

QuickGuide: RealFast[™] CNV on Bio-Rad CFX96

Setup for Relative Quantitation Assays:

- Open the Bio-Rad CFX Maestro software (QuickGuide is based on version 2.2).
- In the Startup Wizard select instrument CFX96 and run type User-defined.
- In the Run Setup select Create New within the Protocol Tab. The Protocol Editor opens.
 - Select a sample volume of 20 µl and setup the PCR program: 10 min at 95°C followed by 40 times 15 sec at 95°C and 60 sec at 60°C. Make sure that the Plate Read is added to the 60°C step. Press OK and save the protocol file. Press Next.

		1	95,0	С	for	10:00				
	\rightarrow	2	95,0	С	for	0:15				
		3	60,0	С	for	1:00				
	+ Plate Read									
П		4	GOT	D 2		39	mo	re time	s	
	END									

- In the tab called **Plate** select **Create New**. The **Plate Editor** opens.
 - Select Settings > Plate Type and choose the correct type of plate: Plate Size and Plate Type.
 - > Select scan mode All Channels.
 - > Click **Select Fluorophores** and select FAM and HEX.
 - Select wells by clicking in the well selector and choose the sample type (NTC or Unknown); a minimal setup should contain triplicates of a negative control template, the calibrator and an unknown sample.
 - Click Load check boxes to load fluorophores FAM and HEX
 - Type target names (FAM: gene of interest; HEX: EC / endogenous control) and press Enter. The name is now available from the drop down menu.
 - > Type sample name and press Enter.
 - > Click check box to load **Replicate** number.
 - Open Experiment Settings and select the endogenous control EC as Reference in the Targets tab.
 - In the Samples and Biological Groups tab select the supplied Calibrator sample as Control. Press OK.
 - > Choose Well Groups in case you are running several assays at the same time
 - > Press **OK** and save the plate file.
- Press Next, load your PCR tubes and start the run.

Select Fluorophores							
Sample Type	Unknown 🔻						
Load FAM HEX	Target Name Gene of Intere ▼ EC ▼						
Load V	Sample Name Calibrator 🗸						
Load	Replicate # 1						
Experiment Settings							
Clear Replicate #							
Clear Wells							

Analysis of Relative Quantitation Assays:

- Open the data file: File > Open > Data File
- Within the **Quantification** tab select your samples and click the check box for **HEX** in the amplification chart.
 - > Right-click on the threshold line and select **Show Threshold Values**.
 - > Set the threshold according to the settings in the Assay Description:
 - Settings > Baseline Threshold > Auto Calculated
 - > Follow the same principle and review the threshold for FAM.
- Select both fluorophores and review the results by clicking on individual wells in the well selector.



Example: Amplification Plot of the Calibrator sample – linear and log graph type (red: gene of interest, green: EC)

• Click on the Gene Expression tab. In the Bar Chart select a Mode from the drop down menu to the right



of the chart. Select **Normalized Expression** ($\Delta\Delta$ **Cq**), **Relative To Control** (Graph Data) and **Calibrator** (Control). Review **Experiments Settings** for correct assignment of reference (EC) and control (ViennaLab Calibrator). For details right-click on the **Graph Expression Data Table** select **Show Details**.

• In the Well Results Tab you can find the Expression column.



The ratio for the **Calibrator** (Control Sample) is set to "1" and values for your samples are relative to the **Calibrator**. Refer to the product description for interpretation of your results.

• To open a report, select **Tools > Reports** and adjust the report according to your needs.