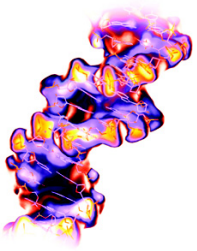


Quick Reference Guide

In This Guide

This quick reference guide describes example analysis workflows for the GeneMapper® Software Version 4.0. It also summarizes the version(s) of the Data Collection Software, Windows® operating system, and sample data files that are supported by the GeneMapper Software for specified instruments.

For More Information

For more information about the workflows described in this guide, refer to the:

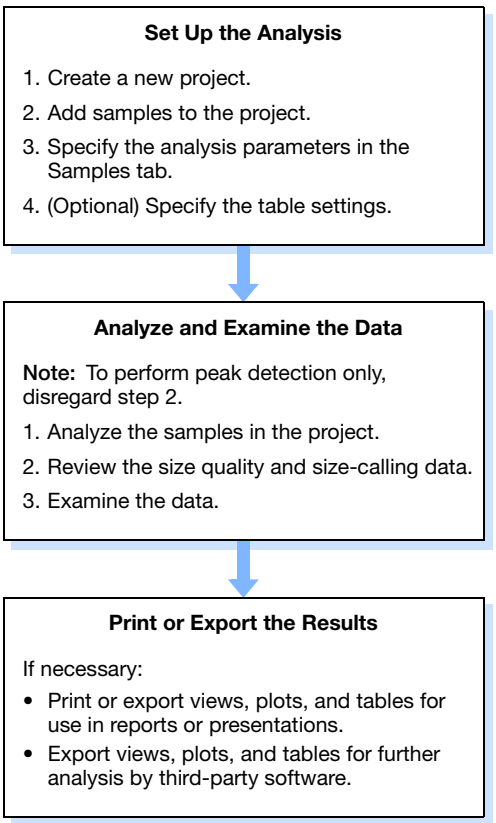
- ***GeneMapper® Software Version 4.0 Getting Started Guides*** – Shipped with the software, as well as available on the *GeneMapper® Software Version 4.0 Documentation CD* as portable document format (PDF) files.
- ***GeneMapper® Software Version 4.0 Online Help*** – Accessible from the GeneMapper Software by doing one of the following:
  - Clicking in the toolbar
  - Selecting **Help** ▸ **Contents and Index**
  - Pressing **F1**

Basic Sizing/Peak Detection Analysis Workflow

Overview

Use the method described in the following workflow to perform a basic sizing and/or peak detection analysis using the GeneMapper Software.

Note: This workflow does not include instructions for performing allele or genotype calling.



Setting Up the Analysis

Note: To perform peak detection only, disregard step 3c.

1. Create a new project:
   a. In the GeneMapper window toolbar, click .
   b. Select the appropriate project type.
   c. Click **OK**.
2. Click to add samples to the project.
3. In the Samples tab, specify the analysis parameters for the samples in the project:

   Note: You can use the fill-down function to apply the parameters to all the samples at one time.

   a. In the Analysis Method column, select or create an analysis method with the following settings:

Tab	Parameter	Setting
Allele	Bin Set	Select **None**.
Peak Detector	Peak Detection Algorithm	Select the appropriate algorithm (**Basic**, **Advanced**, or **Classic**) and the appropriate peak sizing method (as applicable). **IMPORTANT!** If you use the Classic peak detection algorithm, you must select a size standard created in Classic mode.

   b. In the Panel column, select **None**.
   c. In the Size Standard column, select the appropriate size standard.
4. (Optional) In the toolbar, select or create table settings for the analysis.

Analyzing and Examining the Data

Note: If you want to perform peak detection only, disregard step 2.

1. Click  to analyze the samples in the project.
2. Review the size quality and size-calling data.
3. Examine the data.

   Note: In the plot windows, the sizing table shows information about the detected peaks.

Printing or Exporting the Results

If necessary, print or export the results.

To print the results:

1. In the GeneMapper window, select the desired tab.
2. Select **File** ▸ **Print**.

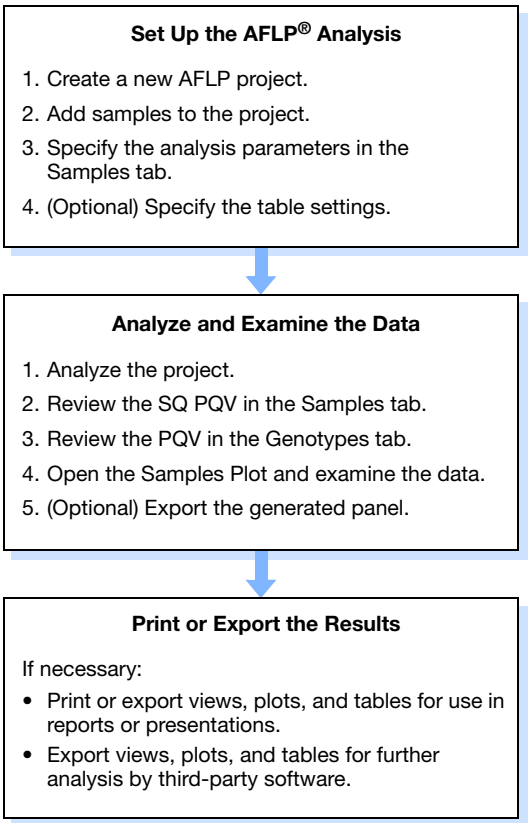
To export the results:

1. Select the desired table setting.
2. Select **File** ▸ **Export Table**.

AFLP® Analysis Workflow

Overview

Use the method described in the following workflow to study band patterns from multiple amplified fragment length polymorphisms (AFLP®) simultaneously.



Automated Generation of AFLP® Panels

The GeneMapper Software can generate panel data algorithmically from AFLP sample files added to a project. The generated panel, which consists of the bin definitions for the peaks of all samples in the project, can be exported for use in other projects after data analysis.

IMPORTANT! The Auto Bin function cannot generate bins from AFLP data. To generate panels from AFLP samples, use the automated panel function of the AFLP analysis method described in this workflow.

Setting Up the AFLP® Analysis

1. Click to create a new project and select **AFLP** for the project type.
2. Click to add samples to the project.
3. In the Samples tab, specify the analysis parameters for the samples in the project:

   Note: You can use the fill-down function to apply the parameters to all the samples at one time.

   a. In the Analysis Method column, select or create an AFLP analysis method with the following settings:

   IMPORTANT! All samples must use the same analysis method.

Tab	Parameter	Setting
Allele	Bin Set	Select **None** to generate the panel automatically, or select an appropriate bin set if you are using an existing panel.
	Analyze Dyes	Select the dyes that you want to analyze.
	Analysis Range	Use the default settings or enter a desired range (bps).
	Panel	Select **Generate panel using samples** to have the software generate the panel automatically.‡
	Allele Calling	Select an appropriate naming method (**Name alleles using bin names** or **Name alleles using labels**).
Peak Detector	Peak Detection Algorithm	Use the default settings, or select the appropriate algorithm (**Basic**, **Advanced**, or **Classic**) and an appropriate peak-sizing method. **IMPORTANT!** If you use the Classic peak detection algorithm, you must select a size standard definition that was created in Classic mode.
Peak Quality	Use the default settings or enter values for the Max Peak Width and Pull-Up Ratio.	
Quality Flags	Use the default settings or enter values for the Quality Flag Settings and PQV Thresholds.	

‡ When configured to generate a panel automatically, the software creates bins from the collective peaks present in all samples of the project, not for each sample individually.

b. In the Panel column, select **None** (the analysis method is configured to generate the panel automatically).

> **IMPORTANT!** The analysis method and panel that you select must use the same bin set.

c. In the Size Standard column, select the appropriate size standard.

4. (Optional) In the toolbar, select or create table settings and plot settings for the analysis.

> **IMPORTANT!** If you create a table setting, select the following options in the Genotype tab of the Table Settings Editor:
> - Limit the number of displayed alleles shown to the number of bins.
> - Show only binned alleles in their respective bin positions.

Analyzing and Examining the Results

1. Click ▶ to analyze the project.
2. In the Samples tab, review the Size Quality (SQ) Process Quality Value (PQV).

   If necessary, fix failed size standards in the Size Match Editor, then reanalyze the samples that failed sizing. Samples that display ● (low quality) fail sizing and are not genotyped. Samples that display ⚠ (check) are genotyped but may have lower Genotype Quality (GQ) values.
3. In the Genotypes tab, review the PQV (BD, OS, and SPU).
4. Open the Samples Plot and examine the data:
   a. (Optional) Overlay and verify the concordance of the size standards data.
   b. Overlay the sample data and review the electropherograms for polymorphisms.
   c. If necessary, edit the genotype calls and generated bins.
5. (Optional) If the software generated a panel for the project:
   a. In the GeneMapper window, select **File ▸ Export Project Panel** to export the panel from the project.
   b. In the Panel Manager, select **File ▸ Import Panels** to import the panel for use in later projects.

Printing and Exporting the Results

If necessary, print or export the results.

To print the results:

1. In the GeneMapper window, select the desired tab.
2. Select **File ▸ Print**.

To export the results:

1. Select the desired table setting.
2. Select **File ▸ Export Table**.

LOH Microsatellite Analysis Workflow

Overview

Use the method described in the following workflow to perform microsatellite-based relative peak height comparisons, such as loss of heterozygosity (LOH) or replication error (RER).

Set Up the LOH Microsatellite Analysis

1. Create a kit and a panel for the project.
2. Create a new microsatellite project.
3. Add samples to the project.
4. Specify the analysis parameters in the Samples tab.
5. Perform an initial analysis.
6. Create a new bin set.
7. Generate bins.

Analyze and Examine the Data

1. Edit the analysis method to specify a bin set.
2. Specify the analysis parameters in the Samples tab.
3. (Optional) Specify the table settings.
4. Analyze the samples in the project.
5. Examine the data.

Sort Data and Evaluate Loss of Heterozygosity

1. Sort the data in the Genotypes tab by sample file and marker.
2. Generate a report.

Print or Export the Results

If necessary:

- Print or export the desired views, plots, and tables for use in reports or presentations.
- Export desired views, plots, and tables for further analysis by third-party software.

Sample-Naming Conventions

When you create sample sheets for LOH samples, Applied Biosystems recommends that you use a consistent sample-naming convention that distinguishes the controls from the test samples for each individual in your data set. Such a naming convention enables the GeneMapper Software to sort the analyzed data to take advantage of report settings that evaluate for LOH.

Setting Up the LOH Microsatellite Analysis

1. Create a kit and a panel for the project:
   a. Click  to open the Panel Manager.
   b. Create or select a kit.
   c. Create or import panels with marker information.
   d. Close the Panel Manager.
2. Click  to create a new project and select **Microsatellite** for the project type.
3. Click  to add samples to the project.
4. In the Samples tab, specify the analysis parameters for the samples in the project:

   Note: You can use the fill-down function to apply the parameters to all the samples at one time.

   a. In the Analysis Method column, select or create a microsatellite analysis method with the following settings:

Tab	Parameter	Setting
Allele	Bin Set	Select **None**.
Peak Detector	Peak Detection Algorithm	Select the appropriate algorithm (**Basic**, **Advanced**, or **Classic**) and the appropriate peak sizing method (as applicable). **IMPORTANT!** If you use the Classic peak detection algorithm, you must select a size standard created in Classic mode.

   b. In the Panel column, select the panel created in step 1.
   c. In the Size Standard column, select the appropriate size standard.

5. Click ▶ to perform the initial analysis on the sample files in the project so they will be available as reference data.
6. Create a bin set to associate with the panel:
   a. Click ▦ to open the Panel Manager.
   b. In the Navigation Pane, select the panel created in step 1 on page 6.
   c. Select **Bins** ▸ **New Bin Set** to create a bin set.
   d. Select **Bins** ▸ **Add Reference Data** to add the analyzed reference data to the panel.

   Note: You can add reference samples collectively in a folder or individually using the Ctrl-click function.

7. Generate bins for the panel and bin set:
   a. In the Navigation Pane, select the panel created in step 1 on page 6.
   b. In the Bin Set drop-down list, select the bin set created in step 6, above.
   c. Select **Bins** ▸ **Auto Bin** to generate the bin set automatically.
   d. Select the markers, then review the bins. Edit if necessary.
   e. (Optional) For faster loading of the panel in the future, remove the reference samples from the panel.
   f. Close the Panel Manager.

Analyzing and Examining the Data

1. Edit the analysis method to use the bin set created in step 6 of "Setting Up the LOH Microsatellite Analysis," above:
   a. Click ▦ to open the GeneMapper Manager.
   b. Select the **Analysis Method** tab.
   c. Select the analysis method created in step 4a on page 6, then click **Open**.
   d. In the Allele tab, select the bin set created in step 6, above.
   e. Click **OK**, then click **Done**.
2. In the Samples tab, specify the analysis parameters for the samples in the project created in step 2 of "Setting Up the LOH Microsatellite Analysis" on page 6:
   a. In the Sample Type column, select the appropriate sample type (**Sample**, **Positive Control**, or **Negative Control**).
   b. Leave the settings for the Analysis Method, Panel, and Size Standard columns the same as those selected in step 4 of "Setting Up the LOH Microsatellite Analysis" on page 6.

   IMPORTANT! The selected analysis method and panel must use the same bin set.

3. (Optional) In the toolbar, select or create table settings for the analysis.
4. Click ▶ to analyze the samples in the project.
5. Examine the data:
   a. In the Samples tab, examine the Size Quality (SQ) scores and the size standards.
   b. In the Genotypes tab, review the Process Quality Value (PQV) columns (BD, BIN, CC, LPH, OBA, OS, PHR, SHP, SP, SPA, SPU, and XTLK).
   c. Display the samples and genotypes plots.

Sorting Data and Evaluating LOH

1. In the Genotypes tab, sort the data by sample file and marker.

   Note: Depending on your sample-naming convention, control (healthy) and test (tumor) samples from the same individual may be listed consecutively, or all control samples may be listed first, followed by all test samples.

2. Generate a report:
   a. Create a report setting that is appropriate for the order in which your data is sorted (this is determined by your sample-naming convention) or use the "LOH Default" report setting.
   b. Select the samples to include in the report.
   c. Select **Analysis** ▸ **Report Manager**, then select the appropriate report setting.

Printing or Exporting the Results

If necessary, print or export the results.

To print the results:

1. In the GeneMapper window, select the desired tab.
2. Select **File** ▸ **Print**.

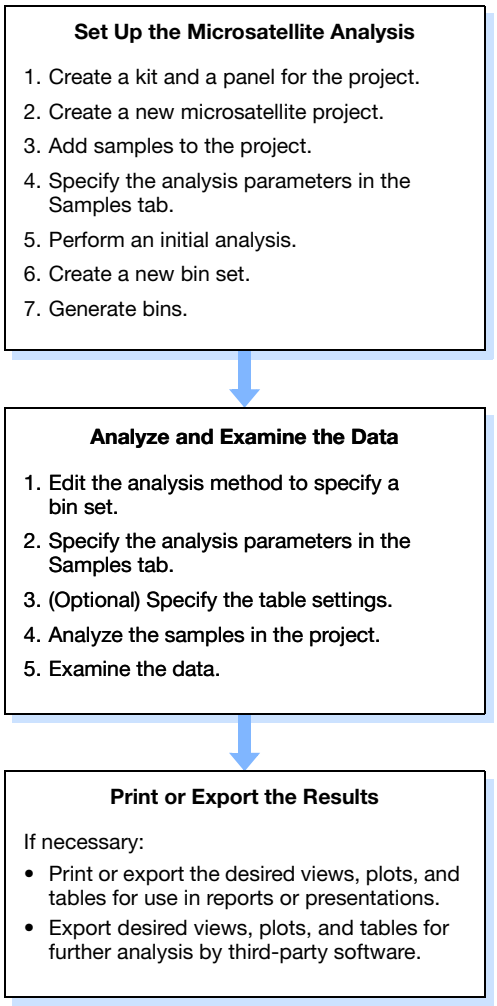
To export the results:

1. Select the desired table setting.
2. Select **File** ▸ **Export Table**.

Microsatellite Analysis Workflow

Overview

Use the method described in the following workflow to analyze polymorphic DNA loci that contain a repeated nucleotide sequence (usually 2 to 7 base pair repeats).



Setting Up the Microsatellite Analysis

1. Create a kit and a panel for the project:
   a. Click to open the Panel Manager.
   b. Create or select a kit.
   c. Create or import panels with marker information.
   d. Close the Panel Manager.
2. Click to create a new project and select **Microsatellite** for the project type.
3. Click to add samples to the project.
4. In the Samples tab, specify the analysis parameters for the samples in the project:

   Note: You can use the fill-down function to apply the parameters to all the samples at one time.

   a. In the Analysis Method column, select or create a microsatellite analysis method with the following properties:

Tab	Parameter	Setting
Allele	Bin Set	Select **None**.
Peak Detector	Peak Detection Algorithm	Select the appropriate algorithm (**Basic**, **Advanced**, or **Classic**) and the appropriate peak sizing method (as applicable). **IMPORTANT!** If you use the Classic peak detection algorithm, you must select a size standard created in Classic mode.

   b. In the Panel column, select the panel created in step 1.
   c. In the Size Standard column, select the appropriate size standard.
5. Click to perform the initial analysis on the sample files in the project so they will be available as reference data.
6. Create a bin set to associate with the panel:
   a. Click to open the Panel Manager.
   b. In the Navigation Pane, select the panel created in step 1.
   c. Select **Bins** ▸ **New Bin Set** to create a bin set.

d. Select **Bins** ▸ **Add Reference Data** to add the analyzed reference data to the panel.

Note: You can add reference samples collectively in a folder or individually using the Ctrl-click function.

7. Generate bins for the panel and bin set:
   a. In the Navigation Pane, select the panel created in step 1 on page 8.
   b. In the Bin Set drop-down list, select the bin set created in step 6 on page 8.
   c. Select **Bins** ▸ **Auto Bin** to generate the bin set automatically.
   d. Select the markers and review the bins. Edit if necessary.
   e. (Optional) For faster loading of the panel in the future, remove the reference samples from the panel.
   f. Close the Panel Manager.

Analyzing and Examining the Data

1. Edit the analysis method to use the bin set created in step 6 of "Setting Up the Microsatellite Analysis" on page 8:
   a. Click  to open the GeneMapper Manager.
   b. Select the **Analysis Method** tab.
   c. Select the analysis method created in step 4 on page 8, then click **Open**.
   d. In the Allele tab, select the bin set created in step 6 on page 8.
   e. Click **OK**, then click **Done**.
2. In the Samples tab, specify the analysis parameters for the samples in the project created in step 2 of "Setting Up the Microsatellite Analysis" on page 8:

Note: You can use the fill-down function to apply the parameters to all the samples at one time.

   a. In the Sample Type column, select the appropriate sample type (**Sample**, **Positive Control**, or **Negative Control**).
   b. Leave the settings for the Analysis Method, Panel, and Size Standard columns the same as those selected in step 4 on page 8.

IMPORTANT! The selected analysis method and panel must use the same bin set.

3. (Optional) In the toolbar, select or create table settings for the analysis.
4. Click  to analyze the samples in the project.
5. Examine the data:
   a. In the Samples tab, examine the Size Quality (SQ) scores and the size standards.
   b. In the Genotypes tab, review the Process Quality Value (PQV) columns (BD, BIN, CC, LPH, OBA, OS, PHR, SHP, SP, SPA, SPU, and XTLK).
   c. Display the samples and genotypes plots.

Printing or Exporting the Results

If necessary, print or export the results.

To print the results:

1. In the GeneMapper window, select the desired tab.
2. Select **File** ▸ **Print**.

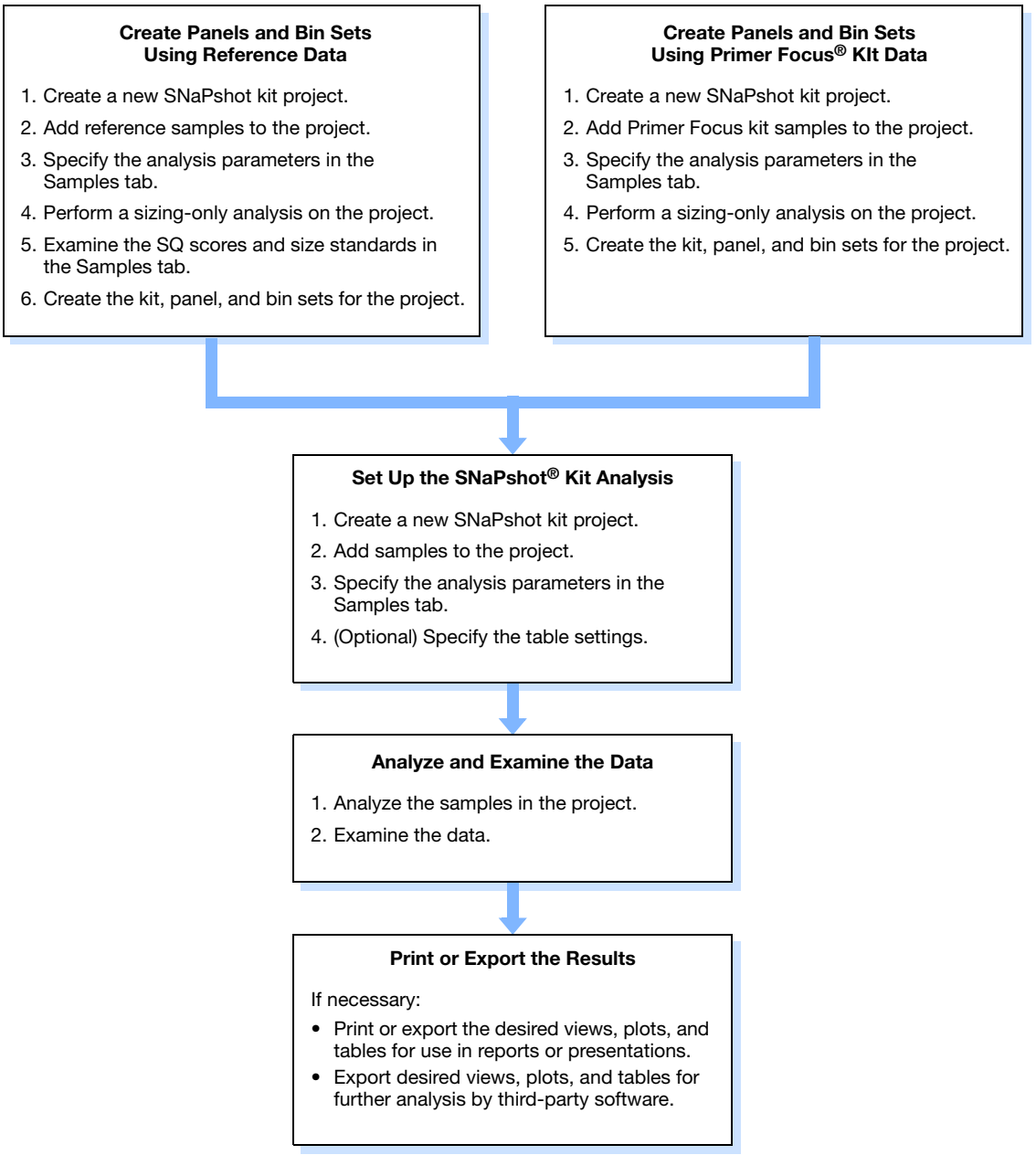
To export the results:

1. Select the desired table setting.
2. Select **File** ▸ **Export Table**.

SNaPshot® Kit Analysis Workflow

Overview

Use the method described in the following workflow to analyze multiplexed, single-base-extension SNP sample data. The workflow for the analysis varies, depending on the chemistry used to prepare the samples.



Creating Panels and Bin Sets Using Reference Data

1. Click to create a new project and select **SNaPshot®** for the project type.
2. Click to add reference sample files to the project.
3. In the Samples tab, specify the analysis parameters for the project:
   a. In the Analysis Method column, select or create a SNaPshot kit analysis method with the following settings:

Tab	Parameter	Setting
Allele	Bin Set	Select **None**.
Peak Detector	Peak Detection Algorithm	Select the appropriate algorithm (**Basic**, **Advanced**, or **Classic**) and the appropriate peak sizing method (as applicable). **IMPORTANT!** If you use the Classic peak detection algorithm, you must select a size standard created in Classic mode.

   b. In the Panel column, select **None**.
   c. In the Size Standard column, select the appropriate size standard.
4. Click to perform a sizing-only analysis on the project.

Note: The GeneMapper Software only sizes samples during the analysis. It does not make allele or genotype calls.

5. In the Samples tab, examine the size quality (SQ) scores and the size standards.
6. Create the kit, panel, and bin sets for the project:
   a. Click to open the Panel Manager.
   b. Click to create a new kit.
   c. For kit type, select **SNP**.
   d. Click to create a panel for the SNP kit.
   e. Select **Bins** ▸ **New Bin Set** to create a bin set for the SNP kit.
   f. Select **Bins** ▸ **Add Reference Data** to add the analyzed reference data to the SNP kit.
   g. Select **Bins** ▸ **Panel Reference Data** to add the analyzed reference data to the SNP panel.
   h. Using the reference sample files, manually create and adjust SNP markers and associated bins.
   i. Create SNP markers as needed.
   j. Using the imported data as a reference, use the tools of the Plot tab to adjust the SNP marker and associated bins.
7. Set up and perform the analysis as described in "Setting Up the SNaPshot® Kit Analysis" on page 12.

Creating Panels and Bin Sets Using Primer Focus® Kit Data

IMPORTANT! The Auto Panel function can be used to generate panels for samples prepared using Primer Focus Kit chemistry only.

1. Click to create a new project and select **SNaPshot®** for the project type.
2. Click to add Primer Focus kit sample files to the project.
3. In the Samples tab, specify the analysis parameters for the project:
   a. In the Sample Type column, select **Primer Focus**.
   b. In the Analysis Method column, select (or create) a SNaPshot kit analysis method with the following settings:

Tab	Parameter	Setting
Allele	Bin Set	Select **None**.
Peak Detector	Peak Detection Algorithm	Select the appropriate algorithm (**Basic**, **Advanced**, or **Classic**) and the appropriate peak sizing method (as applicable). **IMPORTANT!** If you use the Classic peak detection algorithm, you must select a size standard created in Classic mode.

   c. In the Panel column, select **None**.
   d. In the Size Standard column, select the appropriate size standard.

4. Click ▶ to perform a sizing-only analysis on the project.

   Note: The GeneMapper Software only sizes samples during the analysis. It does not make allele or genotype calls.

5. Create the kit, panel, and bin sets for the project:
   a. Click to open the Panel Manager.
   b. Click to create a new kit.
   c. For kit type, select **SNP**.
   d. Select **Bins** ▸ **New Bin Set** to create a bin set for the SNP kit.
   e. Select **Bins** ▸ **Add Reference Data** to add the Primer Focus kit data to the SNP kit.
   f. Select **Bins** ▸ **Auto Panel** to create the panel, markers, and bin set automatically.
   g. Review the panels and bins created with the Auto Panel function.

6. Set up and perform the analysis as described in "Setting Up the SNaPshot® Kit Analysis," below.

Setting Up the SNaPshot® Kit Analysis

1. Click to create a new project and select **SNaPshot®** for the project type.
2. Click to add sample files to the project.
3. In the Samples tab, specify the analysis parameters for the project:

   Note: You can use the fill down function to apply the parameters to all the samples at one time.

   a. In the Sample Type column, select the appropriate sample type (**Sample**, **Positive Control**, or **Negative Control**).
   b. In the Analysis Method column, select or create a SNaPshot kit analysis method with the following settings:

Tab	Parameter	Setting
Allele	Bin Set	Select the bin set created in either of the previous procedures.
Peak Detector	Peak Detection Algorithm	Select the appropriate algorithm (**Basic**, **Advanced**, or **Classic**) and the appropriate peak sizing method (as applicable). **IMPORTANT!** If you use the Classic peak detection algorithm, you must select a size standard created in Classic mode.

   c. In the Panel column, select the panel created in either of the previous procedures.

   IMPORTANT! The selected analysis method and panel must use the same bin set.

   d. In the Size Standard column, select the appropriate size standard.

   Note: If you imported analysis parameters from the sample sheet, verify that the settings are correct.

4. (Optional) In the toolbar, select or create table settings for the analysis.

Analyzing and Examining the Results

1. Click ▶ to analyze the samples in the project.
2. Examine the data:
   a. In the Samples tab, examine the Size Quality (SQ) score and the size standards.
   b. In the Genotypes tab, review the Process Quality Value (PQV) columns (AN, BD, CC, DP, LPH, NB, OS, PHR, and SPU).
   c. Display and examine the samples and genotypes plots.

Printing or Exporting the Results

If necessary, print or export the results.

To print the results:

1. In the GeneMapper window, select the desired tab.
2. Select **File ▸ Print**.

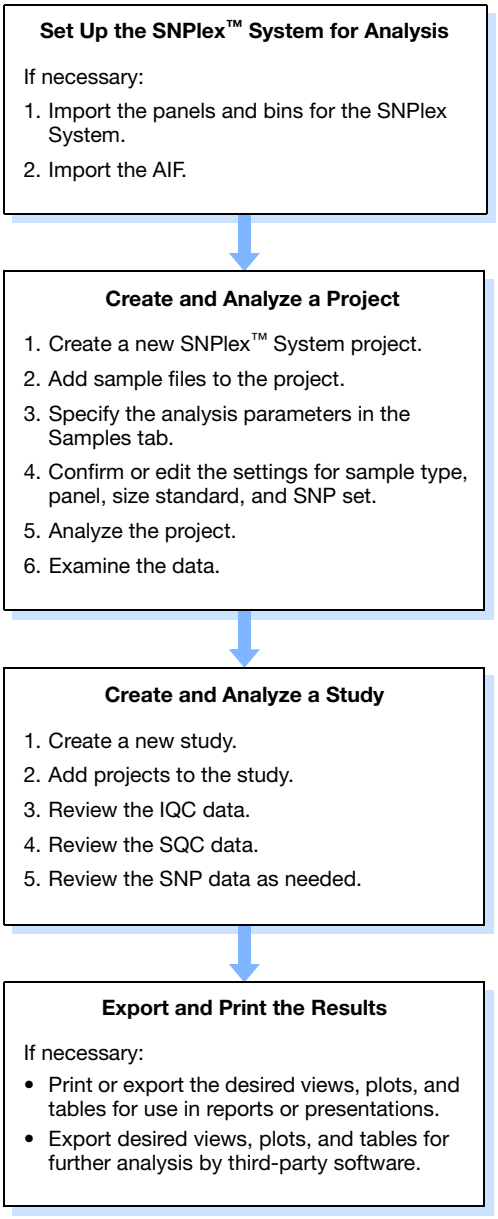
To export the results:

1. Select the desired table setting.
2. Select **File ▸ Export Table**.

SNPlex™ System Analysis Workflow

Overview

Use the method described in the following workflow to analyze multiplexed, oligonucleotide ligation/PCR assay (OLA/PCR) SNPs prepared using the Applied Biosystems SNPlex™ System chemistries.



Setting Up the SNPlex™ System for Analysis

1. If you have not already done so, import the panels and bins for the SNPlex System:
   a. Click to open the Panel Manager.
   b. In the Navigation Pane, select **Panel Manager**, then import the **SNPlex_48plex_3730_Panels.txt** file.
   c. In the Navigation Pane, select the **SNPlex_48_plex** folder, then import the **SNPlex_48plex_3730_Bins.txt** file.
   d. Close the Panel Manager.
2. If you have not already done so, use the GeneMapper Manager to import the Assay Information File (AIF) found on the CD that was shipped with your SNPlex System chemistry kit.

Creating and Analyzing a Project

For each run (electrokinetic injection) performed by the compatible Applied Biosystems electrophoresis instrument:

1. Click to create a new project and select **SNPlex™** for the project type.
2. Click to add the samples of a single run folder to the project.
3. In the Samples tab, specify the analysis parameters and table settings for the project:

   Note: You can use the fill-down function to apply the parameters to all the samples at one time.

   a. In the Sample Type column, select the appropriate sample type.
   b. In the Analysis Method column, select the appropriate SNPlex System analysis method (**SNPlex_Model_3730** or **SNPlex_Rules_3730**).
   c. In the Panel column, select the SNPlex System panel.
   d. In the Size Standard column, select the **SNPlex_48_plex_v1** size standard definitions.
   e. Confirm the sample type (Sample, Positive Control, Allelic Ladder, or Negative Control)
   f. In the SNP Set column, select the SNPlex System SNP set.

   If configured for autoanalysis, the software may automatically fill in the analysis method, panel, and size standard settings.

4. Click ▶ to analyze the project.
5. Examine the data:
   a. Examine the size standards.
   b. Display and examine the cluster plots (using the SNPlex System plot settings).
   c. (Optional) Display and examine the samples and genotypes plots.

Creating and Analyzing a Study

After you create a sufficient number of projects:

1. Select **Tools** ▸ **Study Manager** to open the Study Manager.
2. Click to create a new study.
3. Click to add projects to the study.
4. Review the Initial QC (IQC) data:
   a. Review the Sizing IQC data and resolve any sizing-related issues.
   b. Review the Allelic Ladder IQC data and resolve any binning-related issues.
   c. Review the Positive Hybridization Control (PHC) and Assay IQC signal data (normalized and otherwise) to identify and diagnose any process-related problems.
   d. If necessary, override the IQC status of suspect runs.
5. Review the Secondary QC (SQC) data.
   a. Review the SQC metrics applicable to your analysis and review the test results of runs exhibiting potential problems.
   b. If necessary, override the SQC status of suspect runs.
6. Review the genotype (SNP) data as needed.

Exporting and Printing the Results

If necessary, print or export the results.

To print the results:

1. In the GeneMapper window, select the desired tab.
2. Select **File** ▸ **Print**.

To export the results:

1. Select the desired table setting.
2. Select **File** ▸ **Export Table**.

Instrument, Software, and Data Compatibility

Genetic Analysis Instrument	Compatible Data Collection Software and Operating System	Sample Data Compatibility
 **Applied Biosystems 3730/3730*xl* DNA Analyzer**	• Data Collection v1.0 • Windows 2000, SP 2	• Sample Files
	• Data Collection v2.0 • Windows 2000, SP 3 and 4	• Sample Files • Co-installation • Automation
	• Data Collection v3.0 • Windows XP, SP 1 or later	
 **Applied Biosystems 3130/3130*xl* Genetic Analyzer**	• Data Collection v3.0 • Windows XP, SP 1 or later	• Sample Files • Co-installation • Automation
 **ABI PRISM® 3100 Genetic Analyzer**	• Data Collection v1.0/1.0.1/1.1 • Windows NT, SP 5	• Sample Files
	• Data Collection v2.0 • Windows 2000, SP 3 or later	• Sample Files • Co-installation • Automation
 **ABI PRISM® 3100-*Avant* Genetic Analyzer**	• Data Collection v1.0 • Windows NT, SP 5	• Sample Files
	• Data Collection v2.0 • Windows 2000, SP 3 and 4	• Sample Files • Co-installation • Automation
 **ABI PRISM® 3700 DNA Analyzer**	• Data Collection v1.0/1.0.1/1.1 • Windows NT 4.0, SP 5	• Sample Files
	• Data Collection v2.0 • Windows NT 4.0, SP 5	
 **ABI PRISM® 377 DNA Sequencer**	• Data Collection v3.0 • Windows NT 4.0, SP 5	• Sample Files
 **ABI PRISM® 310 Genetic Analyzer**	• Data Collection v1.0/1.0.1/1.1/3.0 • Windows NT 4.0, SP 3,4, 5, and 6a	• Sample Files
	• Data Collection v3.0 • Windows 2000, SP 3 and 4	• Sample Files • Co-installation
	• Data Collection v3.1 • Windows XP, SP 1 or later	

Compatible Data Collection Software and Operating System Column

This column displays the version(s) of the Data Collection Software, Windows operating system, and any associated service pack(s) supported by the GeneMapper Software Version 4.0 for the specified instrument.

Sample Data Compatibility Column

This column indicates the methods by which the GeneMapper Software Version 4.0 can process sample data produced by the associated combination of instrument, Data Collection Software, and Windows operating system.

- **Sample Files** – The software can import sample files created by the indicated combination of the Data Collection Software and Windows operating system.
- **Co-installation** – The software can be installed on the same computer that contains the indicated combination of the Data Collection Software and Windows operating system.
- **Automation** – The software can automatically retrieve and analyze data generated by the indicated combination of the Data Collection Software and Windows operating system.

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