

How to use STEP ONE Plus -Quick start-

Turn on the PC.

Login to Windows. (Administrator / no password)

Launch the StepOne Software v2.2.

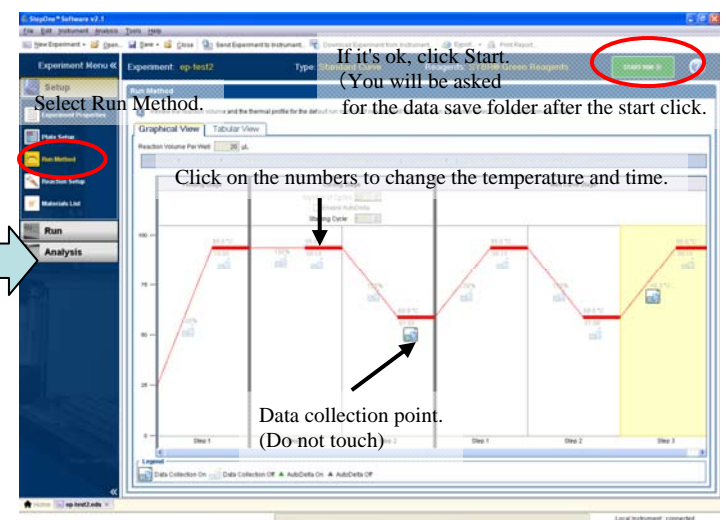
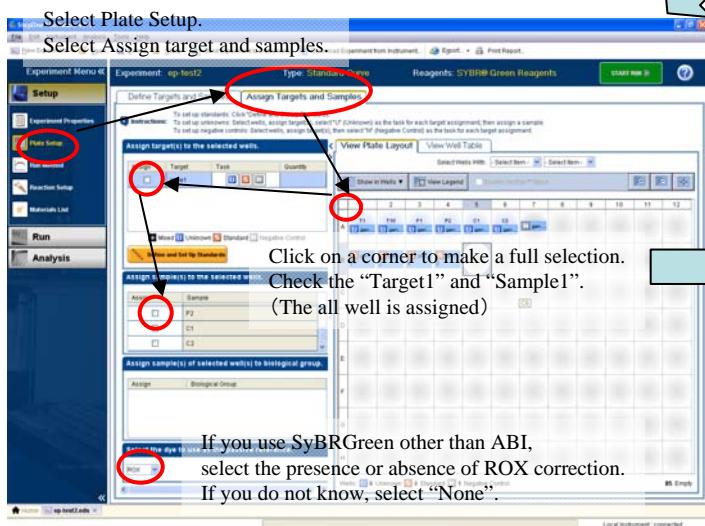
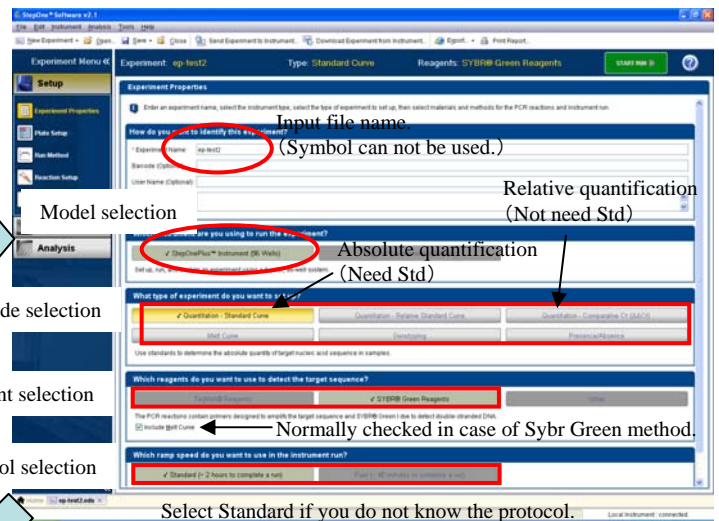
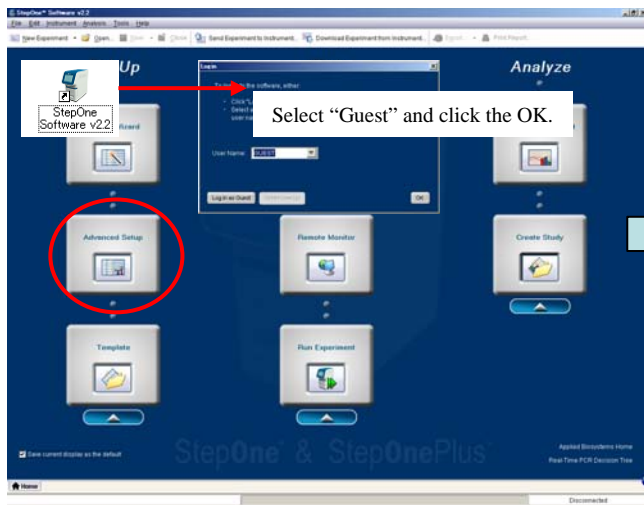
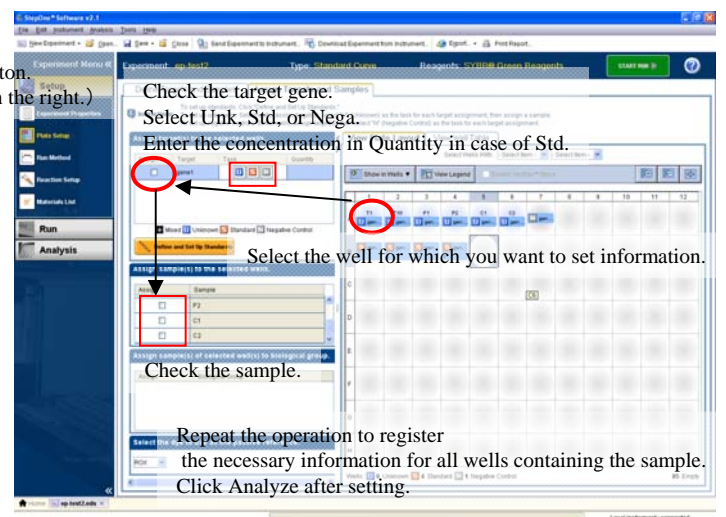
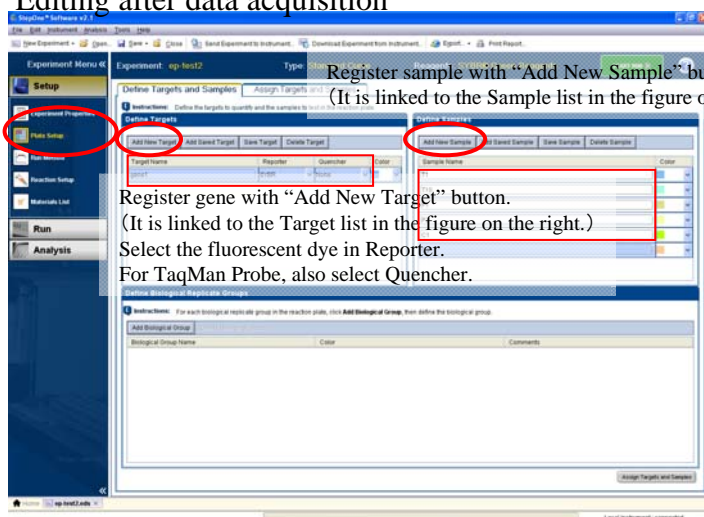


Plate Setup information can be edited after data acquisition.
Give priority to starting.

Editing after data acquisition



How to use STEP ONE Plus

Genotyping with TaqMan

Up Login as Guest

Select "Advanced Setup".

Open "Experiment Properties".

Enter the experiment name

Select "Step one plus".

Select "Genotyping".

Select "TaqMan".

Select a polymerase type.
Select Standard if you do not know.

Open "Plate setup".

Select "Edit SNP Array" and set SNP information.
If register new SNP click "Create New SNP Assay" button.

Click "Add New Sample" button and register the sample.

Change the sample name

Select dye

Set gene name and SNP
<ABI kit labeling rules>
Gene name (N/n)
N=VIC , n=FAM

Select the place of the well and link the sample and gene.
(The task select unknown)

Set the Negative Control.
(Do not select a sample at this place)

Click on analyze after changing settings.

Open "Run Method".

Check the temperature program.
Start if there is no problem.

Click the number you want to change and enter the value.
(temperature or time)

This icon is a sign of data collection.
(Do not touch)

After measurement

(When not automatically analyzed)
Drag the group and select a type from "Apply Call".

The Well and plot are linked to each other.

Memo

Use export if you want to use the data in Excel or Power Point.

Right-click on plot or plate layout and select Save as, you can save the figure with Jpeg.

If you want to reproduce the View Well Table, right click on the upper left of A1, select Copy, and paste in Excel.

How to use STEP ONE Plus

Absolute quantitative method (Standard curve method)

Use a sample of known absolute amount for standard curve preparation.
Prepare dilution series of known amount samples and use as standard sample.

Launch the app → Login as Guest → Advanced setup

Open "Experiment Properties".

Enter the experiment name

Select "Step one plus".

Select standard curve.

Select TaqMan or SYBR

When using SYBR, be sure to check "Include Melt Curve".

Select a polymerase type.
Select Standard if you do not know.

Change to "Assign Targets and Samples" tab.

Select the place of the well and link the sample, gene and task.
(If the task is standard, enter a standard quantity.)

Open "Run Method".

Click the number you want to change and enter the value.
(temperature or time)

This icon is a sign of data collection.
(Do not touch)

Check the temperature program.
Start if there is no problem.

The genuine reagent contains ROX.
Set to None when using a reagent that does not contain ROX.

I can not explain the analysis.

The problematic sample is displayed here.
Improve it referring to the name column of table.

How to create template file.

1. Open the file after measurement.
2. Create a template file by the following operation.
File – Save as template
3. Close the file after measurement.
4. Open the created template file.
5. Create a new data file by the following operation.
File – Save as (You can now click the start button.)

How to use STEP ONE Plus

Relative quantification method (Standard curve method)

Launch the app → Login as Guest → Advanced setup

The sample with the highest concentration is selected as the standard sample. Prepare a low standard sample by diluting the standard sample. After creating a standard curve, calculate the relative values of target and endogenous control. (Target / E-Control)
Recalculate the sample specified in reference as 1.

Open "Experiment Properties"

Enter the experiment name.

Select "Step one plus".

Select relative standard curve.

Select TaqMan or SYBR.

When using SYBR, be sure to check "Include Melt Curve".

Select a polymerase type.
Select Standard if you do not know.

Open "Plate setup"

Select dye

Click "Add New Sample" and enter sample name.

Click "Add New Target" and enter gene name.

Assign Targets and Samples

Change to "Assign Targets and Samples" tab.

Select the place of the well and link the sample, gene and task. (If the task is standard, enter a standard quantity.)

Select reference sample.

Select endogenous control.

The genuine reagent contains ROX. Set to None when using a reagent that does not contain ROX.

Run Method

Check the temperature program. Start if there is no problem.

Click the number you want to change and enter the value. (temperature or time)

This icon is a sign of data collection. (Do not touch)

I can not explain the analysis.

The problematic sample is displayed here. Improve it referring to the name column of table.

Well	Name	Task	Wells
1	Amplification in negative control	Amplification	1-12
2	First positive reference signal	Amplification	1-12
3	Second positive reference signal	Amplification	1-12
4	Amplification in reference	Amplification	1-12
5	First endogenous control in replicates	Amplification	1-12
6	Second endogenous control in replicates	Amplification	1-12
7	Amplification in sample	Amplification	1-12
8	First endogenous control in sample	Amplification	1-12
9	Second endogenous control in sample	Amplification	1-12
10	Amplification in biological group	Amplification	1-12
11	First endogenous control in biological group	Amplification	1-12
12	Second endogenous control in biological group	Amplification	1-12
13	Amplification in reagent	Amplification	1-12
14	First endogenous control in reagent	Amplification	1-12
15	Second endogenous control in reagent	Amplification	1-12
16	Amplification in reagent	Amplification	1-12

- How to create template file.
1. Open the file after measurement.
 2. Create a template file by the following operation.
File – Save as template
 3. Close the file after measurement.
 4. Open the created template file.
 5. Create a new data file by the following operation.
File – Save as (You can now click the start button.)

