Gene editing software at your fingertips.

Personal genetic analysis environment, made more accessible.

User Manual

Version 1

目次

1. Introduction

1.1 What is GeneQuick?

GeneQuick is a desktop application designed for molecular biology research using DNA sequences and plasmids. It allows users to carry out essential tasks in a single integrated environment, including viewing and editing sequences, visualizing plasmid maps, analyzing restriction enzymes, performing sequence alignment, analyzing chromatogram (AB1) data, and designing primers.

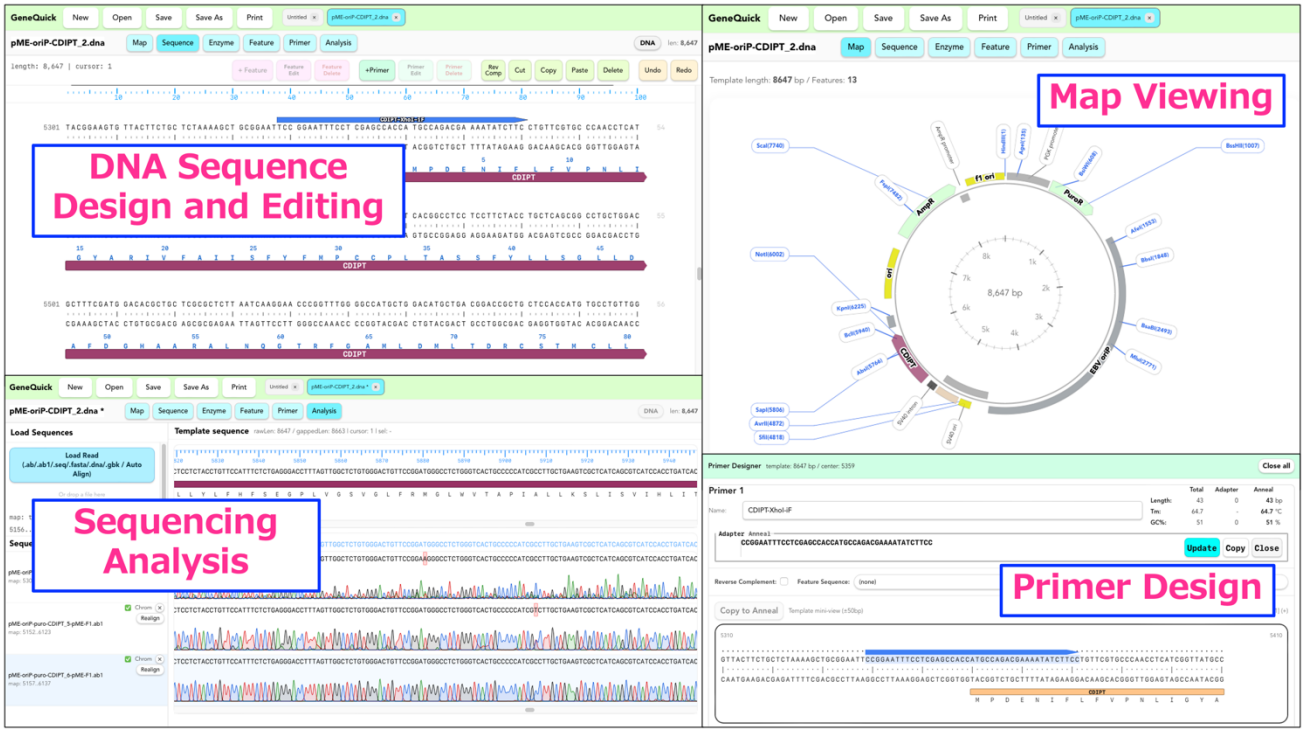


Figure 1-1. Overview of GeneQuick

GeneQuick supports major file formats such as **.gb, .fasta, .seq, .ape, .dna, and .ab1**, allowing users to import existing data directly and use it for analysis without additional conversion.

This software is designed not only for use in research laboratories, but also as a **personal tool** that individual researchers and students can easily use on their own computers. This allows users to carry out sequence analysis and design work efficiently, regardless of location or working environment.

In addition, GeneQuick supports multiple languages, including **English, Japanese, Chinese (Simplified and Traditional), Korean, German, French, Spanish, and Italian**, providing a multilingual environment accessible to researchers around the world.

GeneQuick offers a **14-day free trial** from the first launch, during which all features are available at no cost. After the trial period ends, users can continue using the software indefinitely by purchasing a license.

1.2 Key Features

- Perform sequence editing and analysis in one integrated software application
- Intuitive visualization of plasmid maps
- Fast and detailed viewing of AB1 chromatograms
- Sequence comparison with high-speed alignment
- Built-in primer design tools
- Personal-use design suitable for individual researchers and students
- High compatibility with major file formats
- Multilingual support for users around the world
- 14-day free trial and a perpetual license available through one-time purchase

1.3 System Requirements

GeneQuick can be used in the following environment.

Supported Operating Systems
Mac: Apple Silicon Macs (M1 or later), macOS Sonoma or later
Windows: Windows 11 or later

Supported operating system versions may change in future updates.

Recommended Environment
Memory: **8 GB or more**
Storage: **At least 500 MB of free space**
Internet connection: **Required only for license activation** (normal use is available offline)

GeneQuick is designed as a desktop application that runs comfortably not only on shared computers in laboratories, but also on personal laptops used by individual researchers and students.

2. Installation and Initial Setup

2.1 Installation

Download the version of GeneQuick that matches your computer environment from the GeneQuick introduction webpage (https://gene-quick.com/index.html).

For Mac
Open the **.dmg** file, then drag and drop the application icon into the **Applications** folder.

For Windows
Open the **.exe** file and follow the on-screen instructions to complete the installation.

[Installing the Windows Version]

During installation, you may see a message from Microsoft Defender SmartScreen stating, "Windows protected your PC." This message does not necessarily mean that the application is unsafe. It may appear for new applications that do not yet have a sufficient reputation on Windows.

If this warning appears, you can proceed as follows:

1. Click "More info".

2. Click "Run anyway".

3. Then follow the on-screen instructions to continue the installation.

2.2 First Launch

2.2.1 For Mac

When launching GeneQuick for the first time, the application may not open from Launchpad or other standard shortcuts.

In that case, open **Finder** and select: **Go → Applications**

Then select the **GeneQuick** application, **Control-click** it (or right-click it), and choose **Open**.

An alert message may appear, but please click “Open” to proceed.

After the first launch, GeneQuick can be opened normally from Launchpad and other standard shortcuts.

2.2.2 For Windows

Click the GeneQuick icon created after installation to open the application.

3. License and Usage

3.1 Free Trial

When you launch GeneQuick for the first time, a **14-day free trial** will begin automatically.

Please note that an internet connection is required during the free trial period. After purchasing a license, GeneQuick can be used offline.

After the 14-day trial period ends, the use of the application will be restricted. We therefore recommend purchasing a license before the trial expires.

Figure 3-1. Screen displayed during the free trial period

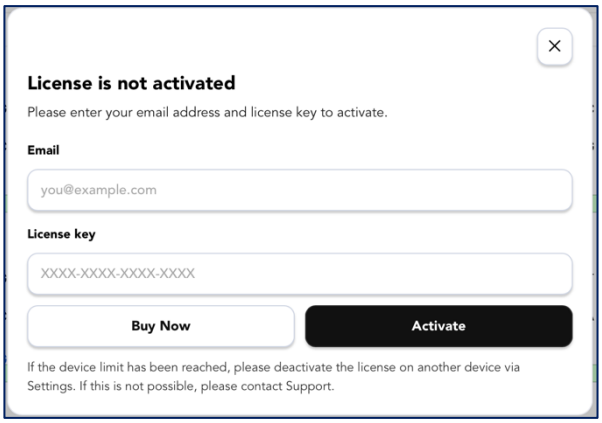
3.2 How to Purchase a License

To purchase a license, click the **Buy** button displayed in the lower-right corner of the application, or visit the purchase page available on the GeneQuick introduction website (https://gene-quick.com/index.html).

On the purchase page, please enter the required information, such as your **institution, name, and email address**, and complete the payment process.

After the purchase is completed, a **license key** will be sent to your registered email address.

3.3 License Activation



To activate your license, click the **Activate** button in the lower-right corner of the screen, or open the **Settings** menu in the menu bar and select **Activate**.

Enter your **email address** and the **license key** provided in the email you received after purchase, and then click the **Activate** button.

If the activation is successful, the free trial display in the lower-right corner of the screen will disappear, and GeneQuick will become available as a licensed version.

3.4 License Deactivation and Management

With a standard license, GeneQuick can be used on up to **two PCs**.
With a student license, GeneQuick can be used on **one PC** only.

The software cannot be used on more devices than the number allowed by your license.

If you would like to move your license to another PC, you must first deactivate the license on the PC currently in use.

To deactivate the license, open the **Settings** menu from the menu bar and select **Deactivation (This PC)**.

A confirmation dialog will appear. Click **OK** to complete the deactivation.

If you are unable to deactivate the license on your old PC due to hardware failure or another issue, please contact us and provide your **institution, name, and email address**.

4. Screen Layout

4.1 Menu Bar

The GeneQuick menu bar consists of the following menus: **GeneQuick, File, View, Sequence, Settings,** and **Language**.

Figure 4-1. Menu bar

4.1.1 “GeneQuick” Menu

GeneQuick: Displays application version information.
Hide GeneQuick: Hides the GeneQuick window.
Hide Others: Hides all running applications except GeneQuick.
Show All: Shows all running applications that are currently hidden.
Quit GeneQuick: Closes the GeneQuick application.

4.1.2 The “File” Menu

New: Creates a new file.
Open: Opens an existing file.
Save: Saves the current file.
Save As: Saves the file with a specified file format and file name.
Print: Prints the current file.
Export: Exports the file in **GenBank (.gb), FASTA (.fa),** or **Sequence (.seq)** format.

4.1.3 The “View” Menu

Map: Displays the map view of the sequence.
Sequence: Displays the nucleotide sequence.
Show Features: Displays the list of features.
Show Primers: Displays the list of primers.
Show Enzymes: Displays the list of restriction enzymes.
Enter Full Screen: Switches the display to full-screen mode. Press **Esc** on the keyboard to return to the normal view.

4.1.4 The “Sequence” Menu

Show Sequence: Switches to the sequence view.
Show Alignment: Switches to the analysis view.
Find: Displays a search box at the bottom of the screen.
Go to Position: Moves the cursor to a specified position in the sequence view.
Go to Top: Moves to the beginning of the sequence view.

4.1.5 The “Settings” Menu

Activate: Activates the license. See **Section 3.3**.
Deactivate: Deactivates the license. See **Section 3.4**.

4.1.6 The “Language” Menu

You can select the display language from **English, Japanese, Chinese (Simplified), Chinese (Traditional), Korean, German, French, Spanish,** and **Italian**.

4.2 Common Screen Buttons

4.2.1 Top of the Screen (First Row)

The first row at the top of the screen contains the following buttons: **New, Open, Save, Save As,** and **Print**.

Files that are currently open are also displayed in this row as tabs.

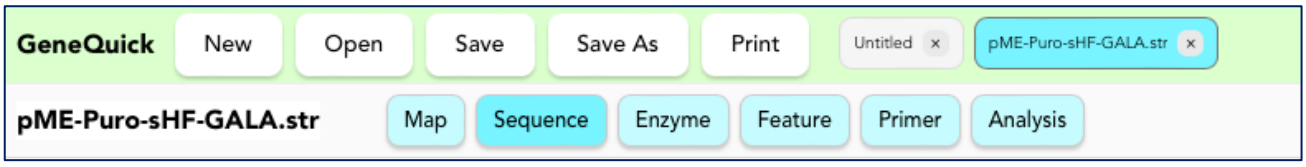


Figure 4-2. Common screen buttons

4.2.2 Top of the Screen (Second Row)

The second row at the top of the screen contains the following buttons: **Map, Sequence, Enzyme, Feature, Primer,** and **Analysis**.

The file name is displayed on the left side.

Clicking the **DNA** button on the right side allows you to switch between **DNA** and **RNA** mode.

5. Basic Operations

5.1 Opening Files

5.1.1 Creating a New File

To create a new file, select **New** from the **File** menu in the menu bar, or click the **New** button at the top of the screen.

5.1.2 Opening an Existing File

To open an existing file, select **Open** from the **File** menu in the menu bar, or click the **Open** button at the top of the screen. Then, move to the folder containing the file you want to open and select the file.

In addition to **.geneq** files, GeneQuick supports **.gb, .fasta, .seq, .dna,** and **.ab1** files.

Files can also be opened by drag and drop. When you drag a file onto the GeneQuick window, the message **“Drop a file to open”** will appear. Drop the file onto this area to open it.

5.2 Saving Files

To save a file, select **Save** from the **File** menu in the menu bar, or click the **Save** or **Save As** button at the top of the screen.

5.2.1 GeneQuick Format (.geneq)

We recommend saving files in the native GeneQuick format (**.geneq**).

Once a file has been saved in this format, it can be overwritten directly the next time by using **Save**.

In addition to sequence data, the **.geneq** format can store features, primer information, and alignment data used in analysis, including alignments with Sanger sequencing data.

GeneQuick can also save files in **GenBank (.gb, .gbk)**, **FASTA (.fasta, .fa)**, and **Sequence (.seq)** formats.

5.2.2 GenBank Format (.gb, .gbk)

In **GenBank** format, feature and primer information can be saved, but alignment data, including alignments with Sanger sequencing data, cannot be saved.

If you want to open the file in other software such as **ApE** or **SnapGene**, please save it in **GenBank** format.

5.2.3 FASTA Format (.fa, .fasta) and Sequence Format (.seq)

In **FASTA (.fa, .fasta)** and **Sequence (.seq)** formats, feature and primer information are not saved. Only the nucleotide sequence itself is stored.

6. How to Use the Sequence View

In the **Sequence** view, you can display and edit nucleotide sequences, as well as add and edit features and create and edit primers. However, **.ab1** files cannot be edited in the Sequence view. For editing **.ab1** files, please refer to **Section 12. How to Use the Analysis View**.

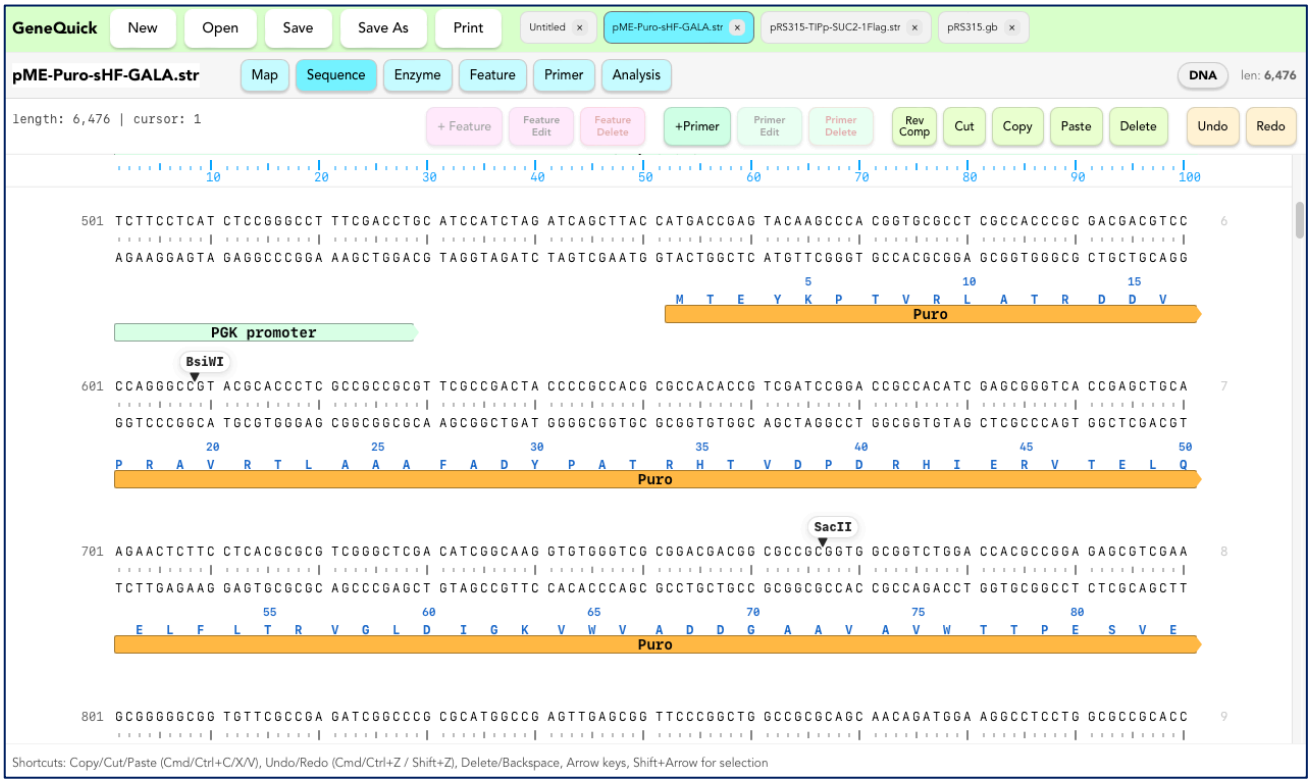


Figure 6-1. Sequence view

6.1 Viewing and Editing Nucleotide Sequences

When a file is opened, the nucleotide sequence is displayed in the **Sequence** view. To edit the sequence, move the cursor to the desired position.

To select multiple bases, click and drag across the sequence. You can also select multiple bases by holding down the **Shift** key while using the arrow keys on the keyboard.

6.1.1 Copying Bases

Select the nucleotide sequence you want to copy, then use **Copy** (**Command** + **C**) or click the **Copy** button in the third row at the top of the screen.

6.1.2 Cutting Bases

Select the nucleotide sequence you want to cut, then use **Cut** (**Command** + **X**) or click the **Cut** button in the third row at the top of the screen.

6.1.3 Inserting Bases

Move the cursor to the desired position and type **A, G, C, T,** or **U**.

If you have copied a sequence, move the cursor to the desired position and use **Paste** (**Command** + **V**) or click the **Paste** button in the third row at the top of the screen.

6.1.4 Deleting Bases

Press the **Backspace** key to delete the base immediately before the cursor. Press the **Delete** key to delete the base immediately after the cursor.

To delete multiple bases at once, select the desired region and then press **Backspace** or **Delete**. Multiple bases can be selected either by clicking and dragging across the sequence or by holding down the **Shift** key while using the arrow keys.

You can also delete selected bases by clicking the **Delete** button in the third row at the top of the screen.

6.1.5 Replacing Bases

Select the region you want to replace, then paste the previously copied nucleotide sequence by using **Paste** (**Command** + **V**).

6.1.6 Reverse Complementing a Sequence

To convert a nucleotide sequence into its reverse complement, select the region you want to change and click the **RevComp** button in the third row at the top of the screen.

If no sequence is selected, the entire file will be converted into the reverse complement sequence.

6.1.7 Undo and Redo

To undo an edit, click the **Undo** button in the third row at the top of the screen. To redo an action, click the **Redo** button.

Please note that **Undo** and **Redo** have limitations, so we recommend saving your sequence regularly.

6.1.8 Switching Between DNA and RNA Mode

By default, GeneQuick is set to **DNA** mode. If your sequence is RNA, or if you want to convert a DNA sequence to RNA display mode, click the **DNA** button on the right side of the second row at the top of the screen.

The label will change to **RNA**, indicating that RNA mode is active. Click the **RNA** button again to return to **DNA** mode.

6.1.9 Selecting Features, Primers, and Amino Acid Sequences

Clicking a feature or primer track selects the corresponding nucleotide sequence, allowing it to be copied, cut, or deleted.

In addition, if you select amino acid residues within a **CDS** and right-click, the following options will appear:

- **Copy amino acid sequence for selection**
- **Copy amino acid sequence for entire CDS**

Selecting either option will copy the amino acid sequence.

6.2 Adding and Editing Features

Features can be displayed on the nucleotide sequence. If you open a file from **GenBank**, **Addgene**, or another source in which feature regions have already been defined, those features will be displayed automatically.

6.2.1 Adding a Feature

Select the region of the nucleotide sequence where you want to add a feature. With the region selected, click the **+ Feature** button in the third row at the top of the screen. The **Add Feature** window will open.

In the **Add Feature** window, enter the following information:

Feature name: Enter the name of the feature.
Type: Select the feature type, such as **CDS**, **gene**, or **promoter**. If **CDS** is selected, the translated amino acid sequence will be displayed on the nucleotide sequence.
Start and **End**: The start and end positions of the selected region are displayed automatically. If

necessary, you can change these positions manually.
Color: Select the label color for the feature. By default, colors are assigned according to feature type.
Note: Enter any notes if needed.

After entering the required information, click **OK** to register the feature.

If you click **Cancel** or the × button, the feature will not be added and the **Add Feature** window will close.

6.2.2 Editing a Feature

To edit a feature, click the feature track. Then right-click and select **Edit Feature**. Alternatively, you can click the **Feature Edit** button in the third row at the top of the screen to open the editing window.

Make the necessary changes in the **Edit Feature** window, then click **OK**.

6.2.3 Deleting a Feature

To delete a feature, click the feature track and then right-click. Select **Delete Feature** from the menu. A confirmation dialog will appear. Click **Delete** to complete the deletion.

Alternatively, after selecting the feature track, you can click the **Feature Delete** button in the third row at the top of the screen.

6.3 Adding and Editing Primers

Primers can also be displayed on the nucleotide sequence.

6.3.1 Adding a New Primer

Select the region for which you want to design a primer, then click the + **Primer** button in the third row at the top of the screen. The **Primer Designer** window will open.

For details on how to use the Primer Designer, please refer to **Section 11**.

6.3.2 Editing a Primer

To edit a primer, click the primer track. Then right-click and select **Edit Primer**. Alternatively, you can click the **Primer Edit** button in the third row at the top of the screen to open the editing window.

Make the necessary changes in the **Primer Designer** window, then click **Update**.

6.3.3 Deleting a Primer

To delete a primer, click the primer track and then right-click. Select **Delete Primer** from the menu. A confirmation dialog will appear. Click **Delete** to complete the deletion.

Alternatively, after selecting the primer track, you can click the **Primer Delete** button in the third row at the top of the screen.

7. How to Use the Map View

In the **Map** view, you can check the positions of nucleotide sequences, features, and restriction enzyme sites. You can also select a region on the map and jump to the corresponding sequence in the **Sequence** view.

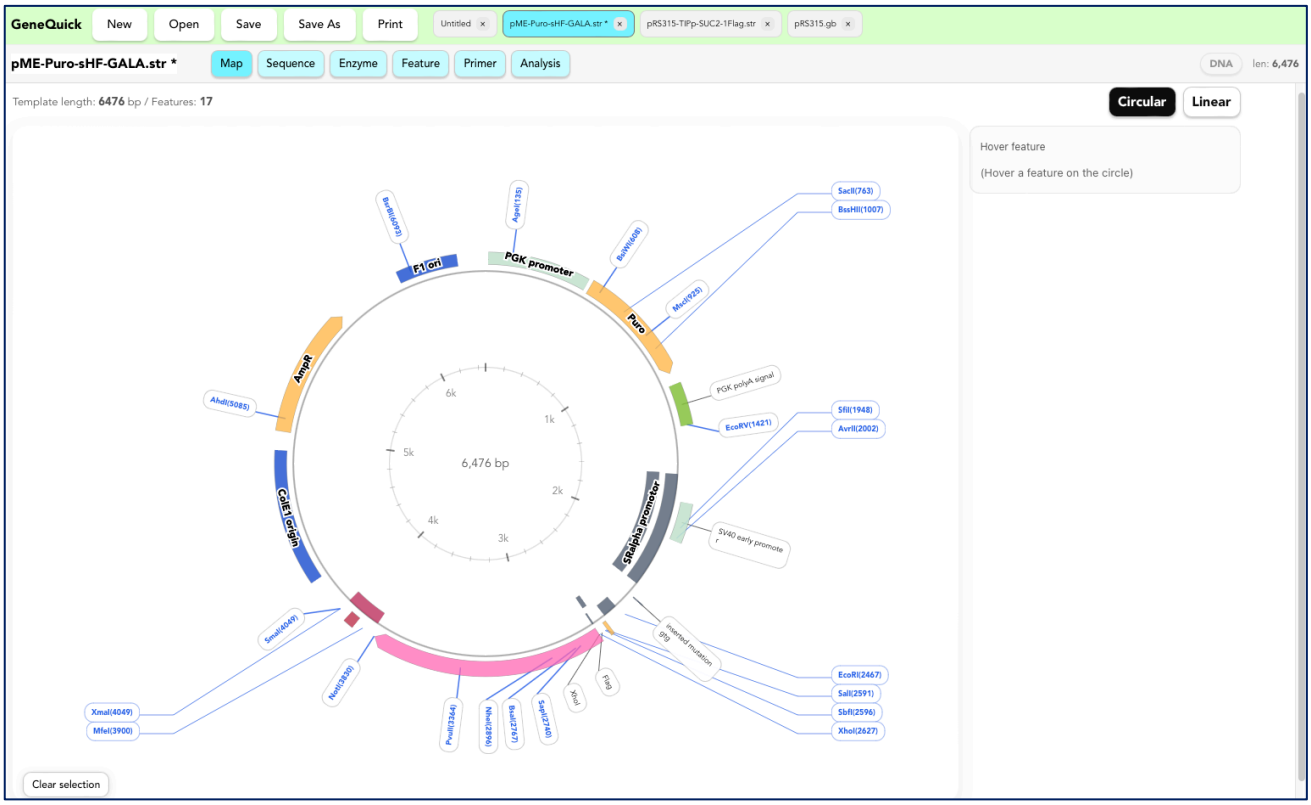


Figure 7-1. Map view

7.1 Displaying the Map

With a sequence file open, click **Map** in the second row at the top of the screen. The map will be displayed based on the nucleotide sequence, features, and restriction enzyme sites.

The displayed restriction enzyme sites are based on the enzymes selected in the **Enzyme** view.

In the upper-left corner of the screen, **Template length** and **Features** are shown.

When you place the mouse cursor over a feature, the position and direction of that feature are displayed in the upper-right corner.

7.2 Selecting Circular or Linear View

By default, the map is displayed automatically as either **Circular** or **Linear**, depending on the file information.

If you want to change the display format, click the **Circular** or **Linear** button in the upper-right corner of the screen.

7.3 Selecting and Clearing Regions

You can select specific regions directly on the map.

When you click a feature track, **sel** (selected position and length) and **Selected** (the name of the selected feature) are displayed in the upper-left corner of the screen.

If you double-click a feature track, GeneQuick will switch to the **Sequence** view and jump to the nucleotide sequence of the selected feature.

You can also double-click a restriction enzyme site to move to the **Sequence** view and jump to the nucleotide sequence at that restriction site.

In addition, if you click one restriction enzyme site and then **Shift-click** another restriction enzyme site, the sequence between the two sites will be selected and shown as a **yellow region**.

If you double-click the selected yellow region, GeneQuick will switch to the **Sequence** view and jump to that selected region.

To clear the selected region, click **Clear selection** in the lower-left corner of the screen.

8. How to Use the Enzyme View

In the **Enzyme** view, information about restriction enzyme sites in the nucleotide sequence is displayed. You can also change which restriction enzymes are shown.

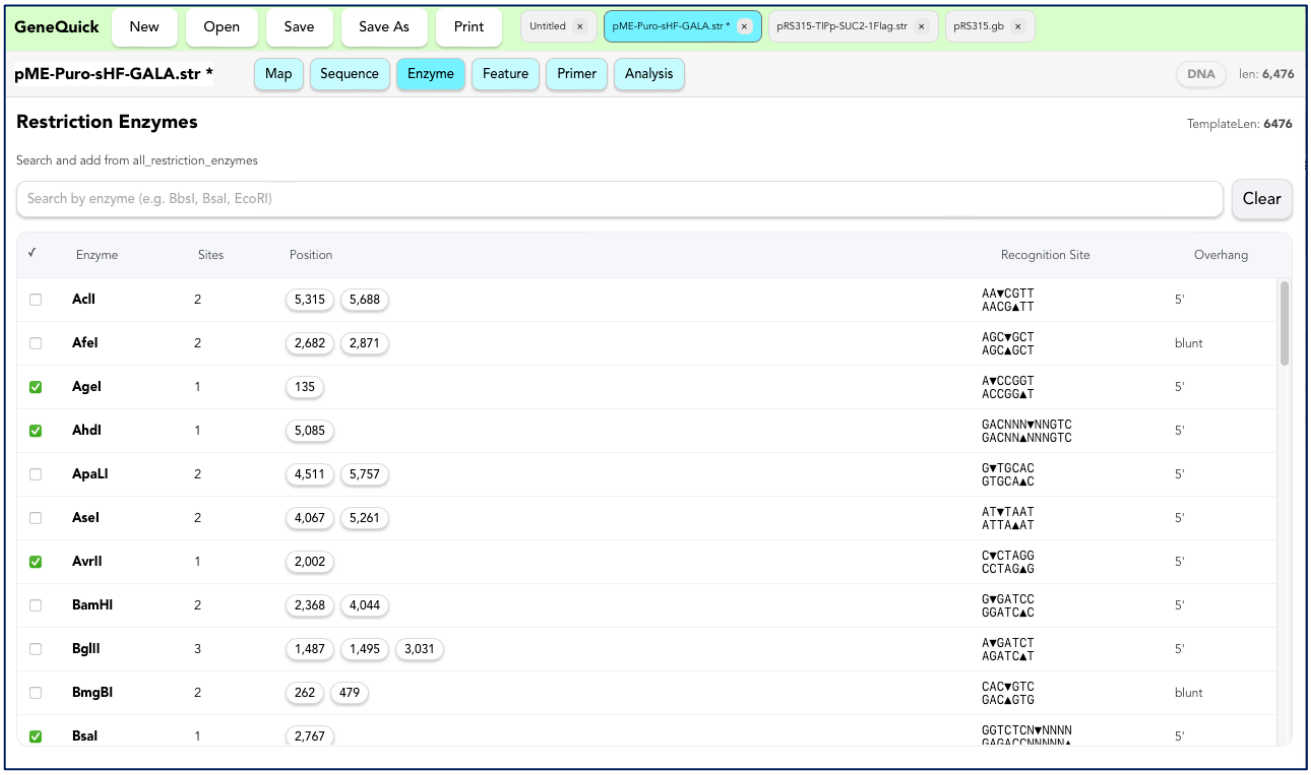


Figure 8-1. Enzyme view

8.1 Displaying Restriction Enzymes

With a sequence file open, click **Enzyme** in the second row at the top of the screen. A list of restriction enzyme sites in the nucleotide sequence will be displayed.

In the list, you can check the following information: **Enzyme** (enzyme name), **Sites** (number of sites), **Position**, **Recognition Site**, and **Overhang**.

By default, the list includes commonly used restriction enzymes.

Among them, restriction enzyme sites that are **unique** within the nucleotide sequence, meaning they appear only once, are checked and displayed in the **Sequence** view and the **Map** view.

You can turn the display of each enzyme on or off by checking or unchecking the box on the left side of the enzyme list.

8.2 Searching for and Adding Restriction Enzymes

In the **Enzyme** view, you can search for a restriction enzyme by entering its name in the search box above the enzyme list. Matching enzymes will then be displayed.

If you find an enzyme you want to add, click **Add** on the right side.

If an enzyme has already been added to the list, it will be marked as **Added**.

For enzymes that have already been added, check **Show** if you want them to be displayed in the **Sequence** view or the **Map** view.

To close the search box, click the **Clear** button on the right side of the search field.

To remove an added enzyme, click the – symbol shown next to the enzyme name in the list.

8.3 Jumping to a Restriction Enzyme Site

If you click a number in the **Position** column of the restriction enzyme list, GeneQuick will switch to the **Sequence** view and jump to the corresponding restriction enzyme site.

9. How to Use the Feature View

In the **Feature** view, information about features in the nucleotide sequence is displayed. You can also edit or delete existing features.

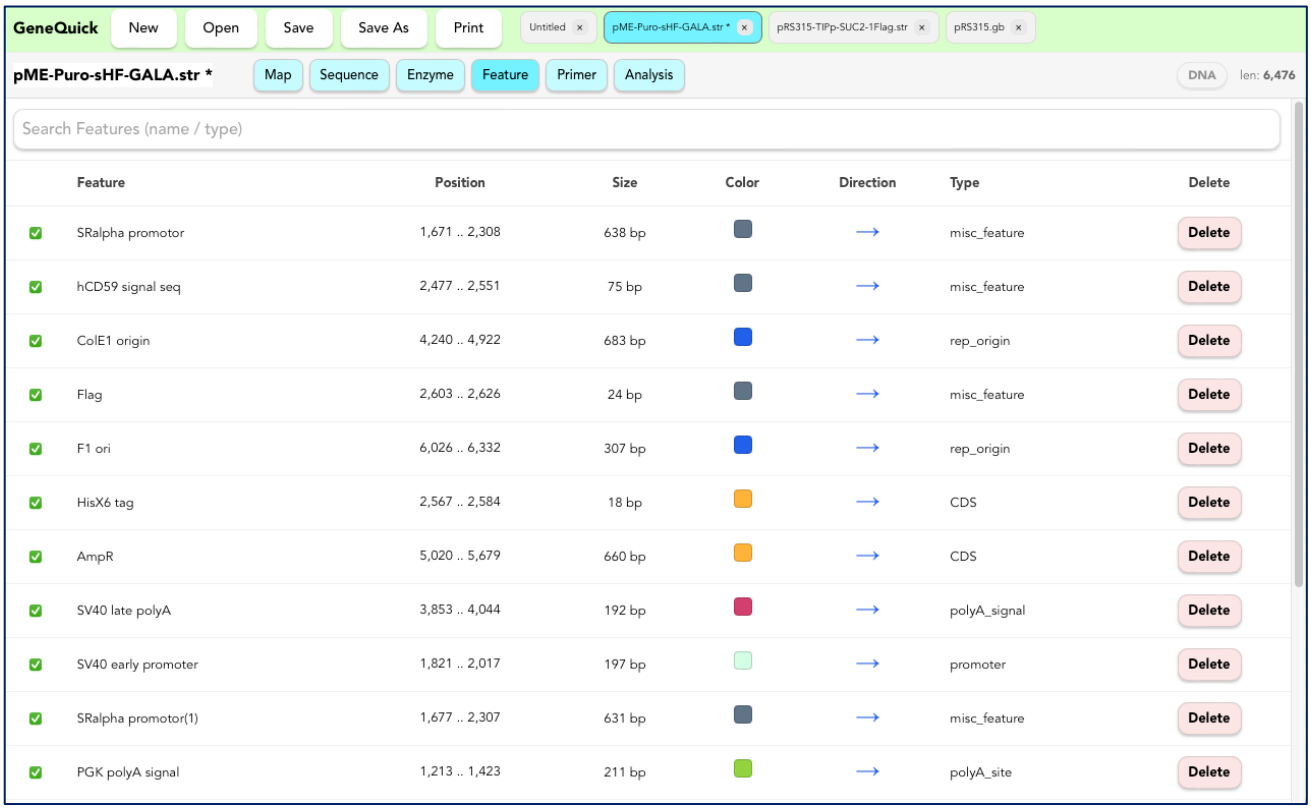


Figure 9-1. Feature view

9.1 Displaying Features

With a sequence file open, click **Feature** in the second row at the top of the screen. A list of features in the nucleotide sequence will be displayed.

In the list, you can check the following information: **Feature** (feature name), **Position**, **Size**, **Color**, **Direction**, and **Type**.

9.2 Searching for Features

You can search for features in the list by entering a keyword in the search box.

9.3 Editing and Deleting Features

To edit a feature, double-click the feature in the list. The **Edit Feature** window will open.

After making your changes, click **OK** to save them. To cancel and return without saving, click **Cancel** or the × button.

To delete a feature, click the **Delete** button on the right side of the feature in the list. A confirmation dialog will appear. Confirm the deletion to remove the feature.

9.4 Jumping to a Feature

If you single-click a feature in the list, its background will be highlighted in blue.

When you then move to the **Sequence** view, GeneQuick will jump to and display the nucleotide sequence corresponding to the selected feature.

10. How to Use the Primer View

In the **Primer** view, information about primers in the nucleotide sequence is displayed. You can also edit or delete existing primers.

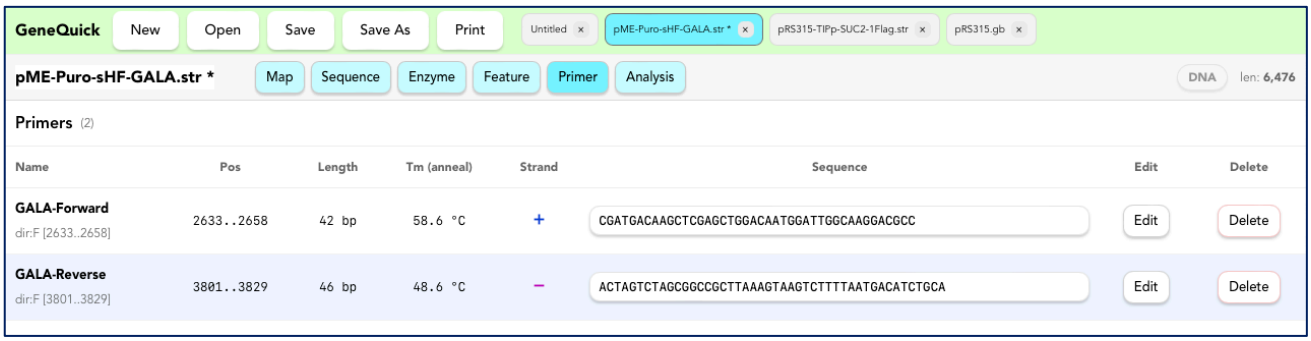


Figure 10-1. Primer view

10.1 Displaying Primers

With a sequence file open, click **Primer** in the second row at the top of the screen. A list of primers in the nucleotide sequence will be displayed.

In the list, you can check the following information: **Name**, **Pos** (position), **Length**, **Tm (anneal)**, **Strand**, and **Sequence**.

10.2 Editing and Deleting Primers

To edit a primer, click the **Edit** button for the primer in the list. The **Primer Designer** window will open.

After making your changes, click **Update** to apply them.

To delete a primer, click the **Delete** button on the right side of the primer in the list. A confirmation dialog will appear. Confirm the deletion to remove the primer.

11. How to Use the Primer Designer

The **Primer Designer** allows you to design multiple primers at the same time while comparing them side by side.

You can add additional primer cards by clicking the + **Primer** button in the lower-left corner of the **Primer Designer** window.

Figure 11-1. Primer Designer view

11.1 Opening the Primer Designer

To open the **Primer Designer**, go to the **Sequence** view and click + **Primer** in the third row at the top of the screen.

If you select a nucleotide sequence before opening the Primer Designer, the selected sequence will be entered automatically when the window opens.

To edit an existing primer from the **Sequence** view, click the primer track and then click **Primer Edit**.

You can also open the **Primer Designer** from the **Primer** view by clicking **Edit** for the primer in the list.

11.2 Using the Primer Designer

11.2.1 Entering Name, Adaptor, and Anneal

When the **Primer Designer** window opens, first enter the **Name**, **Adaptor**, and **Anneal** fields.

Name: Enter the name of the primer.
Adaptor: Enter the sequence of the adaptor region.
Anneal: Enter the sequence used for annealing. By default, the sequence selected in the **Sequence** view is entered automatically.

When designing the **Adaptor** and **Anneal** sequences, refer to the **Length**, **Tm**, and **GC%** values shown in the upper-right corner, as well as the **Template mini-view** shown at the bottom of the window.

11.2.2 Useful Functions for Primer Design

Reverse Complement:
If this option is checked, the sequence will be converted to its reverse complement. When this option is enabled, feature sequences and restriction enzyme sequences described below will also be entered in reverse-complement form.

Feature Sequence:
Commonly used sequences, such as **Kozak sequences** and **protease recognition sequences**, are available here. When selected, the sequence is automatically entered into the **Adaptor** field.

Restriction Enzyme:
If you select a restriction enzyme recognition sequence from the list, that sequence will be automatically entered into the **Adaptor** field.

Copy to Anneal:
Select any region from the sequence shown in the **Template mini-view**, then click **Copy to Anneal** to add the selected sequence to the **Anneal** field.

11.2.3 Add, Copy, and Close

After entering the **Name**, **Adaptor**, and **Anneal** fields, click **Add** to register the primer sequence. The primer will then also be displayed in the **Sequence** view.

Copy:
Clicking **Copy** copies the full primer sequence (**Adaptor** + **Anneal**), which can then be pasted into another text file such as a Word document.

Close:
Clicking **Close** closes the current primer design window. Please note that any primer currently being designed will not be saved unless it has been added.

11.2.4 Close All

Click **Close all** to close the **Primer Designer** window.

12. How to Use the Analysis View

The **Analysis** view is mainly used to align and compare **template DNA** with **Sanger sequencing data** such as **.ab1** files. Based on the Sanger sequencing results, you can also edit the sequence.

In addition to **Sanger sequencing data (.ab1 files)**, the Analysis view also supports multiple file formats, including **.seq, .fasta, .dna,** and **.gb**, allowing you to compare sequences from different sources.

Figure 12-1. Analysis view

12.1 Opening the Analysis View

With a sequence file open, click **Analysis** in the second row at the top of the screen.

The nucleotide sequence will be displayed as the **template sequence**.

12.2 Loading Sequence Files (.ab1 and Others)

Click **Load Read** in the upper-left corner of the screen to select a file.

Choose the sequence file you want to load, then click **Open**. The file will be loaded into the Analysis view.

Alternatively, you can drag and drop a sequence file onto the **Load Read** area. In this case, multiple files can also be loaded at the same time.

12.3 Aligning Sequence Files

When a sequence file such as an **.ab1** file is loaded, it is automatically aligned to the template sequence.

If the loaded file is an **.ab1** file, you can display the chromatogram trace data by checking **Chrom** for each file shown on the left side of the screen.

If a base in the loaded sequence differs from the template sequence, or if there is no corresponding base (**gap**), that position is shown with a **red background**.

If a base is present in the loaded sequence but not in the template sequence, that position is shown with a **blue background**.

12.4 Editing Sequences

12.4.1 Editing the Template Sequence

To edit the template sequence, move the cursor to the target position and insert, delete, or replace bases as needed.

You can edit the sequence by selecting bases and using standard operations such as **Copy** (**Command + C**), **Paste** (**Command + V**), and **Delete** (**Delete** or **Backspace**).

When bases are inserted into or deleted from the template sequence, the alignment is automatically recalculated.

12.4.2 Editing Sanger Sequencing Data

Aligned sequence files can also be edited by selecting bases and using standard operations such as **Copy** (**Command + C**), **Paste** (**Command + V**), and **Delete** (**Delete** or **Backspace**).

When trimming bases from the **5′ end** or **3′ end**, it is recommended to delete all bases up to the sequence end for a cleaner result.

Please note that editing a loaded sequence file does **not** automatically realign it to the template sequence. If realignment is needed, click the **Realign** button for the corresponding file on the left side of the screen.

12.5 Notes on Analysis

If you edit the **template sequence** in the Analysis view, those changes will also be reflected in the **Sequence** view.

In contrast, edits made to loaded sequence files during analysis are **not saved**. These edits are intended only for checking and reviewing Sanger sequencing data.

When you save the file in **.geneq** format, the loaded sequence files are saved together with the project.

13. Printing

13.1 How to Print

The following views can be printed: **Map**, **Sequence**, **Enzyme**, **Feature**, and **Primer**.
The **Analysis** view cannot be printed.

To print, open the view you want to print and click **Print** in the first row at the top of the screen.

You can also print from the menu bar by selecting **File → Print**.