the Ignore First by selecting the value 5 cycles. If it does not lead to a proper result, try to increase this value by 1 - 5
	The threshold line crosses descending fluorescence curves at the initial cycles	The red threshold line crosses (or touches) fluorescence curves at the left (initial cycles) on the chart of processed fluorescence curves	Use the Eliminate cycles before ... option by setting 5 (crossing the threshold and the fluorescence curve at the first 5 cycles is ignored)
Sensitivity decrease due to impurity of the instrument lenses	Impurity of lenses leads to reduction of effectiveness of fluorescence excitation and detection. It primarily affects to samples with small quantity of specific DNA, which show low fluorescence growth	Low values of the background signal in all 4 detection channels (<1) at the maximum value of the gain parameter (10)	Clean the horizontal and vertical lenses of the instrument by a dry disposable cotton disc at least once a month
The absence of the fluorescence curves when the fluorescence values are less than 1 or more than 100	The autocalibration parameter from 5FI to 10FI is not set or it is a failure of the first tube in the rotor (tube is absent, DNA sample or reaction mixture is added incorrectly)	Most of fluorescence background signals are less than 1 or greater than 20	Repeat the PCR after setting the autocalibration parameters. Make sure that the well 1 is filled with any test tube except for an empty one

The information about all set parameters of the experiment and the autocalibration report can be found by browsing the experiment settings (the **Settings** button). Particularly, **Autocalibration Log Messages** point in the **Messages** tab is the autocalibration report.

AMPLIFICATION AND DATA ANALYSIS USING iCycler iQ5

(Bio-Rad, USA) INSTRUMENTS

Carry out the sample pretreatment and reaction mixture preparation stages according to the PCR kit *Instruction Manual*. When carrying out the amplification it is recommended to use thin-walled PCR tubes (0.2 ml) with domed or flat optically transparent caps, or tubes (0.2 ml) with transparent caps from the eight-pieces-strips (e.g. Axygen, USA) (detection through the cap of the tube).

Programming the thermocycler


1. Turn on the instrument and the power supply unit of the optical block of the instrument.

NOTE: The lamp is to be warmed up during 15 min before starting the experiment.

2. Start the program iCycler iQ5.
3. Insert the tubes or strips into the reaction module of the thermocycler and program the instrument according to the *Instruction Manual* given by the manufacturer of the instrument.

NOTE: Monitor the tubes. There must not be drops left on the walls of the tubes as falling drops during the amplification process may lead to the signal failure and complicate the results analysis. Don't turn the tubes (strips) upside down while inserting them into the instrument.

Creating the template for the run

1. Set the plate setup (set the order of the tubes in the reaction chamber and the detection of fluorescent signal).
 - click the **Create New** button in the **Selected Plate Setup** window of the **Workshop** module;
 - in the opened window click the **Whole Plate loading** button and set the plate setup using the buttons of the upper toolbar. Enter the samples' names in the **Identifier/Condition** column in the bar appeared in the screen bottom. Select the fluorescent signal detection in the FAM, JOE/HEX, ROX channels. Click the **Select/Add Fluorophores** button, select the fluorophore and tick it in the **Selected** column. Click **OK**. The fluorophore name will appear in the **Fluorophore** window. For addition of fluorescence signal measuring for each sample it is necessary to click the fluorophore (activate it) and select the samples on the plate using the **Fluorophore loading in whole Plate mode**  button under the scheme;
 - set the reaction volume (**Sample Volume**) as **25 µl**, the caps type (**Seal Type**) as **Domed Cap**, and the tubes type (**Vessel Type**) as **Tubes**;
 - save the set plate setup by clicking the **Save&Exit Plate Editing** button. Enter the

file name and click **Save**.

2. Set all the biological samples as **Unknown**, negative controls as «-».

Set the calibrators C1 and C2 in the test channels as **Std (Standard)**. Enter the values specified in the *Important Product Information Bulletin* enclosed to the given lot of the PCR kit in the **Quantity** column. If different calibrators' values in the detection channels are set then the **Whole Plate Loading** button should be **inactive**.

3. Set the amplification program. To do this, in the **Selected Protocol** window of the **Workshop** module click the **Create New** button. Set the amplification parameters and save the protocol by activating the **Save&Exit Protocol Editing** button. Enter the name of the file and then click **Save**.

AmpliSens unified amplification program

Step	Temperature, °C	Time	Fluorescence detection	Number of cycles
1	50	15 min	–	1
2	95	15 min	–	1
3	95	10 s	–	45
	60	20 s	FAM, JOE/HEX, ROX	

NOTE: Any combination of the tests can be performed in one instrument simultaneously with the use of the unified amplification program. If only the tests for pathogen agent DNA detection are performed in one instrument then the first step of reverse transcription (50 °C – 15 minutes) can be deleted from the program for time saving.

Note – The Cy5 channels are enabled when required if the “multiprime” format tests are performed.

4. Before a run it is obligatory to check if the selected protocol (**Selected Protocol**) and the plate scheme (**Selected Plate Setup**) are correct. To begin a run click the **Run** button. For the well factors measurement the **Use Persistent Well Factors** type is selected by default. Click the **Begin Run** button, save the experiment (the results of this experiment will be automatically saved in this file) and click **OK**.
5. At the end of the run it is necessary to close the software and turn off the instrument (the thermocycler and the optical block).

Using the ready template for the run

The test parameters and the plate setup set earlier can be used for the further runs. To do this:

- select the needed file with the run in the upper left window of the **Workshop** module;
- click the **Edit** button in the **Selected Plate Setup** area of the **Workshop** module and edit the plate setup (the files of protocols are saved in the **SampleFiles** folder by default);
- click the **Edit** button in the **Selected Protocol** area of the **Workshop** module and check

the correctness of the selected protocol (the files of protocols are saved in the **Users** folder by default).

Data analysis:

The obtained results are analyzed by the iCycler iQ5 software. The results are interpreted according to the crossing (or not-crossing) of the S-shaped (sigmoid) fluorescence curve with the threshold line set at the specific level, that corresponds to the presence (or absence) of the *Ct* (threshold cycle) value in the corresponding column of the results table. The calibration curve plotting and calculation of the *HHV7* DNA concentration are performed automatically in accordance with the *Ct* values.

1. Start the software and open the needed file with data of the analysis in the **Data File** window of the **Workshop** module. Click the **Analyze** button.
2. Select the **Analysis Mode: PCR Base Line Subtracted Curve Fit** (is set by default).
3. Check the correctness of threshold line automatic choice for each channel. The threshold line is to cross only with S-shaped (sigmoid) curves describing the accumulation of the signal detecting positive samples and controls. The threshold line is not to cross the base line. If it happens, it is necessary to set the threshold line level for each channel manually. To do this, click the **Log View** (logarithmic scale selection) and set (with the left mouse button) the threshold line at the level where the fluorescence curves have a linear character and do not cross with the curves of the negative samples. As a rule, the threshold line is set at the level of 10-20 % of maximum fluorescence obtained for the Positive control in the last amplification cycle. Make sure that the fluorescence curve of the Positive control has the typical exponential growth of fluorescence.
4. In order to analyze the results click the **Results** button situated under the buttons with the fluorophores' names.

Results interpretation

The result of the PCR analysis is considered reliable only if the results for the controls of the amplification and the extraction are correct in accordance with the table of assessment of results for controls (see the *Instruction manual*) and boundary values specified in the *Important Product Information Bulletin* enclosed to the PCR kit.

The interpretation of the test samples is to be carried out in accordance with the *Instruction Manual* and the *Important Product Information Bulletin* enclosed to the PCR kit.

Possible problems and special aspects of results analysis with the use of iCycler iQ5 for research software

Possible problems	Characters	Ways to eliminate
The threshold level is set incorrectly	The threshold line passes with the negative samples or above some or all positive curves (herewith, curves are S-shaped in a linear scale)	Set the threshold line at the level of 10-20 % of maximum fluorescence obtained for the Positive control in the last amplification cycle (in logarithmic scale)
The drops are not sedimented from the walls of the tubes before the run	The appearance of negative or positive "steps" in the curves of the fluorescence accumulation	Open the BaseLine Threshold window by clicking the right mouse button on the fluorescence curve. Set the range for calculation of the base line beginning from the first cycle after the step.

AMPLIFICATION AND DATA ANALYSIS USING CFX96 (Bio-Rad, USA)

Carry out the sample pretreatment and reaction mixture preparation stages according to the PCR kit *Instruction Manual*. When carrying out the amplification it is recommended to use thin-walled PCR tubes (0.2 ml) with domed or flat optically transparent caps, or tubes (0.2 ml) with transparent caps from the eight-pieces-strips (e.g. Axygen, USA) (detection through the cap of the tube).

Programming the thermocycler

1. Turn on the instrument and start the Bio-Rad CFX Manager software.
2. Program the instrument according to the *Instruction Manual* provided by the manufacturer.

Creating the template for the run

1. In the **Startup Wizard** window it is necessary to select the **Create a new Run/Experiment** (or select **New** in the **File** menu and then select **Run.../Experiment...**). Click **OK**.
2. In the **Run Setup** window, select **Protocol** tab and click the **Create new....** Set the amplification parameters in the opened **Protocol Editor – New** window. Set **Sample Volume – 25 µl**.

AmpliSens unified amplification program

Step	Temperature, °C	Time	Fluorescence detection	Number of cycles
1	50	15 min	–	1
2	95	15 min	–	1
3	95	10 s	–	45
	60	20 s	FAM, HEX, ROX	

NOTE: Set **Ramp Rate 2,5 °C/s** by clicking the **Step Options** button for each step of cycling (see the figure below). Click **OK**.

1	50,0	C for 15:00
2	95,0	C for 15:00
3	95,0	C for 0:10 Slow Ramp Rate to 2,5 C per second
4	60,0	C for 0:20 + Plate Read Slow Ramp Rate to 2,5 C per second
5	GOTO 3	.44 more times
END		

NOTE: Any combination of the tests can be performed in one instrument simultaneously with the use of the unified amplification program. If only the tests for pathogen agent DNA detection are performed in one instrument then the first step of reverse transcription (50 °C – 15 minutes) can be deleted from the program for time saving.

Note – The Cy5 and Quasar 705 channels are enabled when required if the “multiprime” format tests are performed.

3. Save the protocol: in the **Protocol Editor New** window select **File**, then **Save As**, name the file and click **Save**.
4. Set the plate setup: in the **Plate** tab click the **Create new...** button. Set the tube order in the opened **Plate Editor – New** window. Click the **Select Fluorophores...** button and click the **Selected** checkbox next to the **FAM, HEX, ROX** fluorophores and click **OK**. In the **Sample type** menu select **Unknown** for all the samples, except for the DNA-calibrators. Then in the **Load** column (in the right part of the window) tick the fluorescence signal acquiring for all the samples in the required channels. Define sample names in the **Sample name** window, moreover the **Load** function is to be ticked.

Set the calibrators C1 and C2 for all the channels as **Sample type – Standard**. Enter a concentration in the **Concentration** box according to the *Important Product Information Bulletin* enclosed to the PCR kit, moreover the **Load** function is to be ticked.

5. Save the plate setup: select **File** and then **Save as** in the **Plate Editor New** window. Enter the file name, click **Save**.
6. Select the **Start Run** tab. Open the lid of the instrument by the **Open Lid** button. Insert the reaction tubes in the wells of the instrument in accordance with the entered plate setup. Close the lid by the **Close Lid** button.

NOTE: Monitor the tubes. There must not be drops left on the walls of the tubes as falling drops during the amplification process may lead to the signal failure and complicate the results analysis. Don't turn the tubes (strips) upside down while inserting them into the instrument.

7. Click the **Start Run** button and start the program with the selected plate setup. Select the directory for the file saving, name the file, click **Save**.

Using the ready template for the run

The test parameters and the plate setup set earlier can be used for the further runs. To do this:

- click the **Select Existing...** button in the **Run Setup** window of the **Protocol** tab. Select the needed file with the amplification program in the **Select Protocol** window. Click **Open**.
- go to the **Plate** tab in the **Run Setup** window. Click the **Select Existing...** button. Select the needed file with the plate setup in the **Select Plate** window. Click **Open**. Click the **Edit selected** button to edit the plate setup.

Data analysis

The obtained results are analyzed by the software of the CFX96 instrument. The results are interpreted according to the crossing (or not-crossing) of the S-shaped (sigmoid) fluorescence curve with the threshold line set at the specific level, that corresponds to the presence (or absence) of the *C_t* (threshold cycle) value in the corresponding column of the results table. The calibration curve plotting and calculation of the *HHV7* DNA concentration are performed automatically in accordance with the *C_t* values.

1. Start the software and open the saved file with data of the analysis. To do this, select **File** in the menu, then **Open** and **Data file** and select the needed file.
2. The fluorescence curves, the tube order in the plate and the table with the *C_t* values are represented in the **Data Analysis** window of the **Quantification** tab.

Check the correctness of threshold line automatic choice for each channel. The threshold line is to cross only with S-shaped (sigmoid) curves describing the accumulation of the signal detecting positive samples and controls. The threshold line is not to cross the base line. If it happens, it is necessary to set the threshold line level for each channel manually. To do this, tick the **Log Scale** item (logarithmic scale selection) and set (with the left mouse button) the threshold line at the level where the fluorescence curves have a linear character and do not cross with the curves of the negative samples. As a rule, the threshold line is set at the level of 10-20 % of maximum fluorescence obtained for the Positive control in the last amplification cycle. Make sure that the fluorescence curve of the Positive control has the typical exponential growth of fluorescence. To select the curve of C+ sample (or another one appropriate sample), set the cursor to the plate setup or to the results grid.

3. Click the **View/Edit Plate...** button on the toolbar and set the samples names and calibrators concentrations in the opened window.

Results interpretation


The result of the PCR analysis is considered reliable only if the results for the controls of the amplification and the extraction are correct in accordance with the table of assessment of results for controls (see the *Instruction manual*) and boundary values specified in the *Important Product Information Bulletin* enclosed to the PCR kit.

The interpretation of the test samples is to be carried out in accordance with the *Instruction Manual* and the *Important Product Information Bulletin* enclosed to the PCR kit.

Possible problems and special aspects of results analysis with the use of CFX96 for research software

Possible problems	Characters	Ways to eliminate
The threshold level is set incorrectly	The threshold line passes with the negative samples or above some or all positive curves (herewith, curves are S-shaped in a linear scale)	Set the threshold line at the level of 10-20 % of maximum fluorescence obtained for the Positive control in the last amplification cycle (in logarithmic scale)
The drops are not sedimented from the walls of the tubes before the run	The appearance of negative or positive "steps" in the curves of the fluorescence accumulation	Repeat the amplification for the sample

List of Changes Made in the Guidelines

VER	Location of changes	Essence of changes
31.05.18 EM	Amplification and data analysis using Rotor-Gene 3000/6000 (Corbett Research, Australia)	The value of <i>Eliminate cycles before</i> was changed from 1 to 5
31.01.19 SK	Amplification and data analysis using Rotor-Gene 3000/6000 (Corbett Research, Australia) AND Rotor-Gene Q (QIAGEN, Germany) instruments	The information about <i>Dynamic tube</i> option was added to the table with settings
11.09.20 MM	Troubleshooting	The section was deleted
	Calculation of HHV7 DNA	The section was deleted
28.12.20 MM	Through the text	The symbol  was changed to NOTE:
	Cover page	The phrase “Not for use in the Russian Federation” was added
23.03.21 EM	Front page	The name, address and contact information for Authorized representative in the European Community was changed