SCI Digital PCR System and SCI Digital Software

User Guide

2023.03.16 Version 1.0

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1. SCI Digital PCR System

1.1 Introduction to SCI Digital PCR System

SCI Digital PCR is a digital PCR (dPCR) method based on water-in-chamber droplets technology. SCI Digital PCR uses a combination of microfluidic chip and curable oil to divide each sample into water-in-chamber droplets.

The SCI Digital PCR System combines droplet generation, thermal cycling, and droplet reading technologies into a single instrument. SCI Digital PCR system can generate more than 20,000 droplets, and contains 5 optional fluorescent channels (FAM, HEX, ROX, Cy5, Quasar 705).

The dPCR system uses reagents and workflows similar to those used for most standard TaqMan probe-based assays. It provides absolute quantification of nucleic acid target sequences by counting nucleic acid molecules encapsulated in discrete volumetrically defined chamber of the chip partitions.

SCI Digital PCR is highly effective in the following areas:

- Absolute quantification
- Copy number variation (CNV)
- Validate NGS results
- Genome edit detection
- Detection of rare sequences
- Gene expression & microRNA analysis
- Viral load analysis
- NIPT

Fig 1.1 SCI Digital PCR System

SCI Digital PCR has the following benefits for nucleic acid quantification:

- **Unparalleled precision：** The massive sample partitioning afforded by dPCR enables small fold differences in target DNA sequence between samples to be reliably measured.
- **Increased signal-to-noise ratio：** High-copy templates and background are diluted, effectively enriching template concentration in target-positive partitions. This allows for the sensitive detection of rare targets and enables a ±10% precision in quantification
- **Removal of PCR efficiency bias：** Error rates are reduced by removing the amplification efficiency reliance of qPCR, enabling accurate quantification of targets.
- **Simplified quantification：** There is no requirement for a standard curve for absolute quantification.

SCI Digital PCR Workflow：

- You prepare your samples for dPCR by combining DNA or RNA with primers, probes dye, and buffer.
- The sample is injected into more than 20,000 uniform nanoliter-sized chambers of the chip, with target and background DNA distributed randomly into the chambers during the partitioning process.
- Following the droplets in the chip are amplified through a thermal cycler, which performs PCR amplification of the nucleic acid target in each individual droplet.
- Imager reads each chamber to determine the fraction of positive chambers in the original sample. Positive chambers containing at least one copy of the target DNA molecule exhibit increased fluorescence compared to negative chambers.

1.2 Instrument Specifications

Element	**Specifications**
Power	220 V, 50 Hz
Air pressure	86 KPa ~ 106 KPa

Temperature	Room temperature (25°C)
Relative humidity	30%-70%
Weight	100 kg
Size (W×D×H)	453×518×498 mm
Samples	12
Partitions per sample	Approximately 20,000
Detection channels	FAM/HEX/ROX/Cy5/Quasar705

2. SCI Digital Software

Double-click the shortcut icon to open the SCI Digital Software.

SCI Digital organizes and provides one-click access to the four main steps of dPCR analysis in the left navigation bar, moving you through the entire workflow:

- New-enter information about the assays and experiments (see Section 2.1)
- Select-select and enter information about the samples (see Section 2.2)
- Run-start the run and control the instrument, if needed (see Section 2.3)
- Analyze-compute nucleic acid concentration (see Sections 2.4)

2.1 New

1. Click the  icon to edit the assay.

2. To enter information about the assay and experiment in the ***"Experimental information"*** dialog box.

3. Click the "***Edit project"*** to edit program of the thermal cycle and fluorescent channel about the assay.

4. In the Edit project interface, you can enter project, select fluorescent channel and set thermal cycling program.

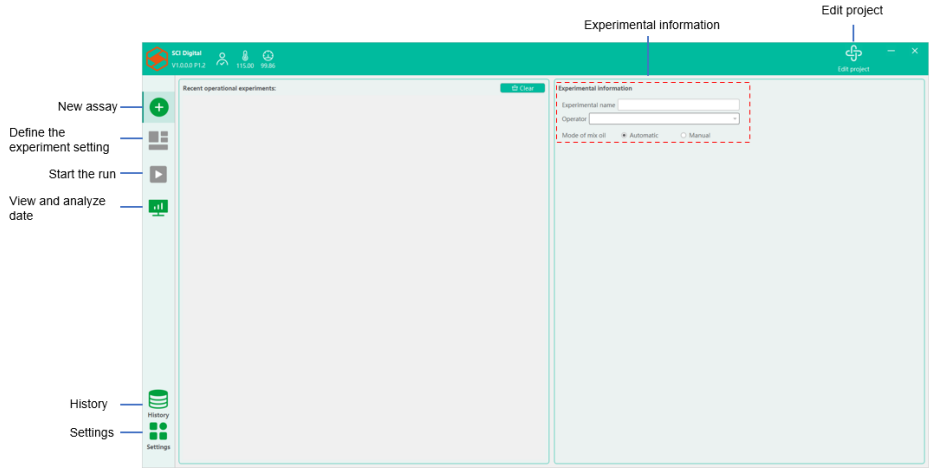

Fig 2.1 New assay interface

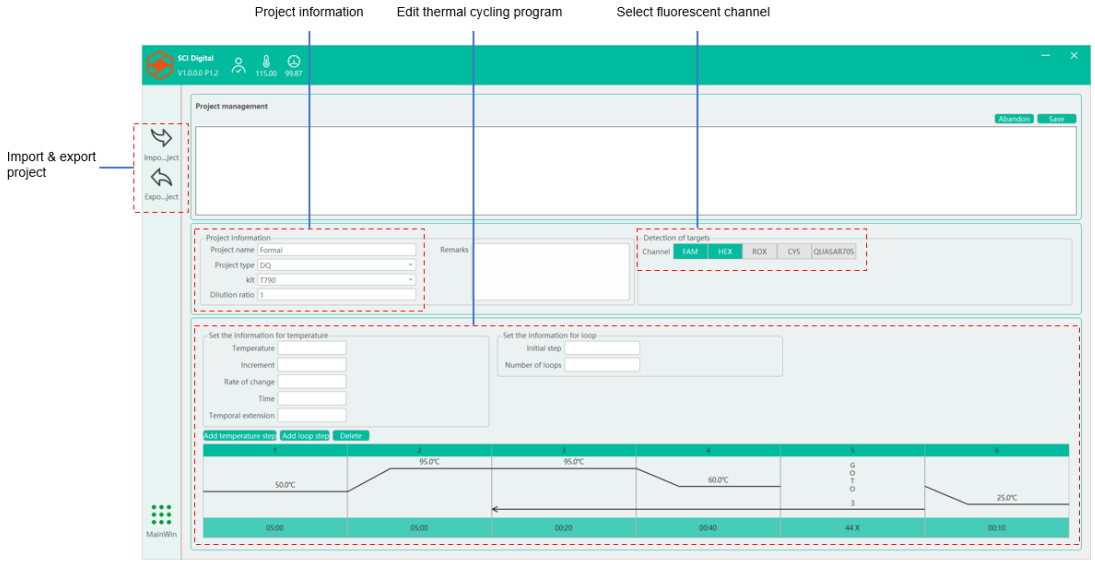

Fig 2.1 Edit project interface

2.2 Setup

1. Click the  Setup icon to define the experiment setting.

2. In the Setup interface, you can select the samples ❶, project ❷, chips ❸, pipette tips ❹, and edit sample information ❺.

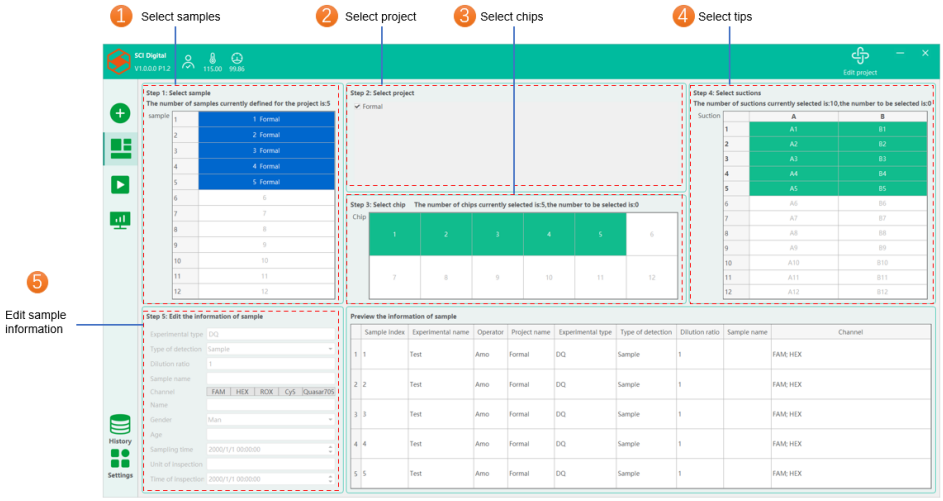

Fig 2.2 Setup interface

2.3 Run

1. Click  in the left navigation bar to double-check the settings.

2. In the Run Options window, Click Run to start the run.

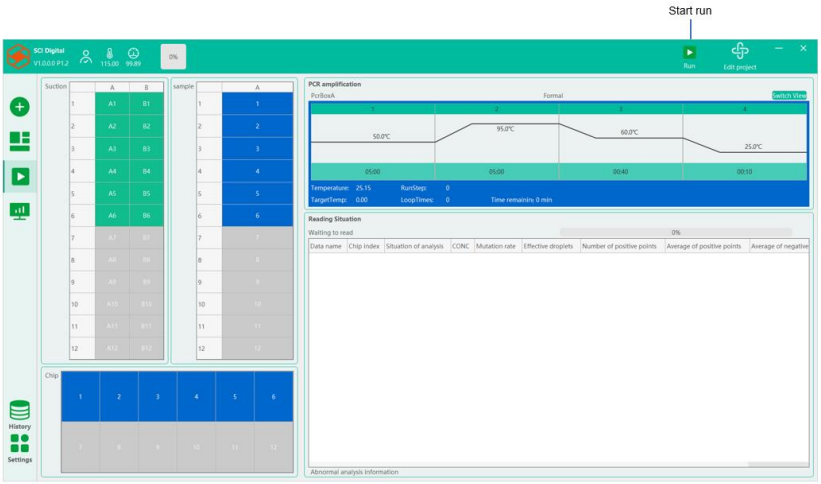

Fig 2.3 Run Options window

2.4 View and analyze date

1. Click  in the left navigation bar to view and analyze date.

2. In the View and analyze date window, Click  to import the date.

3. In the View and analyze date window, you can view the 1D Amplitude, 2D Amplitude, results and export report.

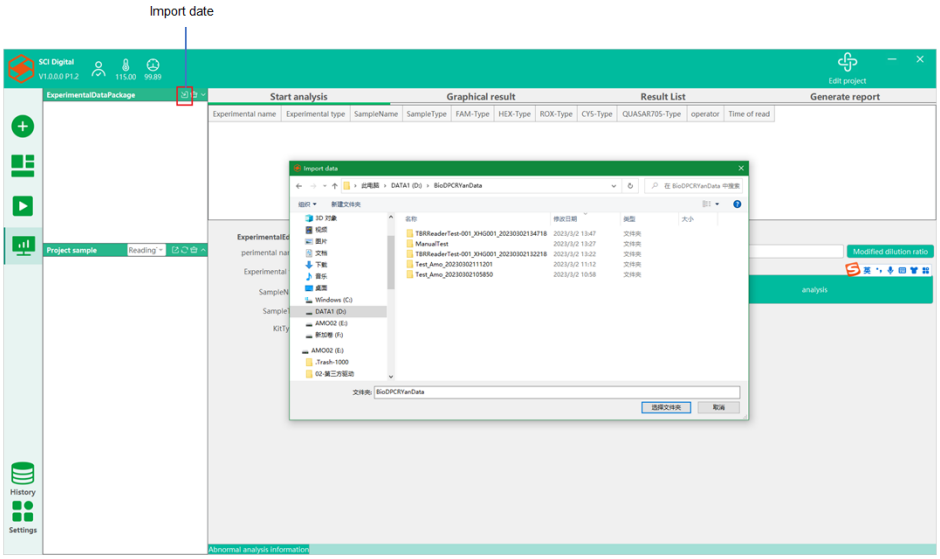

Fig 2.4 Import date window

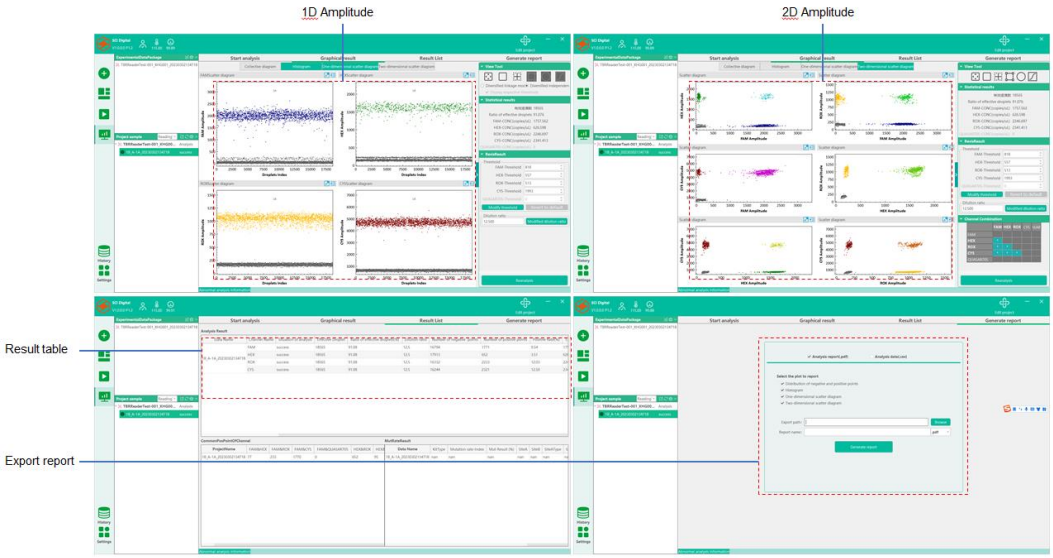

Fig 2.5 View and analyze window