

TaqMan™ Genotyper Software

Create and analyze a study

Pub. No. 4448638 Rev. C

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Create a study

Enter the study properties

1. In the toolbar on the **Home** screen, click **Create Study**.
2. In the **Workflow Menu** pane, select **Setup ▶ Properties** to open the **Properties** screen.
3. Enter a study name, then select a genotyping experiment type.

IMPORTANT! A study can support only one type of experiment. The experiment type can be changed after an experiment is imported. This allows for all of the experiments in the study to be the same type.

4. (Optional) Enter a description of the study and/or enter comments.

Set the analysis settings

1. In the toolbar, click **Analysis Settings** to open the **Analysis Settings** dialog box.
2. Select the **Call Settings** tab, select **Autocalling** or **Classification Scheme** as the call method, then complete the remaining fields as appropriate for your laboratory.

Note: If you select **Autocalling**, the software algorithm is used to call the data points. If you select **Classification Scheme**, you define the cluster boundaries that are used to call the data points.

If the **Show Cycle** slider in the scatter plot was adjusted, the cycle number is also updated in the **Analysis Settings** dialog box. It is updated for the assay in the **Assay-Specific Settings** pane.

When the cycle number is edited in the **Analysis Settings** dialog box, the **Show Cycle** slider in the scatter plot is updated.

3. Select the **Control Identifiers** tab, select or deselect **Override Control Settings from Experiments**, then complete the remaining fields as appropriate for your laboratory.

Note: If you select **Override Control Settings from Experiments**, the software uses the control identifiers that you set in the **Control Identifiers** tab and overrides any control identifiers (tasks) that may have been set in the original experiment file. If a sample ID does not match a control identifier, the software assumes the sample is an Unknown.

4. Select the **QC Settings** tab, select the flags that the software uses for analysis, then select condition and threshold values as appropriate for your laboratory.

5. Click **OK** to save the changes and close the dialog box.

Note: To apply the analysis settings to all assays in the study, make the changes in the **Study-Level Settings** pane. To apply the analysis settings to individual assays, make the changes in the **Assay-Specific Settings** pane.

Optional workflow to customize the analysis settings

The following steps can be used to customize and save the analysis settings:

1. Set up a study with the applicable analysis settings.
2. Generate a template from the study (LAT file) .
3. Create a new study from a template, selecting the new template that was generated.
The analysis settings from the template are applied to the new study.

Import experiments into the study

IMPORTANT! Be sure that the experiments you import meet all of the criteria specified in the *TaqMan™ Genotyper Software Getting Started Guide* (Pub. No. 4448637).

1. In the **Workflow Menu** pane, select **Setup ▶ Experiments** to open the **Experiments** screen.
2. Click **Import**, browse to and select the experiments of interest, then click **Import**.
3. View the imported data in the **Experiments** screen to verify that the data is correct.

(Optional) Import information files

Import assay information files

1. In the **Workflow Menu** pane, select **Setup ▶ Assays** to open the **Assays** screen.
2. Click **Import**, browse to and select the assay information file of interest, then click **Import**.

IMPORTANT! The assay information file must include an assay ID (in the **Assay ID** column) for each assay listed in the file. The software matches the assay IDs in the file with the existing assay IDs in the study.

3. If the assay information file contains information for an assay ID that is already in the study, the software prompts you to ignore the new information, replace the existing information, or cancel the import. Click the appropriate option.
4. View the imported assay information in the **Assays** screen. If the assay information file contained incorrect information, you can:
 - Edit the information in the **Assays** screen: Select the assay of interest, then click **Edit** to open the **Edit Assay** dialog box.
 - Edit the information in the assay information file, then re-import it.
 - Import a different assay information file to replace the incorrect information.

Import an SSI file

1. In the **Workflow Menu** pane, select **Setup ▶ Samples** to open the **Samples** screen.
2. Click **Import**. At the prompt, click **Yes** to update/replace the sample information in the study or click **No** to cancel the import.
3. Browse to and select the SSI file of interest, then click **Import**.

IMPORTANT! The SSI file must include a sample ID (in the **Sample ID** column) for each sample listed in the SSI file. The software matches the sample IDs in the SSI file with the existing sample IDs in the study.

4. View the imported sample information in the **Samples** screen. If the SSI file contained incorrect information, you can:
 - Edit the information in the **Samples** screen: Select the sample of interest, then click **Edit** to open the **Edit Sample** dialog box.
 - Edit the information in the SSI file, then re-import it.
 - Import a different SSI file to replace the incorrect information.

Import a reference panel file

A *reference panel file* is a user-generated TaqMan™ Genotyper Software file that contains reference samples. *Reference samples* are data points in an experiment that you select to be representative of the clusters for an individual assay. Reference samples are similar to positive controls in that the software can use both to bias the calls of Unknown data points.

1. If no reference panel files exist, you must first generate a reference panel file according to the procedures in the *TaqMan™ Genotyper Software Getting Started Guide* (Pub. No. 4448637).
2. In the **Workflow Menu** pane, select **Setup ▶ References** to open the **References** screen.
3. Click **Import**, browse to and select the reference panel file of interest, then click **Import**.

View and analyze the data

Analyze the data using Autocalling

1. In the **Workflow Menu** pane, select **Analysis ▶ Results** to open the **Results** screen.
2. In the toolbar, click **Analysis Settings**, select the **Call Settings** tab, select **Autocalling** as the call method, then click **OK**.
3. View the data in the scatter plot. If needed, perform manual calling.
4. View the data in the **Results** table. If needed, you can bookmark wells, omit wells, tag wells as reference samples, and/or enter comments about the wells.
5. View the data in the **Reference Samples** table. If needed, you can tag wells as reference samples.
6. View the data in the **Population Statistics** table.
7. Click **Analyze** to view the new results, then click **Save**.

Analyze the data using Classification Schemes

1. In the **Workflow Menu** pane, select **Analysis ▶ Results** to open the **Results** screen.
2. In the toolbar, click **Analysis Settings**, select the **Call Settings** tab, select **Classification Scheme** as the call method, then click **OK**.
3. View the data in the scatter plot.
4. Click **Select New Scheme**, select an appropriate scheme, click **OK**, then click **Analyze** to view the new results.
5. Adjust the classification regions for the current scheme: Click **Edit Classification Boundaries**, then click and drag the boundary lines and crosshairs as needed.
6. Click **Analyze** to view the new results, then click **Save**.

View the data in the Quality Control screen

1. In the **Workflow Menu** pane, select **Analysis ▶ Quality Control** to open the **Quality Control** screen.
2. Select the **Flags Summary** tab. Look for any flags that were generated by the analysis. Refer to the *TaqMan™ Genotyper Software Getting Started Guide* (Pub. No. 4448637) for a list of flag descriptions and recommended actions.
3. Select the **Assays** tab. In the **Assays** table, look for any assays that have a low call rate and/or value in a flag column. Select an assay to view detailed information in the scatter plot and **Results** table.
4. Select the **Experiments** tab. In the **Experiments** table, look for any experiments that have a low call rate and/or value in a flag column. Select an experiment to view detailed information in the plate layout and **Results** table.
5. Select the **Samples** tab. In the **Samples** table, look for any samples that have a low call rate and/or value in a flag column. Select a sample to view detailed information in the **Results** table.
6. Bookmark any wells of interest.
7. (If needed) Modify the data or reset the analysis settings (see “Analyze the data using Autocalling” on page 3 and “Analyze the data using Classification Schemes” on page 3, or “Set the analysis settings” on page 1).

(Optional) Enter comments for the study

1. In the **Workflow Menu** pane, select **Setup ▶ Properties** to open the **Properties** screen.
2. In the **Comments** field, enter comments about the study, then click **Add**. The software records the comment, your user name, and the date/time you added the comment.

Export and transfer data

Export analysis data

1. In the **Workflow Menu** pane, select **Export ▶ Analysis Data**.
2. Select the type of data to export (you can select both options at the same time):
 - **Analysis Results**, then select **Basic** or **Advanced**
 - **Analysis Settings**
 - **QC Summary**
3. Complete the remaining fields as desired, then click **Export**. If prompted, analyze and save the study to proceed with the export.
4. Locate the exported file (CSV or TXT file), then select **Open With ▶ Microsoft™ Office Excel™** to view the contents as a spreadsheet in the Microsoft™ Excel™ software.

Export an audit trail

1. In the **Workflow Menu** pane, select **Export ▶ Audit Trail**.
2. Complete all fields as desired, then click **Export**. If prompted, analyze and save the study to proceed with the export.
3. Locate the exported audit trail (CSV or TXT file), then select **Open With ▶ Microsoft™ Office Excel™** to view the contents as a spreadsheet in the Microsoft™ Excel™ software.

Transfer a study

1. To transfer out a study:
 - a. In the **Home** screen, select the study of interest, then click **Transfer out Study**.
 - b. Browse to a save location, enter a name for the study file (LAS), then click **Save**.
2. To transfer in a study:
 - a. In the **Home** screen, select the study of interest, then click **Transfer in Study**.
 - b. Browse to a save location, enter a name for the study file (LAS), then click **Open**.

Note: If you modify a study outside of the TaqMan™ Genotyper Software (that is, in another software program), you will not be able to open the study in the TaqMan™ Genotyper Software. The software will display an error message stating that the study is corrupt.

Limited product warranty

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Revision history: Pub. No. 4448638

Revision	Date	Description
C	29 November 2022	• The statement covering Limited Use Label Licenses was removed. • The instructions to enter the study properties were updated to remove the selection of an instrument type ("Enter the study properties" on page 1). • The information about the experiment type was updated to indicate that it can be changed after importing the experiments ("Enter the study properties" on page 1). • Information was added about the Show Cycle slider in the instructions to set the analysis settings ("Set the analysis settings" on page 1). • A workflow was provided in order to customize and save analysis settings ("Optional workflow to customize the analysis settings" on page 2). • The option to export the QC summary was added ("Export analysis data" on page 4).
B	7 January 2020	Updated for general style and formatting.
A	1 April 2010	New document.

The information in this guide is subject to change without notice.

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