

User Manual **HLA Fusion™ Research**

v. R2.x.x

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For Research Use Only. Not For Use In Diagnostic Procedures.



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Advancing Transplant Diagnostics

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All One Lambda software products are designed to assist personnel experienced in HLA analysis by suggesting typing results. However, any clinical or diagnostic results must be carefully reviewed by a person qualified in HLA typing to assure correctness. This software may be used to aid in suggesting results, but should not be used as the sole method for determining reportable results. This software is meant as a laboratory aid, not as a source of definitive results. The software design does not mitigate hazards associated with the software. The laboratory director or technologist trained in histocompatibility testing is required to review all data to detect any problems with the software.

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Chapter 1 Introduction

What is HLA Fusion™ *Research*?

HLA Fusion *Research* is a companion to One Lambda's ConsenSys™, SSO, and Micro SSP™ products. This software runs in both stand-alone (on a single computer) and network environments.

The features of this software allow you to do the following:

- Import raw data
- Manually enter reaction patterns
- Analyze the raw data and review the results in graphical form
- Easily update product information (new product and lot information)
- Search for specific data and create standard or custom reports
- Compare results to One Lambda quality control (QC) data

README Files

A README file is provided. with software update This file provides a list of significant changes to the software and also critical information that is not included in the user's manual.

Program Updates

Note: For best results, always make sure you are using the latest version of HLA Fusion™ <Emphasis>Research software.

You may obtain updates of HLA Fusion™ <Emphasis>Research by request. Please contact your One Lambda, Inc. representative for a copy of the software or see the Technical Support section below for more contact information. Product information updates (catalog files, etc.) for HLA Fusion™ <Emphasis>Research are available through your One Lambda Inc. representative, or from the One Lambda website:

<http://download.onelambda.com>

Limitations of the Program

All One Lambda software products are designed to assist personnel experienced in HLA analysis by suggesting typing results. However, results must be carefully reviewed by a person qualified in HLA typing to assure correctness. This software may be used to aid in suggesting results, but should not be used as the sole method for determining reportable results. This software is meant as a laboratory aid, not as a source of definitive results.

For the reliability of patient information stored in the database, users must ensure that the identifier for each patient is unique and that each sample identifier is unique. The storage capability of HLA Fusion™ <Emphasis>Research is limited by Microsoft SQL Server Desktop Engine or SQL Server 2000. (The user must manually archive data.)

HLA Fusion™ <Emphasis>Research assumes that data for each required input is in standard format that has not been modified.

The HLA Fusion™ <Emphasis>Research analyzes a data file in the following format.

- The data file is one of the following:
 - .ab1 file for ConsenSys
 - .csv file for SSO
 - .csv file for Micro SSP.
- The data file name (also known as a session ID) can be up to 100 characters and includes the .csv extension.
- The data is generated based on original, unmodified templates provided by One Lambda, Inc.
- The user is responsible for final assignments and must review all suggested results.

Technical Support

For technical support or to report software problems, contact your One Lambda representative. From the United States, call 800-822-8824 or from the Greater Los Angeles Area, call 818-702-0042. Contact us by e-mail at: techsupport@onelambda.com.

For system requirements, see the *HLA Fusion Research Installation Guide*.

Scope of This Manual

This manual provides information on how to import raw data and then to analyze it, making adjustments in cut-off values as necessary. It is very important to recognize that the QC (Quality Control) data used with this program and the defaults set in this program are based on One Lambda's experience with the product in a tightly-controlled research and development environment. Thus, a laboratory performing HLA typing in another environment may need to reset cut-off values to meet specific laboratory requirements.

From the Main Menu of HLA Fusion™ <Emphasis>Research, you can access the three major components of the program:

- Analyze Data
- Manage Records
- Manage Samples

In addition, you may also access the following features:

- Patient Information
- Utilities
- Help
- Exit button

This manual helps you start using One Lambda's HLA Fusion™ <Emphasis>Research. It includes an overview of the system and then quickly takes you into the process of analyzing data. See the *HLA Fusion Research Installation Guide* for installation instructions.

Chapter 2 Navigation

This chapter describes the various ways to access the HLA Fusion™ *Research* software functions, as well as how to use the Navigator tool to access and move between sessions and samples.

Logging On To Fusion *Research*

1. Double-click the HLA Fusion *Research* icon on your computer desktop. from **Start > Programs > One Lambda > HLA Fusion Research**.



You can also open the program

The Security Login dialog box is displayed.

Figure 2-1: HLA Fusion Research Login Screen

The login dialog box for HLA Fusion 2.0. It has a blue header with the text 'HLA Fusion™ 2.0'. Below the header, there are two input fields: 'User Name*' and 'Password*'. Under the 'User Name*' field, there is a blue hyperlink 'Forgot User Name'. Under the 'Password*' field, there is a blue hyperlink 'Forgot Password'. To the right of these links are two buttons: 'Log In' and 'Cancel'. At the bottom of the dialog, there is a section for system information: 'Database: C001951-JHA\FUSION\130QA', 'Version: 2.0.0.28314, Created on: 4/23/2010', 'Regional Settings: Client: English (United States)', and 'DB Server: us_english\SQL_Latin1_General_CP1_CI_AS'.

2. Enter your HLA Fusion *Research* User Name and Password.
3. Click Log In to open the program.

Note: The **SQL Database** field displays the database to which you are currently connected.

Retrieving a Forgotten User Name or Password

- If you forget your HLA Fusion *Research* user name, click the **Forgot User Name** link, enter your first and last name, and select your lab role (supervisor or technician). The system displays the user name matching the data you provide.
- If you forget your HLA Fusion *Research* password, click the **Forgot Password** link, and answer the two security questions you were asked when you set up your user profile (see *Editing User Profiles*, p. 301). The password is displayed when the questions are answered correctly.

Figure 2-2: Forgot Password Dialog Box

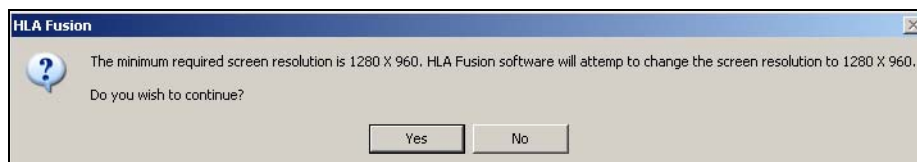
The screenshot shows a 'Forgot Password' dialog box for HLA Fusion 2.0. The window has a title bar with the text 'Forgot Password' and standard window controls. The main area has a blue header with 'HLA Fusion™ 2.0'. Below the header, there is a 'UserID*' field and a 'Forgot UserName' link. A 'Security Questions' section contains two questions: 'What is the last name of your best childhood friend ? *' and 'What is the name of the city you were born ? *', each with a text input field. Below the questions is a 'Your Password is :' field. At the bottom right are 'Get Password' and 'Close' buttons. The footer of the window has the 'ONE LAMBDA' logo and three blue dots.

Key System Settings

Screen Resolution

HLA Fusion *Research* software requires a screen resolution of **1280 x 960**. The software displays a message if your current resolution is less than the expected settings.

Figure 2-3: Screen Resolution Message

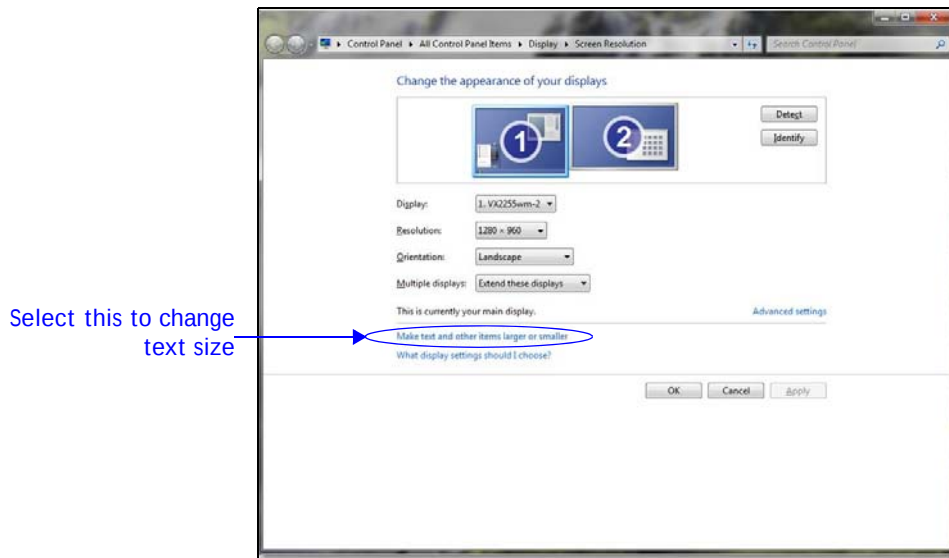


You can select **Yes** to have the system attempt to make the adjustment. It will continue to start the application even if it could not adjust the resolution. Or, you can select **No** and adjust it manually.

In addition, If your computer is running the Microsoft® Windows 7® operating system, the text display setting must be set to **Smaller - 100 % (default)**. Take these steps if you need to adjust the screen text display size:

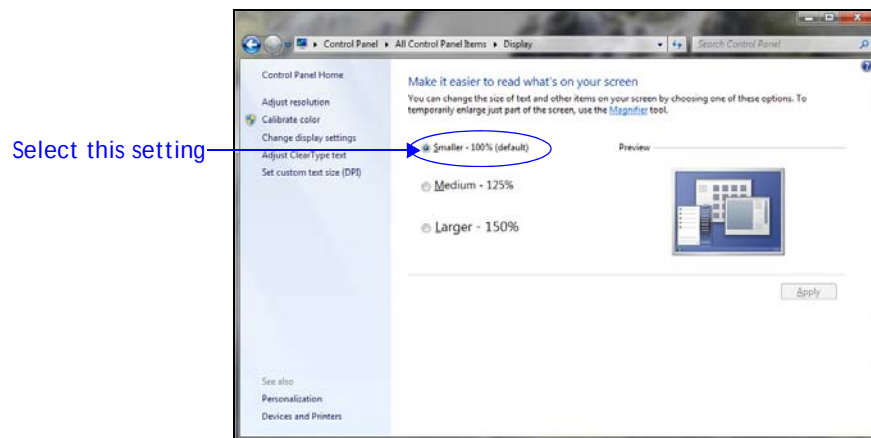
1. Right-click on the computer desktop.
2. Select the Display option. The Screen Resolution window displays.

Figure 2-4: Windows 7 Screen Resolution Window



3. Select the **Make text and other items larger or smaller** (see Figure 2-5).

Figure 2-5: Text Size Options



File Permissions

All HLA Fusion Research users must have read and write permissions to the following directories and files:

-
- OneLambda.Fusion.Interface.exe.config
 - ReportMap.xml
 - C:\OLI Fusion\ and all the sub directories and the files in these directories

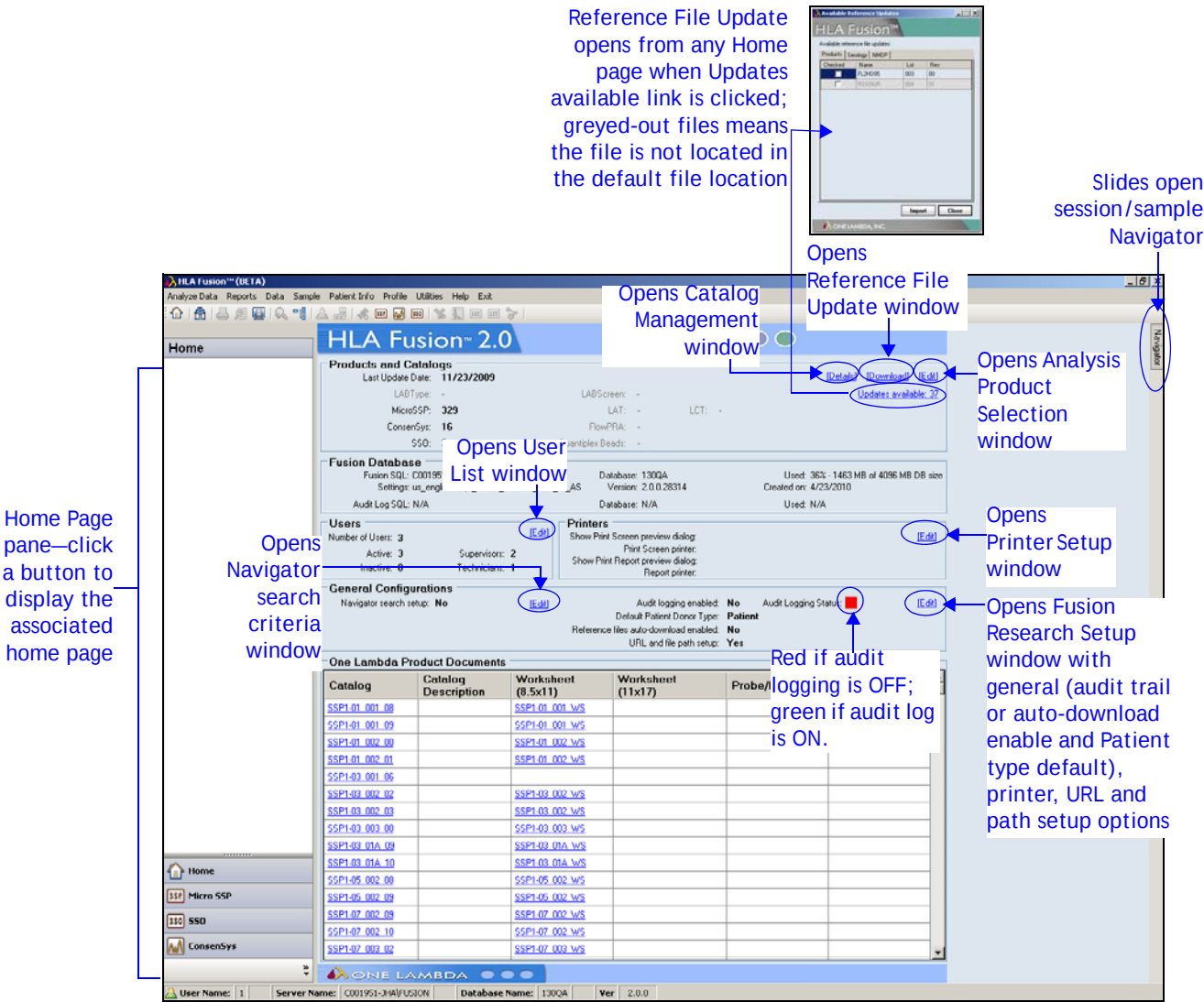
Character Length

If you are using SQL Server 2000 and encounter a report or results that require more than 8000 characters of data, you must update to SQL Server 2005.

User Interface

Fusion Research Home Pages

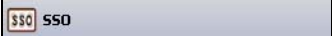
Figure 2-6: Fusion Research Default Home Page



This user interface option allows you access to the product home pages, data import and analysis windows. It also allows you to view or access system or product data, reference file downloads and configuration settings.

Note: If the current page does not show updated information upon modification or downloads, go back to the main Home page, and then return to the product home page to see the changes.

This interface is the default when you first log in to HLA Fusion *Research*. To display the home page for one of the products listed in the bottom left area of the page, click the appropriate button, as in this example for SSO:

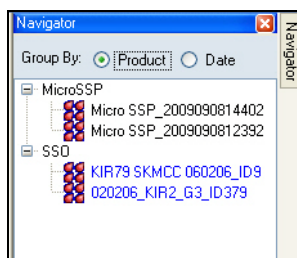
- From the main home page, click the ConsenSys home page button .
- Click the ConsenSys button  from the HLA Fusion *Research* toolbar.
- Select **Analyze Data > LABScreen**.

Note: Migrated and upgraded databases also use this same interface ([Figure 2-6, Fusion Research Default Home Page, p. 9](#)).

Launching Navigator

1. If the Navigator tab is not already displayed on the right of the application window, click the **Show Navigator** toolbar button  to activate the Navigator function. Otherwise, see step 2.
2. Move your cursor over the **Navigator** tab on the right border of the application window to slide the Navigator into view.

Figure 2-7: Navigator Interface



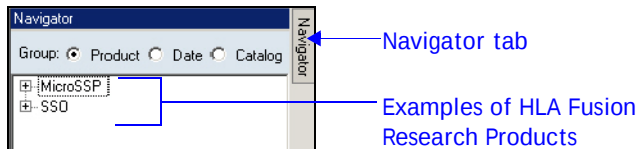
3. To close the Navigator, click the close button .

Navigator Tree

Using the **Navigator** tree, you can easily move between analysis sessions and samples.

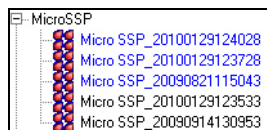
1. Double click on a session, or click the + sign to the left of the catalog, date or product module to display the list of sessions.

Figure 2-8: List of Products



2. Click a sample name to display it in the analysis window.

Figure 2-9: List of Sessions in the Navigator



Results Grouping

The sessions and samples displayed through the Navigator tool can be sorted by various criteria:

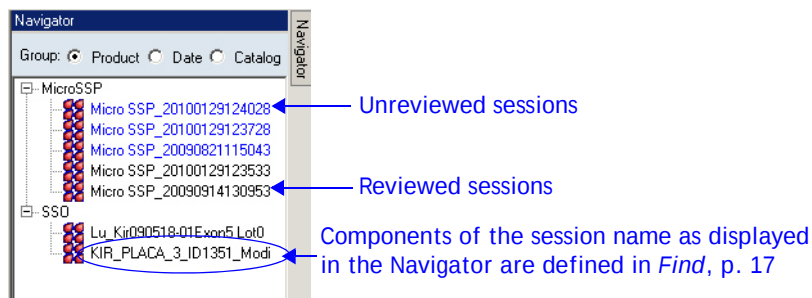
- Product type
- Session Date
- Catalog (Session Name)

The default is to group by Product. See the next few sections for details about these two display options.

Group by Product

The Navigator displays imported sessions for each product type, based on the date range and other criteria set in the **Find** option. If you are already in the analysis mode for a certain product, just the sessions that fit the **Find** criteria for that product display. Click the + sign next to the product type you are interested in to display its sessions.

Figure 2-10: Navigator Sorted by Product Type



-
- The sessions displayed in blue are the ones that have not yet been reviewed. Once you review a session, its color on the Navigator list changes to black.
 - Click a session name to display the samples within this session and a session summary. For LABType and LABScreen, the system also performs a batch analysis and displays the results in the session summary.
 - If a session sample is listed in red, this means the sample failed in batch analysis.
 - Click a sample name to display it in an analysis window.

Group by Session Date

When you select the Date option, sessions are displayed in order of their creation dates.

Figure 2-11: Navigator Sorted by Session Date

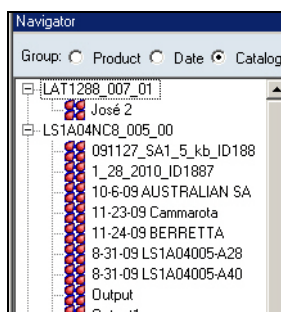


- Otherwise, the use of this tool is the same as described above in [Group by Product](#).

Group by Catalog

When you select the Catalog option, sessions are displayed in alphanumeric order by catalog name.

Figure 2-12: Navigator Sorted by Catalog

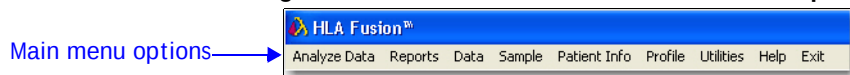


- Otherwise, the use of this tool is the same as described above in [Group by Product](#).

Accessing HLA Fusion™ Research Software Functions

Main Menu Options

Figure 2-13: HLA Fusion Research Main Menu Options



You can access HLA Fusion *Research* functionality at any time from the main menu, which is displayed at the top of all HLA Fusion *Research* application windows. See the following sections for a list of the options available under each main menu item.

Analyze Data

Each option under this menu item is either a molecular or antibody product for which you can import CSV files, or manually enter reactions, and analyze data. For details, see the individual product analysis chapters in this user manual.

Figure 2-14: Analyze Data Menu Options



Reports

When you select this menu item, the Reports page is displayed, allowing you to create reports of your analysis data. See [Chapter 10, Reports, p. 250](#) for information on how to use the Reports window.

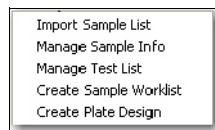
Data

When you select this menu item, a Data window is displayed that allows you to manage (delete, archive, activate and move) sessions and samples, map session alleles to the new NMDP nomenclature, and view/print log files of session data.

Sample

Options under this menu item pertain to importing, creating, managing, and exporting sample information. This is also the menu to use for managing Luminex test lists (see [Chapter 12, Sample Management, p. 275](#) for details) and for creating sample work lists and plate designs.

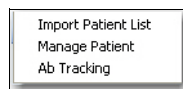
Figure 2-15: Sample Menu Options



Patient Info

Options under this menu item pertain to importing patient/donor lists, managing individual patient/donor information, and tracking patient antibody data. See [Chapter 13, Patient Information, p. 286](#) for details.

Figure 2-16: Patient Info Menu Options



Profile

There are options under this menu item for creating and managing your own user profile, lists of system users and privileges, and lab information. There is also an option for switching between the home page

options, depending on your system navigation preference. See [Chapter 14, Profile Management, p. 299](#) for details.

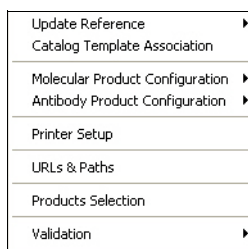
Figure 2-17: Profile Menu Options



Utilities

The options under this menu item pertain to importing catalog, code and serology files, configuring the molecular and antibody products you analyze, setting up your HLA Fusion *Research* system, and system validation. See [Chapter 15, Utilities, p. 305](#) for details.

Figure 2-18: Utilities Menu Options



Help

This menu item allows you to access the following HLA Fusion *Research* Software information:

- Online help, which provides guidance in using HLA Fusion *Research* Software.
- Notification of updates and a description of new features in the latest HLA Fusion *Research* software.
- Dynamically updated Frequently Asked Questions (FAQs) about the HLA Fusion *Research* software.
- The build and version number of the HLA Fusion *Research* Software application you are currently using.

Note: The online help can be accessed from anywhere within the HLA Fusion Research application when you press the **F1** key.

Occasionally, updates are made to the online help between releases of the HLA Fusion Research. To ensure you have the most current help file, you can either check the OLI download site, download.onelambda.com - [/pub/tray_info/Windows/HLA_Fusion_Catalogs/Document/](#), or you can enable the auto-download feature from the Fusion Research default home page (see [Fusion Research Home Pages, p. 9](#)).

Figure 2-19: Help Menu Options

HLA Fusion™ Help	F1
Product Update Notes	
FAQs	
About HLA Fusion™	

Exit

When you select this menu item, a dialog box displays that allows you either to select **Yes** to exit and close the HLA Fusion *Research* application, or to select **No** to keep the current session open.

Toolbar Buttons

HLA Fusion *Research* provides a toolbar, displayed just below the main menu options, with access to commonly used functions.

Figure 2-20: HLA Fusion Research Toolbar



The following table names each toolbar button. The sections below describes the function of each button.

Button	Name
	Home
	Find
	Print Report
	Preview Report
	Print Screen
	Magnify
	Show Navigator

Button	Name
	Patient
	Related Records
	Side-by-Side Analysis
	Product Data Analysis
	Sample Navigation Tools (only visible during sample analysis). The <<Summary link returns to the associated sample summary table.

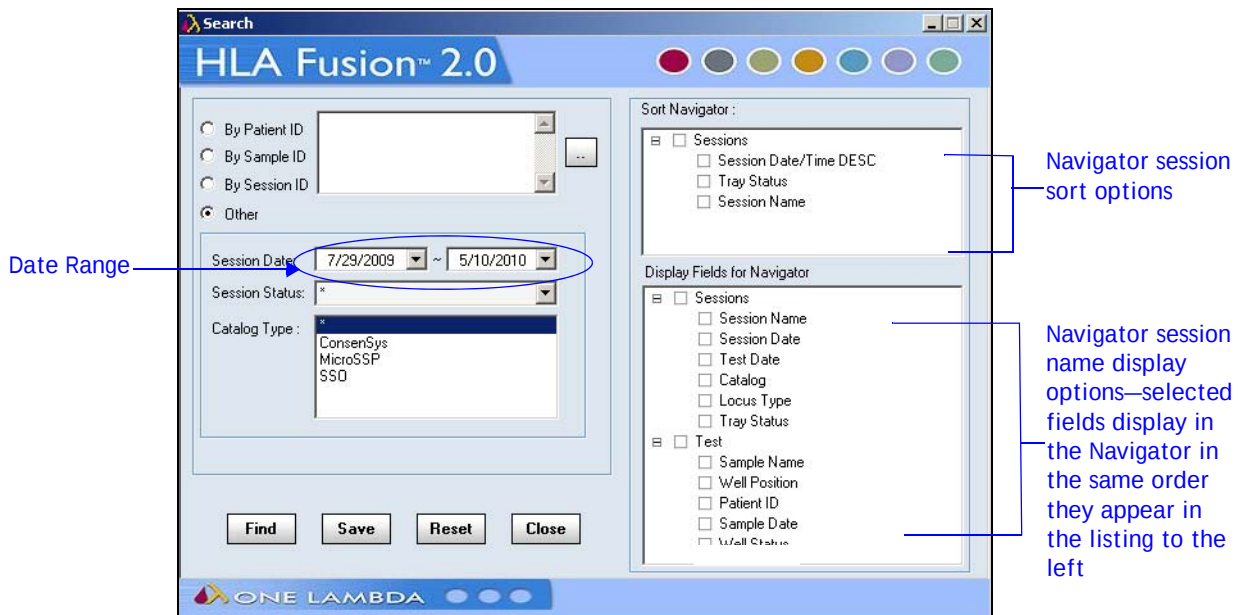
Find

Click the **Find**  button to display a dialog box that allows you to search for records using various criteria. You can choose to search by Patient ID, Sample ID, Session ID, or Other. **Other** allows you to provide multiple search criteria: date range, session status, and catalog type.

The Find dialog box also allows you to modify the Navigator session sort and display criteria.

Note: The date range set here, in the **Session Date** field, is used as the default date range throughout the software, such as in the Navigator and Reports windows. Each time you change it, and click Find, the default changes for the rest of the application.

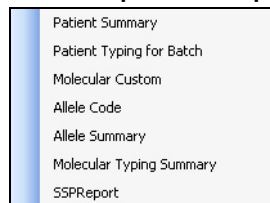
Figure 2-21: Find Records and Navigator Settings



Print Report

From any analysis window, you can click the **Print Report**  button to display a list of the reports that you can print; reports listed are specific to the product you are currently analyzing. If you have set a default printer for your system (configured through **Utilities > Printer Setup**), the selected report is automatically sent to the specified printer. Otherwise, a dialog box is displayed from which you can select a printer. For more information on reports, see [Chapter 10, Reports, p. 250](#).

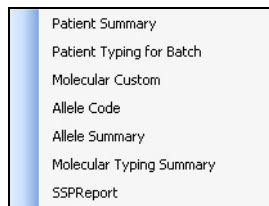
Figure 2-22: Example Print Report Options



Preview Report

From any analysis window, click the **Preview Report**  button to display a list of reports you can preview—reports listed are specific to the product you are currently analyzing. Selected reports display in a preview window. Use the print and export buttons in the preview window to output the report in selected format. Click the close button  to close the preview window.

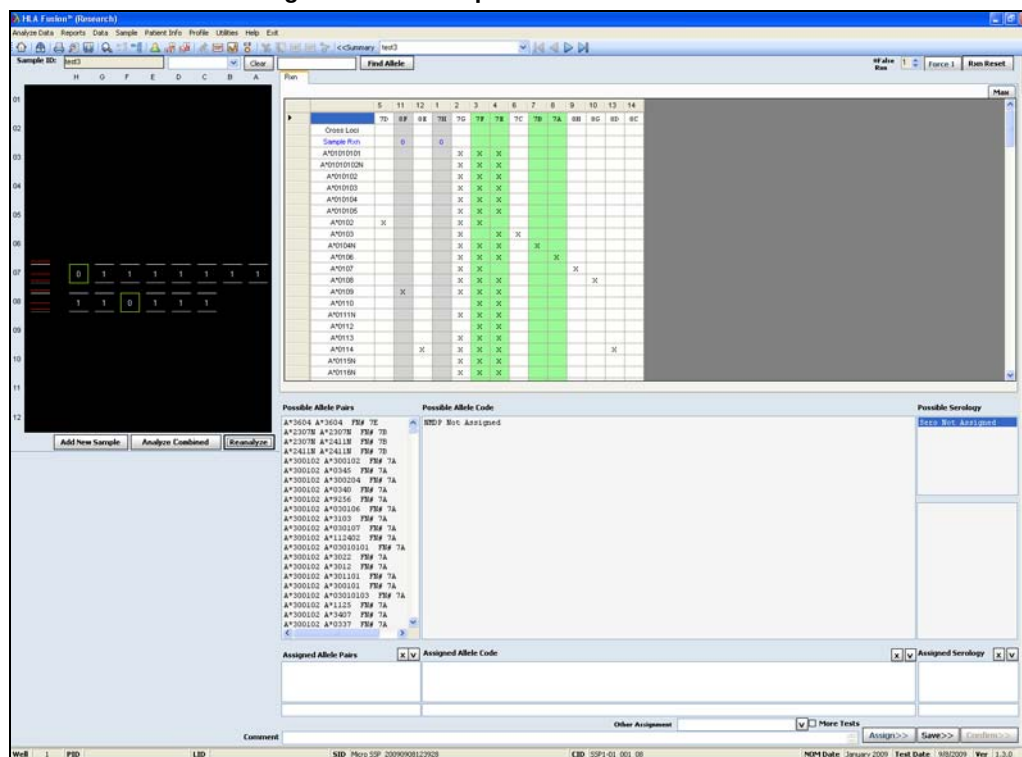
Figure 2-23: Example Preview Report Options



Print Screen

From any analysis windows, click the **Print Screen**  button to display a new window containing the screen shot of the current analysis window. Click the **Print** button to send the screen shot to the printer. To close this window, click the close button .

Figure 2-24: Example of Print Screen Results



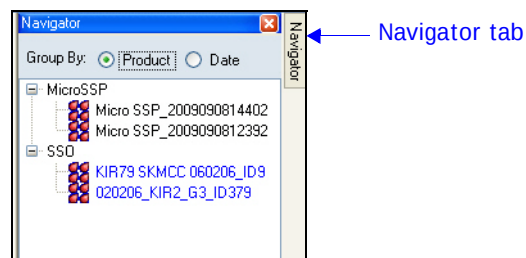
Magnify

From any analysis window, click the **Magnify**  button to activate the magnifying glass and enlarge any section of the window. Use the arrow keys on your computer keyboard to increase or decrease the height and width of the magnified area. Click anywhere on the screen to deactivate the magnifying glass.

				1D	2E	3C	3B
1	1	1		Cross Loci			
				Sample Rxn	X	X	X
8				A*010103			
1				A*010103			
				A*0102			
				A*0103			
				A*0107			
				A*0108			

Show Navigator

Click the **Show Navigator**  button if the **Navigator** tab (normally displayed on the upper right side of the application window) is not visible. Once the **Navigator** tab is displayed, you can move your cursor over it to slide the Navigator panel open.



See [Launching Navigator, p. 10](#) for more information about using the **Navigator**.

Patient

From any analysis window, click the **Patient**  button to display the Patient/Donor Info window where you can enter or edit information related to a patient and associate it with the current sample (see *Managing Patient/Donor Records, p. 287*).

Figure 2-25: Patient/Donor Information Window

Related Records

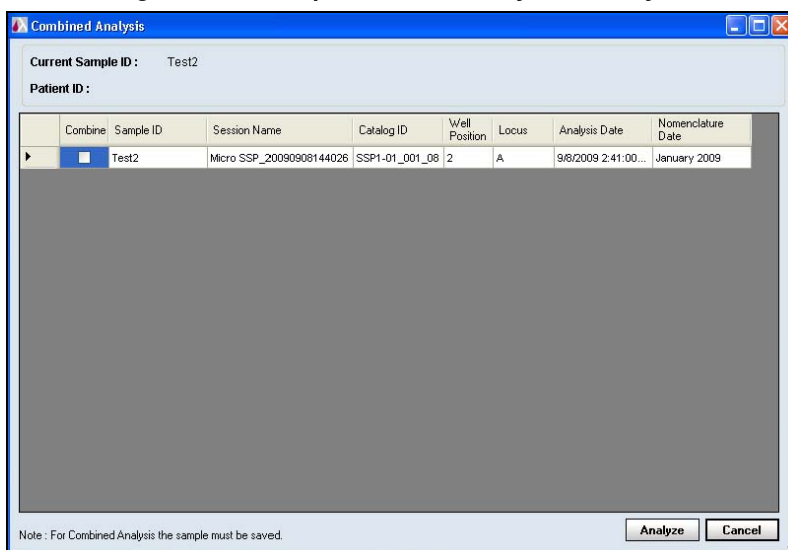
A related record is a sample that is associated in some way with the current sample or patient. From any analysis window, click the **Related Records**  button to load all records related to the current sample into the drop-down list in the Sample ID field. Use the sample navigation arrows to display the analysis of each related record one by one. To exit from the related records mode, click the <<**Summary** link next to the Sample ID field.

Note: This function can be accessed also by right-clicking a sample in the Navigator. See the product-specific chapters of this manual for more information about using this feature.

Side By Side Analysis

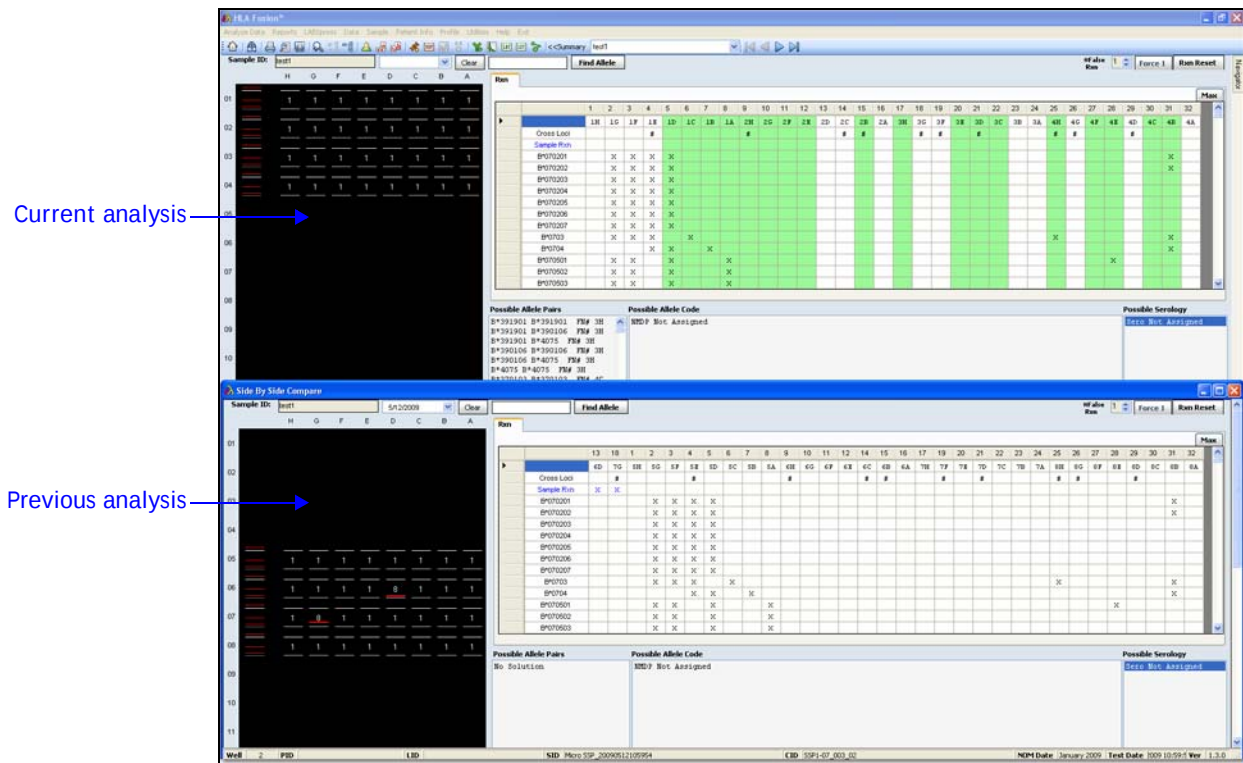
From any analysis window, click the **Side By Side Analysis**  button to compare the current sample analysis with previous analysis sessions for the same sample ID.

Figure 2-26: Sample List for Side By Side Analysis



- Select a previous sample analysis from the displayed list to compare to the current one. The two analysis windows are then displayed in a comparison window.
- Each window can be resized and moved by dragging and dropping. Click again on the **Side By Side Analysis** button to cancel the comparison display.

Figure 2-27: Example of a Side By Side Analysis Window



Note: This function can be accessed also by right-clicking a sample in the Navigator.

Product Data Analysis

Click any of the **Product Data Analysis** buttons  to display the product home page, import a session file, manually enter a session, or select from the Navigator list of already imported sessions for that product.

Sample Navigation

The **Sample Navigation** tools (only accessible from the analysis windows) give you access to all the samples in the current session. You can select a different sample within the same session either by selecting from the drop down list in the Sample ID field, or by clicking the forward/back arrow buttons next to the drop-down field. You can also click **<<Summary** to go to the summary for that session.

Figure 2-28: Sample Navigation Tools



-
- Clicking on the drop-down arrow displays the samples within the current session.
 - Selecting a sample from this list in the Sample ID field makes the selected sample active in the analysis window. Alternatively, you can use the forward/back arrow buttons to select different samples.
 - Clicking <<**Summary** takes you to the session summary for the current sample.

Chapter 3 ConsenSys™ Analysis

HLA Fusion™ <Emphasis>Research ConsenSys analysis uses sequence based typing techniques to analyze sequence data and to determine an HLA typing. To correctly input Ab1 files for analysis, they must be in the expected file name format entered in the Ab1 Filename Configuration Menu (see *Changing Ab1 Filename Configuration*, [p. 87](#)).

Starting a ConsenSys Analysis Session

To begin a ConsenSys analysis session, build a session using Sample IDs or Ab1 files. This information can also be saved as a Plate Record for later use. You can also analyze Ab1 files directly.

HLA Fusion™ <Emphasis>Research analysis uses sequence-based typing techniques to analyze sequence data and determine an HLA typing. Base mismatches or close base calls are flagged by the software and must be resolved by the user.

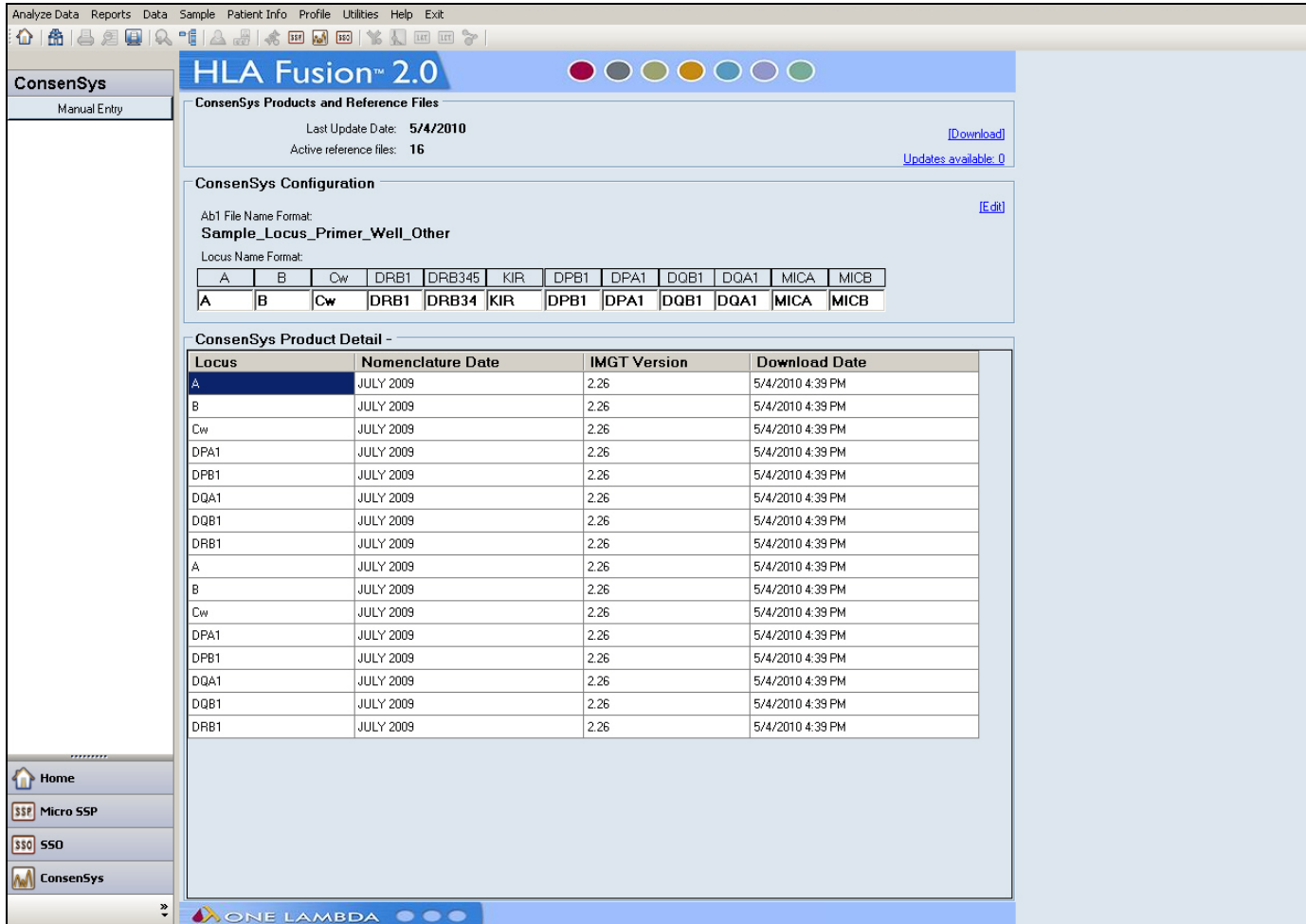
From the Analysis window you can

- View HLA Fusion™ <Emphasis>Research results
- Add sample comments
- Flag a sample for more testing
- Accept or edit base calls

Starting a ConsenSys Session

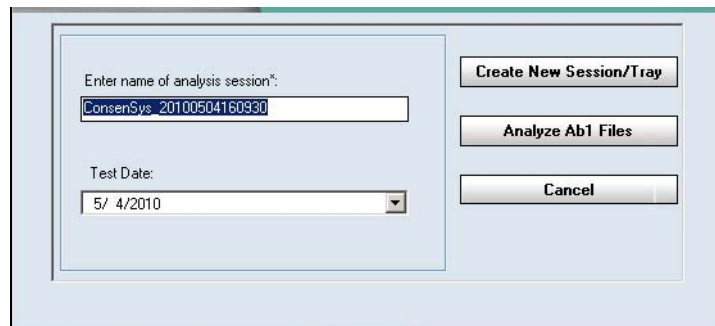
1. Click the ConsenSys home page button  ConsenSys or toolbar button  to open the ConsenSys home page.

Figure 3-1: ConsenSys Home Page



- Click **Manual Entry**. When the dialog box for starting a ConsenSys session manually displays, you will notice that the system has assigned a session name. Optionally, you can rename the session.

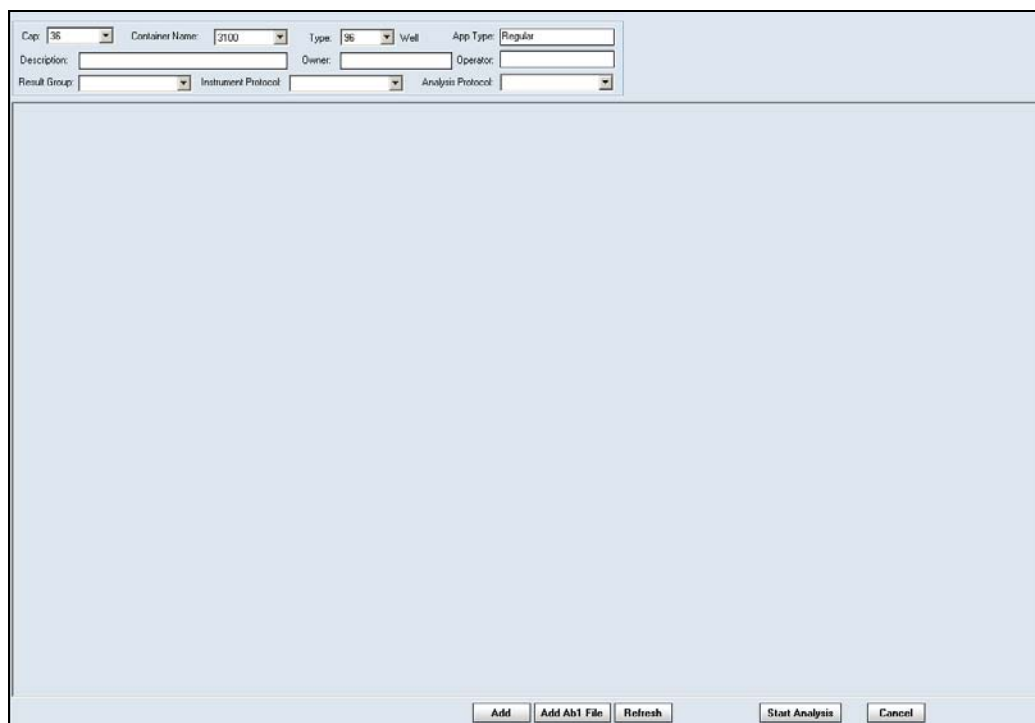
Figure 3-2: ConsenSys Manual Entry Dialog Box



- Accept the current date or select a different test date and click **Next >**.

-
- Click **Create New Session/Tray**. A window is displayed to allow for subsequent session/tray information.

Figure 3-3: Session/Tray Information Window

A screenshot of the 'Session/Tray Information Window'. The window has a light blue background. At the top, there is a header section with several input fields: 'Cap' (dropdown menu showing '36'), 'Container Name' (text box showing '2100'), 'Type' (dropdown menu showing 'S6'), 'Well' (text box), 'App Type' (dropdown menu showing 'Regular'), 'Description' (text box), 'Owner' (text box), 'Operator' (text box), 'Result Group' (dropdown menu), 'Instrument Protocol' (dropdown menu), and 'Analysis Protocol' (dropdown menu). Below these fields is a large, empty rectangular area. At the bottom of the window, there is a row of five buttons: 'Add', 'Add Ab1 File', 'Refresh', 'Start Analysis', and 'Cancel'.

- Enter all required information in the fields at the top of the window. (To add an Ab1 file(s), see [Adding an Ab1 File, p. 27.](#))
- Click **Start Analysis**. The ConsenSys analysis window is displayed.

Adding an Ab1 File

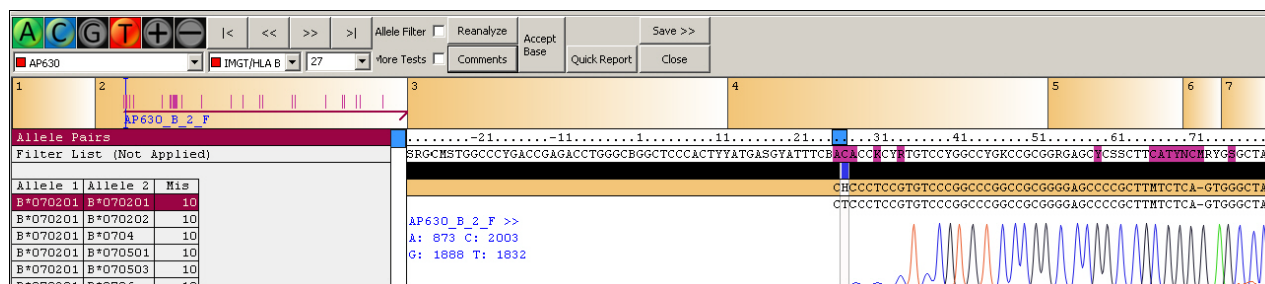
- From the Session/Tray information window, click the **Add Ab1 File** button at the bottom. The file import window is displayed.
- Browse to the folder on your computer containing the Ab1 data file(s) you want, select the file, and click **Open**. The imported Ab1 data file(s) will be displayed on the right side of the Analysis window.

Note: You can select and import more than one file at a time by using the **CTRL** key.

- Click the **Start Analysis** button to analyze the Ab1 files.

Using the ConsenSys Analysis window

The Reference Sequence displays a magenta highlight around bases that differ between the reference and consensus sequences. These bases need to be individually viewed and accepted or edited. Blue highlights between the reference and consensus sequences indicate the location of manually edited bases. The Consensus Sequence is the combined consensus between both the forward and reverse primers. It displays any manually edited bases. A green highlight on a base in the Consensus Sequence indicates an accepted base. To resize the electropherogram, hold down the Shift Key and use the arrow keys to change the size. Right click an electropherogram for more options.



Keyboard Shortcuts

The computer keyboard sequences listed below allow you to navigate and manipulate the ConSensys analysis window.

Key	Shift	CTRL	Description
←	×	×	Go to sequence start position
←	×		Reduce trace width (when not in fixed width view)
←		×	Go to previous marked position
←			Go to previous position
→	×	×	Go to sequence end position
→	×		Increase trace width (when not in fixed width view)
→		×	Go to next marked position
→			Go to next position
↑	×	×	Zoom in on low level signal
↑	×		Decrease the height of the trace window
↑		×	Reduce the trace scale
↑			Go to previous sample
↓	×	×	Zoom out to show high intensity signal
↓	×		Increase the height of the trace window
↓		×	Increase the trace scale
↓			Go to next sample

Key	Shift	CTRL	Description
TAB			Confirm the current IUB code call and move to the next unconfirmed position
A			Set the current IUB code to A
A	×		Show/hide the A trace
A		×	Toggle the amino acid translation view
C			Set the current IUB code to C
C	×		Show/hide the C trace
G			Set the current IUB code to G
G	×		Show/hide the G trace
T			Set the current IUB code to G
T	×		Show/hide the T trace
B			Set the current IUB code to B
D			Set the current IUB code to D
H			Set the current IUB code to H
K			Set the current IUB code to K
M			Set the current IUB code to M
R			Set the current IUB code to R
S			Set the current IUB code to S
V			Set the current IUB code to V
W			Set the current IUB code to W
X			Set the current IUB code to X
Y			Set the current IUB code to Y
+			Add an insertion marker at the current position
-			Add a deletion marker at the current position
F			Open the sequence find dialog
I			Show/hide trace information
[			Step back through the sequence primer layers

Sample Comments

If you choose to enter comments about the sample, they are displayed for the results in the current analysis session in all analysis, data look up and reporting functions in HLA Fusion™ <Emphasis>Research.

1. From the **Analysis** window, click **Comments**.
2. Enter comments about the sample into the **Comments and Warnings** window, and click **Done**.

Flagging a Sample for Further Testing

Marking a sample for more testing displays the More Tests check box for the sample's results in the current analysis session in all analysis, data look up and reporting functions in HLA Fusion™ <Emphasis>Research.

- From the **Analysis** window, select the **More Tests** check box.

Accept Base Calls

You can individually accept the close base calls determined by HLA Fusion™ <Emphasis>Research. When you accept a base call, you are moved to the next marked base position.

- From the **Analysis** window, click **Accept Base** to accept the computer-suggested base call and move to the next base.

Edit Base Calls

The base assignment button is highlighted for the currently selected base. More than one base can be selected at a time and the corresponding base code is displayed. If no bases are highlighted, an asterisk (*) is displayed in the consensus sequence. Any base call can be edited.

- From the **Analysis** window, click on a base and click one or more of the assignment buttons to change the base assignment.



Assignment Buttons

Saving and Confirming ConsenSys Analysis Results

HLA Fusion™ <Emphasis>Research software provides computer suggested typing results. Final assignments can only be made by the user.

From the **Analysis** window you can:

- Save results
- Confirm results

Save Assignments

Lab technicians and supervisors can save analysis results for further review and approval. Samples are marked as *Ready*.

- From the Analysis window, click **Save>>** to save analysis results.

Confirm Assignments

Lab Supervisors can review and confirm analysis results. Samples are marked as *Approved*.

- From the Analysis window, click **Confirm**>> to confirm analysis results.

The SSO Genotyping analysis feature of the program analyzes three Luminex .csv output files as a new session and can continue the analysis of a previously unfinished session.

Starting SSO Analysis

SSO analysis results are based on catalog specifications that are provided with the software. You can analyze samples one at a time to view, adjust, and assign results for each one.

Opening a SSO Analysis Session

1. Select **SSO** home page button  or the SSO toolbar button . The SSO Home page is displayed.

Note: For information on the options available through the links on the right of the window ([Figure 4-1](#)), see [Chapter 11, Utilities](#).

Figure 4-1: SSO Home Page

The screenshot shows the HLA Fusion 2.0 SSO Home Page. The interface includes a menu bar at the top with options: Analyze Data, Reports, Data, Sample, Patient Info, Profile, Utilities, Help, and Exit. Below the menu bar is a toolbar with various icons. The main content area is divided into several sections:

- SSO Product and Catalogs:** Displays the last update date (8/13/2009) and active catalogs (3). It includes links for [Details], [Download], and [Updates available: 0].
- SSO Configuration:** Shows settings for Minimum Positive Control (1000), Minimum Bead Count (100), Minimum Bead Failure Threshold (%) (10), Close Bead Rxxx (3), and Pop-up message for low bead count/low positive (No). It includes an [Edit] link.
- SSO Product Documents:** A table with columns: Catalog, Catalog Description, Worksheet (8.5x11), Worksheet (11x17), and Probe/Primer. The table contains three rows of data with links to various documents.

Annotations on the right side of the page point to specific elements:

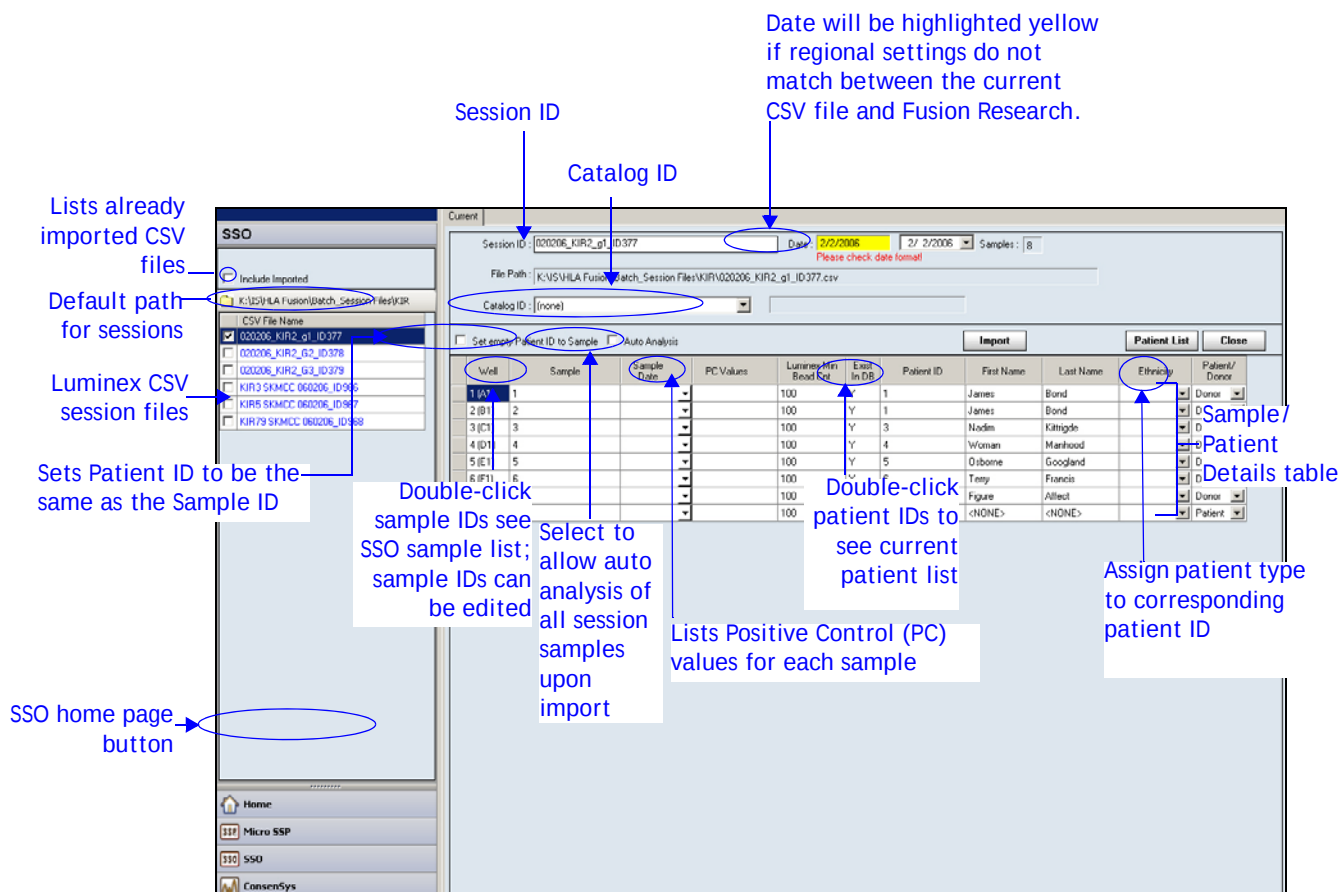
- Click to open Catalog Manager window:** Points to the [Details] link in the SSO Product and Catalogs section.
- Click to open Update Reference File window:** Points to the [Download] link in the SSO Product and Catalogs section.
- Click to open Available Reference Update window:** Points to the [Updates available: 0] link in the SSO Product and Catalogs section.
- Click Edit to modify LABType global settings:** Points to the [Edit] link in the SSO Configuration section.
- Click links to display selected catalog, worksheet, or probe/primer documents:** Points to the links in the SSO Product Documents table.

On the left side, there is a sidebar with a search bar and a list of sessions. At the bottom, there is a navigation pane with links to Home, Micro SSP, SSO, and ConsenSys.

Note: Open worksheets and probe/primer sheets to verify the accuracy of revision numbers (these documents do not contain a revision number in their filename).

2. Select a session from the CSV File Name list. The **SSO Session Import** window displays.

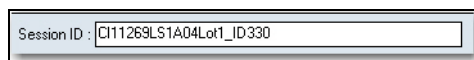
Figure 4-2: SSO Session Import Window



Note: HLA Fusion Research converts Luminex-generated CSV file data, such as date and time, to the local regional code if a regional code is specified in the CSV file. (A regional code cannot be specified for CSV files created with Luminex software version 2.2 or earlier.) If the first date field is highlighted yellow, it indicates a regional code mismatch. In this case, it is recommended that you use the drop-down selector in the second date field to choose the appropriate date, taking into consideration regional date format differences.

3. Select a file from the list of CSV files to import, or click the folder icon above the list to browse to LABType CSV file(s) on your system/network. If samples in a session have a positive control value below the minimum setting, they are flagged so you can easily select and delete them from the session.
4. The system assigns a session ID (the CSV filename) automatically. Optionally, you can change the ID. The ID can be alphanumeric (contain letters and numbers), and will be listed alphabetically with any other SSO session files in your database.

Figure 4-3: Session ID Field



Note: A session ID must be unique to the Fusion Research database. If the session ID already exists, the software prompts you to rename the session. It is also highly recommended that you do not use any special characters in this field since they may serve a specific purpose as field separators (see *Special Characters to Avoid in Filenames*, [p. 339](#)).

5. If a sample is already associated with a patient, the patient ID and any existing, related patient information is displayed. To add patient information, do one of the following:
 - To add data from the system, double-click in the Patient ID column of the Sample/Patient Details table or click the **Patient List** button on the toolbar. The **Import Patient** window is displayed, allowing you to import the patient information file. See *Importing Patient/Donor Lists*, [p. 100](#) for details.
 - To manually add patient data, type data into the patient-related fields of the table.
 - You can assign the sample ID to empty patient ID fields by selecting the check box for *Set empty patient ID to Sample*.
6. Select a catalog file. Your catalog file selection method varies, depending on the CSV file and the catalog files you have imported for LABType:

Note: If you need to import more catalogs, click the **Download** link on the LABtype home page and see [Chapter 11, Utilities, p. 117](#) for instructions on how to add new catalog files to the database.

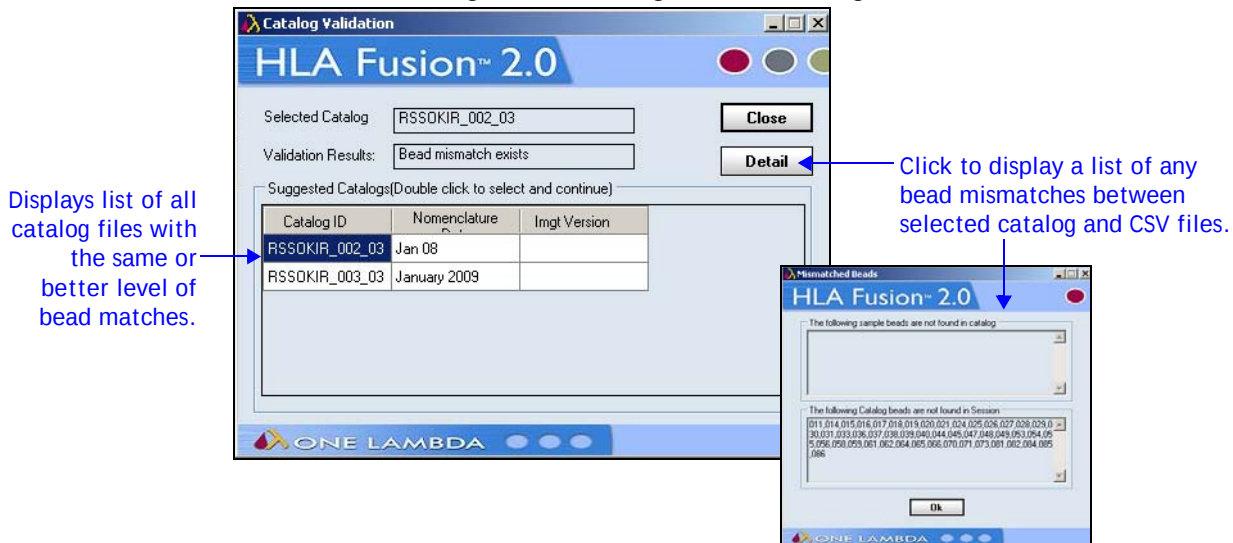
The catalog drop-down list may not be immediately updated if you downloaded the catalogs during this import session. You may need to click the **Home** button and then click the **LABType** button again to return to the import process.

- If the CSV file specifies a template name (only applies to CSV files from Luminex 2.2 and later), and one of the available catalog files is associated with that template, then that catalog file is automatically selected. You can go to [Step 8](#).

Note: You can also select a different catalog file from the one the system has selected by using the drop-down list in the **Catalog ID** field and selecting any catalog file listed.

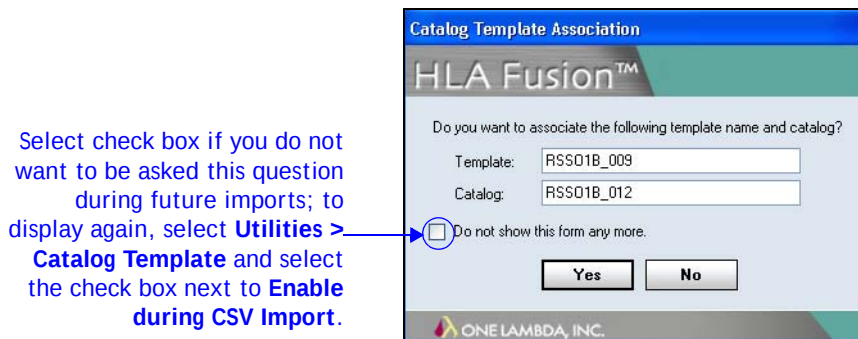
- If there is no template match, the system then considers the closest bead match between the session and all available catalog files. If only one catalog file is a close match, it is automatically selected, and you can go to [Step 8](#). If there is more than one match, a catalog validation dialog box is displayed with the best bead matches. You can confirm the selected catalog file by clicking the **Close** button. Or, you can double-click a catalog file name on the list of **Suggested Catalogs**.

Figure 4-4: Catalog Validation Dialog Box



- Following catalog file validation, the system may ask you if you would like to associate that template name with the specified catalog file (see Figure 4-5). If you click **Yes** to associate the two, the system automatically selects this catalog file for future imports of any CSV files that reference this template.

Figure 4-5: Catalog Template Association Dialog Box



- Check to see if there are any samples that have been flagged as having a low positive control (PC); the rows of low PC samples are highlighted gray. Take the following steps if you want to delete any of these samples:
 - Click in the border to the left of the Well position column to highlight the entire row for the sample (see Figure 4-6).

Figure 4-6: Highlight Sample Row for Deletion

Well	Sample	Sample Date	PC Values	Exist In DB	Patient ID	First Name	Last Name	Ethnicity	Patient/Donor
E4	G0290		2790	Y					
F4	G0114		2701	Y					
G4	G0242		3259	Y					
H4	G0246		2715	Y					
A5	C4916		2619	Y					
B5	G0223		2782	Y					
C5	G0222		2187	Y					
D5	G0141		2606	Y					
E5	G0133		2422	Y					
F5	C4905		1319	Y					
G5	C4726		3253	Y					
H5	C5021		3173	Y					
B6	C5016		3181	Y					
C6	G0067		2634	Y					
D6	G0069		730	Y					
E6	G0082		2904	Y					
F6	G0083		2928	Y					
G6	G0087		3202	Y					

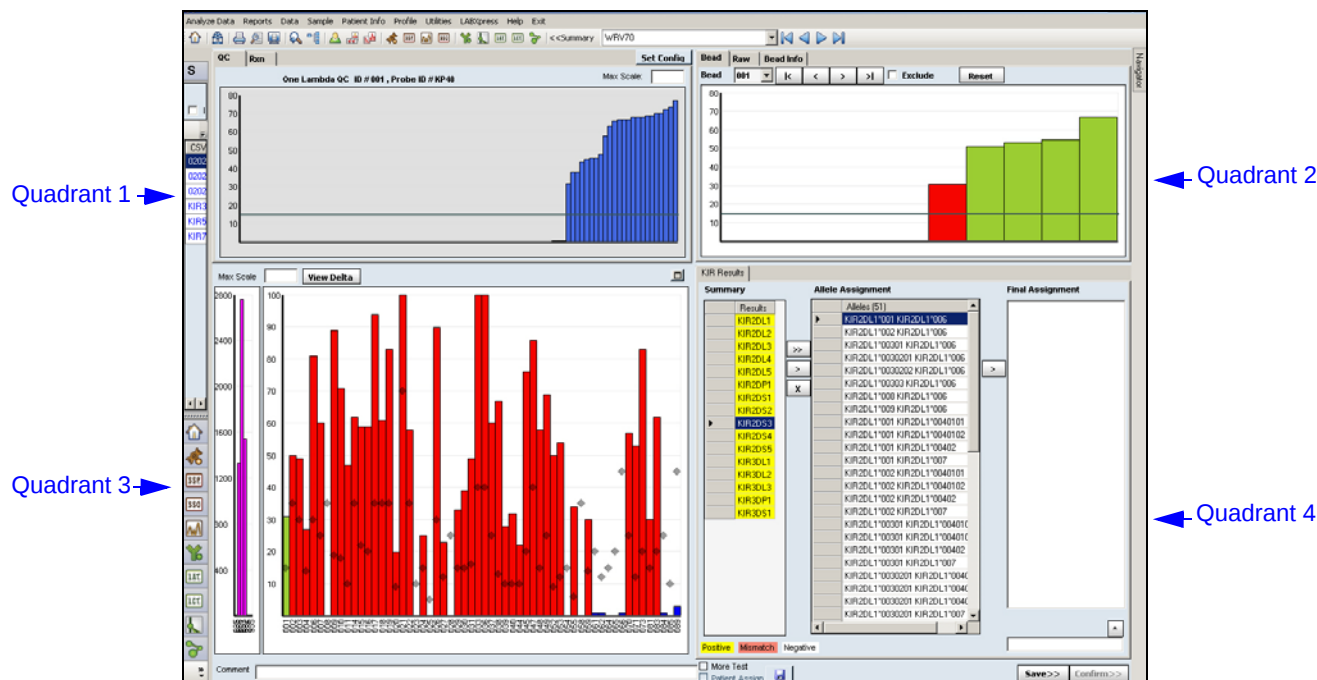
Click here →

- Press the **Delete** key on your computer keyboard to delete the sample and prevent it from being imported as part of the session.
- When session and sample information has been verified, click the **Import** button. The newly imported session is displayed in the **Navigator** tree, in blue at the top of the list. If you select the **Auto Analysis** check box, the session is imported as well as analyzed when you click **Import**; it is displayed on the Navigator as an analyzed session.
 - You can continue importing Luminex session files, or you can click a session on the Navigator to start a batch analysis.

Note: Once a CSV file has been imported, it no longer displays on the Luminex session import list unless you select the **Include Imported CSV** check box.

Displaying a SSO Analysis Window

- Open a SSO session.
- Click on a sample to display its analysis in the **Analysis** window. See [Analyze SSO Data, p. 48](#) for more information.



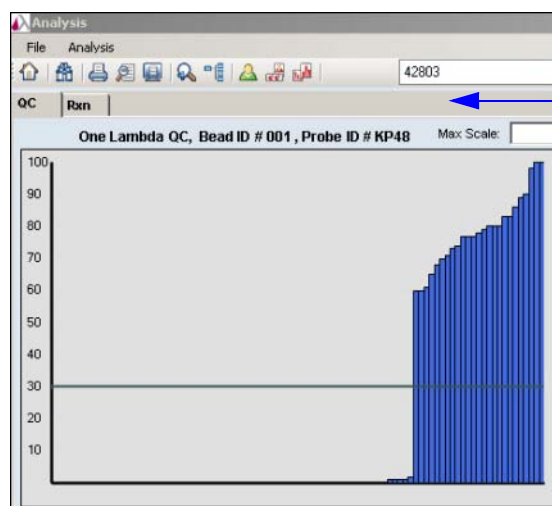
- Select a sample from this list to make the sample active in the **Analysis** window. Alternatively, you can use the arrow buttons to move between the samples.
- Click any column header among the sample list to sort the table by that column. Click the arrow buttons to display the samples per the sorting criteria.

Histograms

Double click on a sample histogram in quadrant 2 to make that sample active. The color of the selected sample histogram in quadrant 2 will change to red and the selected sample profile will be displayed in quadrant 3.

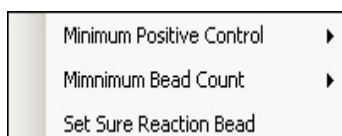
Configuring SSO Data Analysis

The **Configuration** tool allows you to define certain parameters for the analysis. To launch this tool, right-click on the gray panel below the toolbar.

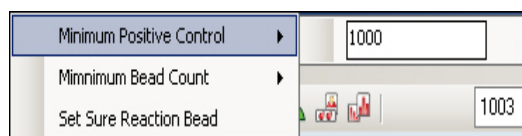


Right click here to launch Configuration tool

The **Configuration** window is displayed, as shown below.



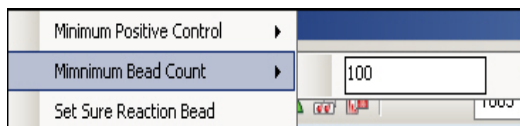
Minimum Positive Control



The default Minimum Positive Control value assigned by the system is 1000. If desired, you can enter a new value into the Minimum Positive Control Value field. If the positive control bead count for a sample is lower than the entered value, a warning is displayed.

In Sample analysis, each sample is processed individually. Results can be viewed and adjusted and final typing assignments made. Using batch analysis, all samples are processed at once and no assignments or changes can be made during analysis. You can continue the session to make adjustments and assignments.

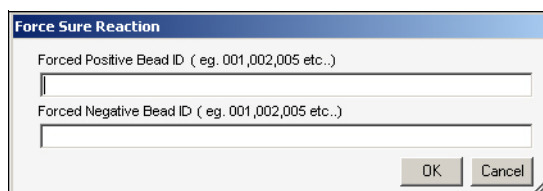
Minimum Bead Count



The default Minimum Bead Count value assigned by the system is 100. If desired, you can enter a new value in the Minimum Bead Count Value field. A warning is displayed if the count for any bead in a test falls below the Minimum Bead Count threshold.

Set Sure Reaction Bead

Selecting the **Set Sure Reaction Bead** option in the configuration menu displays a new window, as shown below. In this window, you can force positive or negative bead ID values by typing in the box.



SSO Analysis window Overview

From the Analysis window you can:

- View sample analysis results
- Change histogram scaling
- Add comments and mark for more testing
- Print analysis information

For each sample in the current session, you can view the test data, adjust the cut-off and assign a typing. HLA Fusion™ *Research* analyzes a sample when you move to view that sample. Any unviewed samples do not have analysis results when the session is saved. To analyze an entire session, all samples in the session must be viewed and typings assigned by the user.

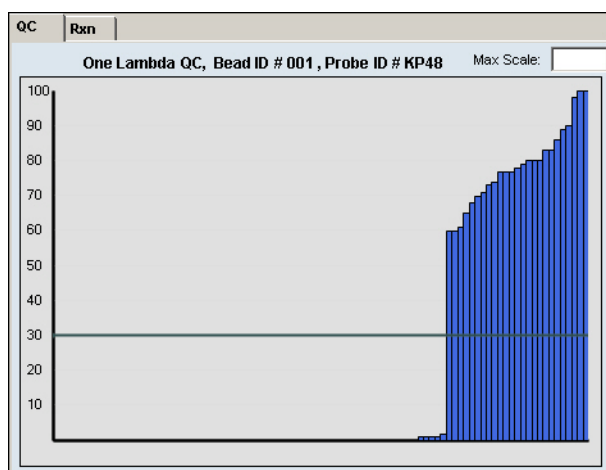
Using the SSO Data Analysis window

The **Sample Analysis Screen** provides detailed analysis information for each sample in the session. You can review the typing assignments suggested by the program and to modify and accept the assignments. HLA Fusion™ *Research* suggests possible typing results, but the final assignment is made by the user. Cut-off adjustments made in the Analysis window are sample-specific and affect only individual samples.

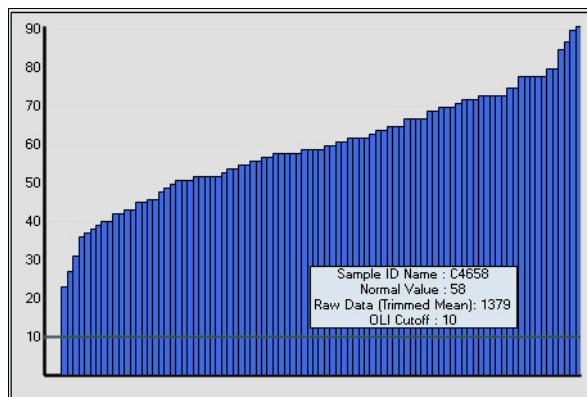
SSO Analysis window - Quadrant 1

QC Tab

Quadrant 1 displays the QC data histogram for the currently selected bead in the QC tab. Each bar represents a QC sample and its height represents the normalized reaction value for the selected bead in that sample.



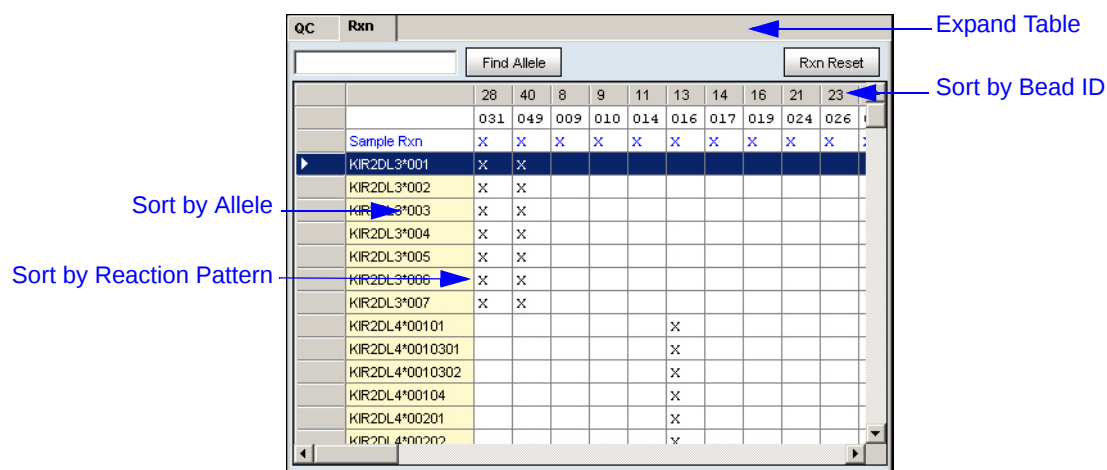
Hover your cursor over any sample to display the sample details, as shown below.



To change the histogram scale, click inside the Max Scale field, type in new limits, and press Enter. This changes the maximum scale for the histograms in quadrants 1 and 2. You can change the scale back to a new value the same way.

Reaction Patterns Tab

1. From the Analysis window Quadrant 1, click on the **Rxn** tab to display the Reaction Pattern Table.



2. Use the **Find Allele** tool to display the reaction pattern in the first row of the table. Type an allele into the text box and click on the **Find Allele** button to **sort by allele**.
3. To **sort beads by reactivity for the allele**, click on the gray area on the left of the allele name. The positive reactions would be moved to the left of the table. Click on the **Rxn Reset** button to reset the table to original configuration.
4. Double-click on the blue panel between the **Find Allele** and **Rxn Reset** buttons and the reaction table will be expanded. To bring the table back to its original size, double-click on the same position again.
5. Click on any column header to **sort the table by well position**.

Positive reactions are listed above the blue line, and negative reactions below.

SSO Analysis window - Quadrant 2

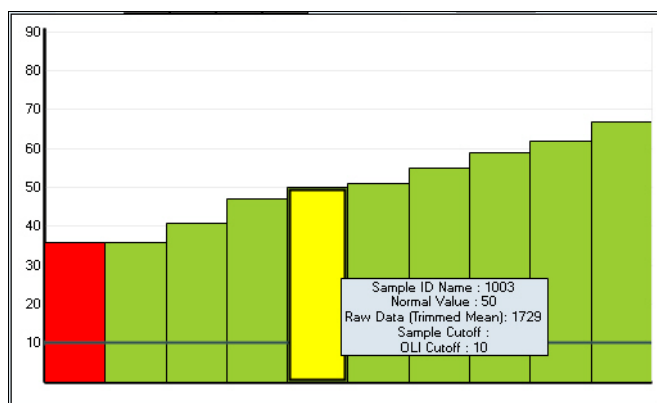
Bead Profile

The Bead profile tab displays the histogram for the currently selected bead. Each bar represents a sample and its height represents the normalized reaction value for the selected bead in that sample. The red bar represents the currently selected sample.

1. Click the arrow buttons to navigate between beads and display the profile of the selected bead in Quadrant 2. Alternatively, you can select the bead from under the **Bead** drop-down choices.



2. Hover your cursor over any sample. The sample details are displayed, as shown below.



3. If you wish to exclude a bead from analysis, you can select the check box for **Exclude**.
4. The **# False** option allows to force false reactions. HLA Fusion™ *Research* re-analyzes the reaction allowing for one false reaction. By default, the software analyzes a sample until an HLA typing can be determined or until the analysis reaches the maximum number of false reactions set in the analysis configuration table. This is a useful tool for checking results, for example, it can be used to look for perfect matches with homozygosity or rare allele assignments. If desired, increase the number of false reaction to be forced and click on the **Reanalyze** button next.

To adjust Sample Cutoff Values, do the following.

1. Select the **Adjust Cutoff** check box to activate the adjust cut-off feature.
2. Click on histogram to set new cut off value to that position. Click the **Reanalyze** button to re-analyze the sample. You can change a bead cut-off value for each sample individually.
3. Clear the **Adjust Cutoff** check box to lock the cut off.

4. Click on the **Reset** button to reset the changed values back to default. The following options would be displayed to choose from.

Current Sample : Current Bead to OLI Default

Current Sample : All Beads to OLI Default

Current Sample : Current Bead to User Setting

Current Sample : All Beads to User Setting

Raw Tab

The Raw Data Table displays all raw data and test details for the current sample.

1. From the **Analysis** window Quadrant 2, click the **Raw** tab to display the Raw Data Table.

Bead

Raw

Bead Info

Threshold 3

Maximize

	Bead ID	Rxn	Raw	Normal	Pos Ctl	OLI Cutoff	Sample Cutoff	Count
▶	001	1	33.24	0.4	057	30	30	119
	002	8	2492.16	61.42	057	38	38	128
	003	8	4086.18	100.97	057	50	50	100
	004	1	54.42	0.92	057	30	30	138
	006	8	2624.54	64.7	057	45	45	116
	007	8	3163.96	78.09	057	32	32	117
	008	1	14.36	0	057	50	50	145
	009	8	4656.72	115.13	057	30	30	134
	010	8	3669.64	90.63	057	30	30	121
	035	1	17.17	0	057	2	2	132
	052	8	1681.47	41.3	057	10	10	124
	057	1	4047.09	100	057	100	100	138

Expand Table

Sort by Column

2. To change the threshold value, enter a new value in the Threshold field and press **Enter**. Normalized bead values that fall within the specified threshold range of the cutoff for that bead are highlighted. The raw table will be updated instantly highlighting the rows in yellow. The Bead IDs for the highlighted row is displayed in the **Close Bead Rxn** box.

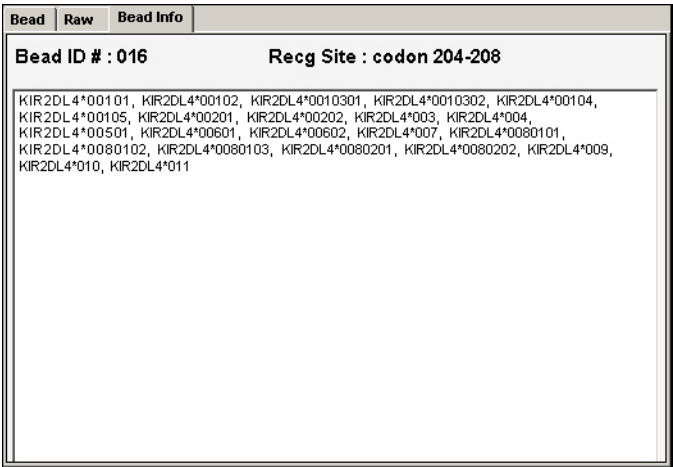
Close Bead Rxn

#001 #005 #006 #007 #008

3. Click the **Maximize** button to expand the Raw Data Table. Click the X to close.
4. Double-click the blue horizontal panel in the raw tab to expand the raw data table within the **Analysis** window. To bring the table back to its original size, double-click the same position.
5. Clicking on any column header would sort the raw data table by that column.

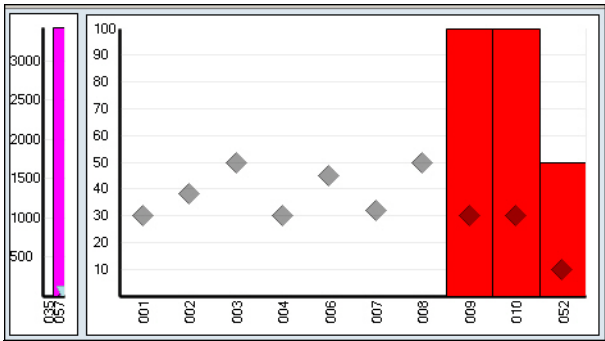
Bead Info Tab

- 1. From the Analysis window Quadrant 2, click the **Bead Info** tab to display the allele specificity of the selected bead.



SSO Analysis window - Quadrant 3 Sample Profile

The Sample Profile displays each bead in the currently selected sample. Each bar represents a bead in the sample sorted by bead number and its height represents the normalized reaction value for the selected bead in that sample.

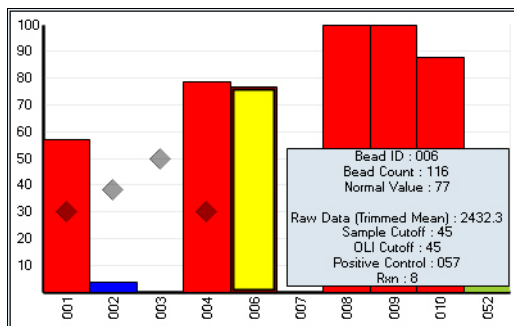


Red = positive reaction; Blue = negative reaction; Green = selected bead in quadrant 2.

The diamonds inside the histograms indicate the current cut-off position. Arrowheads identify the direction and position of cut off changes made to a bead.

- 1. Click arrow buttons on the toolbar to select a sample bar and display the selected sample in Quadrant 3. Alternatively, you can also select a sample from under the **Sample** drop-down list in the toolbar. You can also select a sample by double-clicking on a sample bar in the Bead Profile histogram.

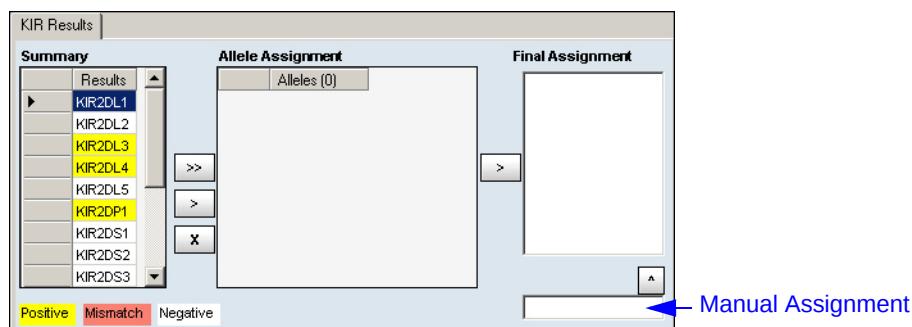
2. Hover your cursor over any sample. The sample details are displayed, as shown below.



3. You can add comments to the sample by typing in the **Comment field** at the bottom. Double-clicking in this text box invokes a new window to type comments in.
4. The magenta bars on the left represent the raw data for positive controls. The up or down arrowheads below indicates the location of the adjusted cut off.
5. You can expand the histogram by double-clicking on the blue panel between quadrants 3 and 4. To resize the histogram to its original size, double-click on the blue panel between quadrants 1 and 3.

SSO Analysis window - Quadrant 4 - SSO Results and Assignment panel

Quadrant 4 displays possible typing assignments for the current sample. The left side shows possible allele pair assignments suggested by the software. You must make assignments manually. The right shows possible coded assignments.



As the color code displayed in the figure above, the alleles highlighted in yellow are positive match, red ones are mismatches, and unhighlighted ones are negative. To make typing assignments, please see [Make Typing Assignments in SSO Analysis, p. 48](#).

Analyze SSO Data

From the **Analysis** window you can:

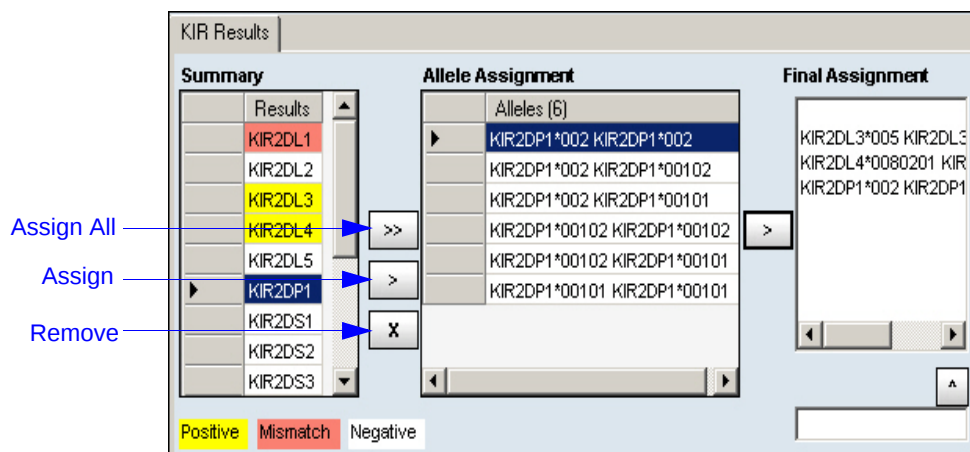
- View raw data
- View reaction patterns
- View bead and sample details
- View results and make typing assignments

The raw data table can be used to easily review raw data, normalized data and cut-off values. The reaction pattern table can be used to compare reaction patterns. Reaction-specific pop-ups display the probe detail and reaction data for the selected sample and probe.

Make Typing Assignments in SSO Analysis

HLA Fusion™ *Research* provides computer suggested assignments. Final typing assignments can only be made by the user. You can save multiple SSO Typing assignments. From the **Analysis** window you can assign typings and make manual assignments.

Typing Assignments



The SSO results are displayed in Quadrant 4 of the Analysis window. This quadrant is divided into three sections. The **Summary** section displays the system suggested results for the SSO locus groups, where the alleles highlighted in yellow are positive match, red are mismatch, and the rest unhighlighted ones are negative. To make a manual assignment, please follow the steps below. The Allele Assignment panel lists the possible allele pair results for the selected SSO locus groups.

-
1. Select an allele or several alleles from the **Summary** using the Control key in your keyboard, and click the **Assign** button to assign the SSO locus group in the Final Assignment panel.
 2. To assign allele pairs, select one or more pair results from the allele assignment panel and click **Assign**.
 3. Click the **Assign All** button to assign all Positive SSO locus groups. The selected allele(s) are displayed under the **Final Assignment**.
 4. To remove any or all alleles from **Final Assignment** sections, select them and click the **Remove (X)** button.

Flagging a Sample for Further Testing

This option flags a sample for further testing in the current analysis session and reports in HLA Fusion™ *Research*. More testing flag is saved with analysis.

- In the **Analysis** window, select the **More Test** check box below the Assignments area.

Reanalyze

Click on the **Reanalyze** button to reanalyze the data based on user changes in the current session or sample.

Manual Assignments

Manual assignments must be entered in standard format with each allele separated by two spaces.

- Type the allele name in the text box below **Final Assignment** section and click on the  button. The newly entered allele is displayed in the **Final Assignment** field.

SSO Batch Analysis

The batch analysis is carried out from the **Session Summary** screen. When the session summary for a new session is activated, a batch analysis is automatically run. Batch analysis allows you to quickly analyze a session and save it for later review and final assignments. You can graphically view samples during batch analysis, but no final typing assignments are made.

From the Session Summary you can:

- Run a Batch analysis for a session
- View the Batch Analysis Summary Chart

Save Assignments

Lab Technicians and Supervisors can save analysis results for further review and approval. Samples are marked as *Ready*.

- From the **Analysis** window, click **Save>>** to save analysis results and move to the next sample. Prior to confirming, a sample can be re-saved, if needed.

Confirm Assignments

When an analysis has been saved, lab Supervisors can review and confirm analysis results. Confirmed samples are marked as *Approved*. The Confirm button is gray when you view a saved but unconfirmed sample. The Confirm button is purple when you view an already confirmed sample. Samples may be reconfirmed.

1. From the **Analysis** window, click **Confirm>>** to confirm analysis results and move to the next sample.

Note: The application records two levels of analysis reviews—Save and Confirm. For re-saved and reconfirmed analysis, only the last user to save or confirm is recorded.

Print Screen

Print Screen prints the currently displayed analysis screen.

- From the **Analysis** window tool bar, click the **Print Screen** button. A screen shot of the current screen is displayed in a new window.

Chapter 5 Micro SSP Analysis

The Micro SSP™ HLA typing trays use the sequence-specific primer technology. These trays are available in 96-well and 384-well format. The Micro SSP analysis feature of the program analyzes manually entered reaction patterns as a new session, and can continue the analysis of a previous session. Analysis results are based on catalog specifications, NMDP code, and serology code references that are provided with the software. Micro SSP analysis uses NMDP cross codes. The software suggests the allele pair assignments, but the final assignment has to be made by the user. The results can be saved in the database for further review by the Lab Technicians and for final approval by the Lab Supervisors.

Starting Micro SSP Analysis

The Micro SSP analysis feature of HLA Fusion™ *Research* analyzes manually input reaction patterns as a new analysis session and can also continue the analysis of a previously unfinished session. Each session consists of as many samples as you wish to analyze with the same catalog information. It can also accept data from eGene and new samples can be added to an existing session.

1. Select **MicroSSP** home page button  or the Micro SSP toolbar button . The Micro SSP Home page is displayed.

Note: If you are not using the default Fusion Research user interface, the data and links shown on the right side of the window in [Figure 5-1](#) are not displayed. For information on accessing this same product data and configuration options, see the [Utilities](#) chapter.

Figure 5-1: Micro SSP Home Page

The screenshot shows the HLA Fusion 2.0 Micro SSP Home Page. The interface includes a menu bar at the top with options like Analyze Data, Reports, Data, Sample, Patient Info, Profile, Utilities, Help, and Exit. On the left, there is a sidebar with a 'Manual Entry' button and a 'CSV File Name' field. The main content area is divided into several sections:

- Micro SSP Product and Catalog:** Displays 'Active Catalogs: 329', 'Serology Equivalent: 2010 January: 5/3/2010', 'Last Updated Date: 11/23/2009', and 'NMDP Update: 5/3/2010'. It includes links for '[Details]', '[Download]', and 'Updates available: 10'.
- Micro SSP Configuration:** Shows settings such as 'Code: NMDP', 'Cross Code Enabled: No', 'Active Demographic / Allele Frequency: (none)', 'Number of False Reaction: 1', and 'Bw4 / Bw6 Information: No'. There is an '[Edit]' link.
- Micro SSP Product Documents:** A table listing various documents with columns for Catalog, Catalog Description, Worksheet (8.5x11), Worksheet (11x17), and Probe/Primer.

Annotations with blue arrows point to specific elements:

- 'Click to open Catalog Manager window' points to the 'Details' link in the 'Micro SSP Product and Catalog' section.
- 'Click to open Update Reference File window' points to the 'Download' link in the same section.
- 'Click to open Available Reference Update window' points to the 'Updates available: 10' link.
- 'Click to modify Micro SSP global settings' points to the '[Edit]' link in the 'Micro SSP Configuration' section.
- 'Click links to display selected catalog, worksheet, or probe/primer documents.' points to the links in the 'Micro SSP Product Documents' table.

Catalog	Catalog Description	Worksheet (8.5x11)	Worksheet (11x17)	Probe/Primer
SSP1-01_001_08		SSP1-01_001_WS		SSP1-01_001_PRI
SSP1-01_001_09		SSP1-01_001_WS		SSP1-01_001_PRI
SSP1-01_002_00		SSP1-01_002_WS		SSP1-01_002_PRI
SSP1-01_002_01		SSP1-01_002_WS		SSP1-01_002_PRI
SSP1-03_001_06				
SSP1-03_002_02		SSP1-03_002_WS		SSP1-03_002_PRI
SSP1-03_002_03		SSP1-03_002_WS		SSP1-03_002_PRI
SSP1-03_003_00		SSP1-03_003_WS		SSP1-03_003_PRI
SSP1-03_01A_09		SSP1-03_01A_WS		SSP1-03_01A_PRI
SSP1-03_01A_10		SSP1-03_01A_WS		SSP1-03_01A_PRI
SSP1-05_002_08		SSP1-05_002_WS		SSP1-05_002_PRI
SSP1-05_002_09		SSP1-05_002_WS		SSP1-05_002_PRI
SSP1-07_002_09		SSP1-07_002_WS		SSP1-07_002_PRI
SSP1-07_002_10		SSP1-07_002_WS		SSP1-07_002_PRI
SSP1-07_003_02		SSP1-07_003_WS		SSP1-07_003_PRI
SSP1-07_003_04		SSP1-07_003_WS		SSP1-07_003_PRI
SSP1-08_001_02				
SSP1-08_002_07		SSP1-08_002_WS		SSP1-08_002_PRI
SSP1-08_002_08		SSP1-08_002_WS		SSP1-08_002_PRI
SSP1-08_003_02		SSP1-08_003_WS		SSP1-08_003_PRI
SSP1-08_003_03		SSP1-08_003_WS		SSP1-08_003_PRI
SSP1-11_001_08		SSP1-11_001_WS		SSP1-11_001_PRI

Note: Open worksheets and probe/primer sheets to verify the accuracy of revision numbers (these documents do not contain a revision number in their filename).

2. Click the **Manual Entry** button. The Manual Entry window is displayed.

Figure 5-2: Micro SSP Manual Entry Window

Catalog	Session	Test Date	Sample Name	Sample Date	Patient ID	First Name	Last Name	Ethnicity	Patient/Donor	Gel Image
---------	---------	-----------	-------------	-------------	------------	------------	-----------	-----------	---------------	-----------

Batch Name: Micro SSP_20100722105001 Existing Batches: Find Batch Date: 7/26/2009 - 1/22/2010

Start new batch — New Batch — Sample — Patient — Gel Image — Save — Next > — Close — Close this window

Open Sample lists — Open Patient list — Browse for Gel Image — Go to analysis window — Save current Batch information

3. The system assigns a Batch Name automatically. Optionally, you can change the name.

Note: A batch name must be unique to the Fusion Research database for each product type. If it already exists, the software prompts you to rename the batch. It is also highly recommended that you do not use any special characters in this field since they may serve a specific purpose as field separators (see [Special Characters to Avoid in Filenames](#), p. 136).

4. Use the drop-down menu in the **Catalog** field to select a catalog file.

Note: If you need to import more catalogs, click the **Download** link on the Micro SSP home page and see [Chapter 11, Utilities](#), p. 117 for instructions on how to add new catalog files to the database.

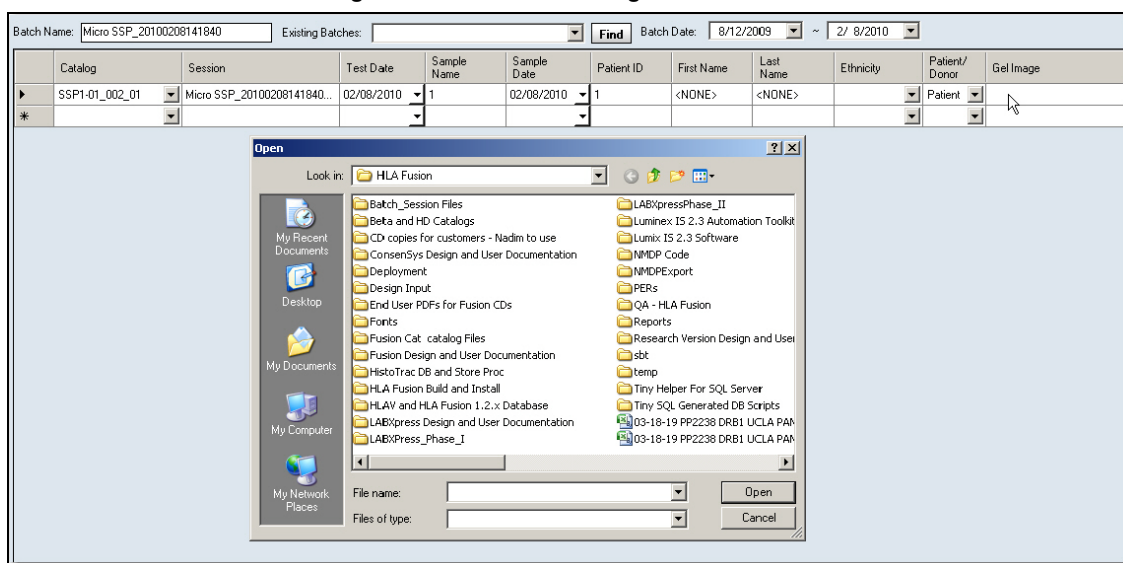
The catalog drop-down list may not be immediately updated if you downloaded the catalogs during this import session. You may need to click the **Home** button and then click the **Micro SSP** button again to return to the import process.

5. Accept the session name in the **Session** field, or modify it.

6. Enter a name in the **Sample Name** field. If this is an existing sample name, other fields, such as the Patient ID and Ethnicity, are populated with existing data.
7. Click the drop-down arrow in the **Sample Date** field and select a date. The analysis window for this session is displayed.
8. If you want to associate a gel image with the sample, double-click in the **Gel Image** field and browse the location of the image you want to add to the sample.

Note: The only format supported for the Gel Image import is JPEG format.

Figure 5-3: Select Gel Image Browser



9. Repeat the above steps until you complete the batch information, or until you want to save and complete the batch later. Each Micro SSP batch session can consist of as many samples as you wish to analyze with the same or with different catalog information.
10. Take one of the following actions once you are ready to stop creating the batch:
 - Click **Next>** to open the Micro SSP analysis window.
 - Click **Save** to save the current batch information to return to later.
 - Click **New Batch** to start creation of a new batch.
 - Click Close to exit the **Manual Entry** window.

Displaying a Micro SSP Analysis Window

1. Open a Micro SSP session.
2. Click on a sample to display its analysis in the **Analysis** window. See [Using the Micro SSP Analysis window](#), p. 57 for more information.

The screenshot shows the Micro SSP Analysis window with several key components and annotations:

- Input and analysis of samples:** A blue box on the left highlights the sample input area, which includes a grid for sample data and a 'View Gel' button.
- Reaction Pattern table:** A blue box on the right highlights the 'Reaction Pattern' table, which displays the results of the analysis.
- Results area:** A blue box on the right highlights the 'Results area', which contains a 'Translate' button and a list of possible serology results.
- Pair displays allele pairs:** A blue box in the center highlights the 'Pair' section, which displays allele pairs.
- Match groups and condenses pairs with same reaction pattern:** A blue box in the center highlights the 'Match' section, which groups and condenses pairs with the same reaction pattern.

Additional annotations include:

- A blue box at the bottom left highlights the 'View Gel' button with the text: 'Click to view or add a gel image (must be a JPEG image to add it)'.
- A blue box at the bottom right highlights the 'Translate' button with the text: 'Click to translate to new allele nomenclature format (only applies if old results; new results will already be in new allele format)'.

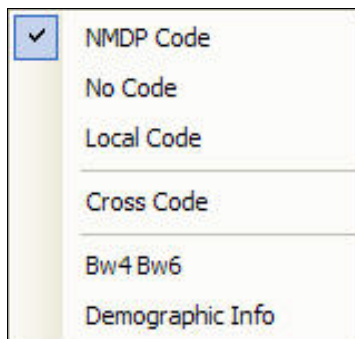
Configuring Micro SSP Data Analysis

The defaults for the configurations can be set from the Utilities menu in the main HLA Fusion™ Research window. Please refer to the **Utilities** chapter for more information on setting the default configurations. Configurations can be set from within the analysis window for the current analysis. If you are starting an analysis session, you can change configuration options before you begin the session.

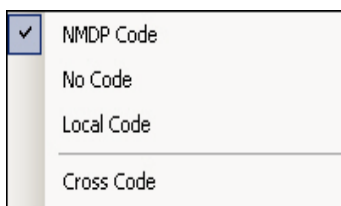
Change Current Configuration

Before starting analysis, you can change analysis options for the current session and all subsequent sessions by using the Configuration menu shown below. Changes to configuration settings in analysis affect the current sample, any samples added after the change for the current session only.

1. To change configuration settings for all new sessions, right click on the blue panel below the toolbar. A list of configuration options will be displayed.

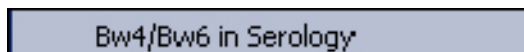


Assign Code



By default, the system assigns the NMDP codes to the alleles. However, the user can optionally change these codes to either No Code, Local Code or Cross Code.

Bw4/Bw6 in Serology



Serology has identified many pairs of HLA-B alleles which appear to differ only at the Bw4/Bw6 region, the two mutually exclusive serological epitopes. If you are involved in Bw4/Bw6 research, you may optionally change the configuration to this option.

Demographic Information



The Demographic Information option offers to determine allele frequency within a particular population.

Entering Micro SSP Reactions Input Panel

The Micro SSP reaction input panel is set up in the same format as the test gel. For multi-test trays, you can skip tray positions to match your gel photos by clicking the Add New Sample button until the correct test position is displayed.

From the Analysis window you can:

- Enter reaction patterns and begin analysis
- Change default reaction pattern values
- Change configuration settings

Entering Micro SSP Reactions

To enter a reaction, simply click on the well until it displays the correct reaction value or type in reaction value for well. The reaction for one sample may be entered at a time. You can enter a new sample at any time during analysis of a new or existing session by clicking **Add New Sample**. New samples use the same catalog information as the rest of the session and also the most current configuration settings.

1. From the Analysis window, enter a sample name in the **Sample ID** box.
2. Enter test reactions by clicking on a well to change the reaction value, or by typing in a reaction value (1, 8 or 0).
3. Click the **Analyze** button.

Note: If the sample has already been analyzed once, click the **Reanalyze** button.

4. To enter a new sample, click the **Add New Sample** button at any time during analysis. Be sure to Save or Confirm any changes to an analysis before adding a new sample.

Using the Micro SSP Analysis window

The **Analysis window** displays detailed analysis information for each sample in the session. You can review the allele assignments suggested by the program, modify and accept the assignments. HLA Fusion™ *Research* suggests possible typing results, but you make the final assignment. Any adjustments made in the Analysis window are sample-specific and affect only individual samples.

From the Analysis window you can do the following:

- View and print sample analysis results
- Use the Reaction Pattern Table
- Add comments and mark for more testing
- Change the allowable number of false reactions
- Force one false reaction

Micro SSP Analysis window Overview

Micro SSP analysis allows you to view analysis details, make adjustments and make typing assignments using the **Analysis window**.

View Well Details

You can view details about the current sample by holding your mouse pointer over a well in the **Reaction Pattern Grid**.

1. From the Analysis window, hold your cursor over a well to view details.

	H	G	F	E	D	C	B	A
01	0	1	0	1	8	8	8	8
02	0	1	0	0	0	0	0	1
03	1	1	1	1	1	1	1	1
04	0	0						
05								

Add New Sample

For multi-test trays, you can skip tray positions to match your gel photos by clicking the **Add New Sample** button until the correct test position is displayed.

Using the Reaction Pattern Table

The Micro SSP reaction pattern table can be sorted by allele name, reaction pattern or well position. The following distinguish the various table entries:

- Positive alleles are highlighted in yellow.
- If a well is a potential false positive, its column is highlighted red.

- If it is a potential false negative, its column is highlighted green.
- Cross Loci wells are indicated with a # symbol in the Cross Loci row for that well position.
- The table can be sorted by typing an allele into the field. This moves the allele to the first row and freezes the row.

The screenshot shows the 'Rxn' (Reaction) table in the HLA Fusion software. At the top, there is a 'Find Allele' button and an 'Expand Table' button. The table itself has columns numbered 1 through 14, representing different wells. The first row is labeled 'Cross Loci' and contains symbols like 3H, 3G, 3F, 3E, 3D, 3C, 3B, 3A, 4H, 4G, 4F, 4E, 4D, 4C. Subsequent rows list various alleles (e.g., A*01010101, A*01010102N, A*010102, A*010103, A*010104, A*0102, A*0103, A*0104N, A*0106, A*0107, A*0108) and show their reaction patterns with 'X' marks in specific wells. Some columns (3F, 3E, 3B, 3A) are highlighted in green. On the left side of the table, there are buttons for 'Sort by Allele' and 'Sort by Reaction Pattern'. On the right side, there is a button for 'Sort by Well Position'. A gray panel is visible on the right side of the table, which can be expanded or collapsed.

1. To **Sort by Allele**, double click on an allele name to bring that allele to the top of the table. Type an allele or partial allele name in the **Find Allele** field, and click the **Find Allele** button. Matches are moved to the top of the Reaction Pattern Table.
2. To **Sort by Reaction Pattern**, click on the left most column of the allele name on the gray area. The positive reactions would be skewed to the left of the table. Click the **Rxn Reset** button to reset the table to original configuration.
3. To **Sort by Well Position**, click on any column header to sort all alleles by reaction value.
4. Double-click the gray panel above the table. The reaction table is expanded. To bring the table back to its original size, double-click the gray panel once again.

Number of Allowable False Reactions

If HLA Fusion™ *Research* cannot determine any results that exactly match the reaction pattern entered, it analyzes the reaction assuming that there is one false reaction in the sample. If a solution still cannot be found, the system continues to search through additional false reactions until the number of allowable false reaction has been reached or a solution is found. The number of false reactions sets the maximum allowable false reactions for an analysis.

- In the **# False Rxn** field within the **Analysis** window, click the up or down arrow to change the number of allowable false reactions.

Force One False Reaction

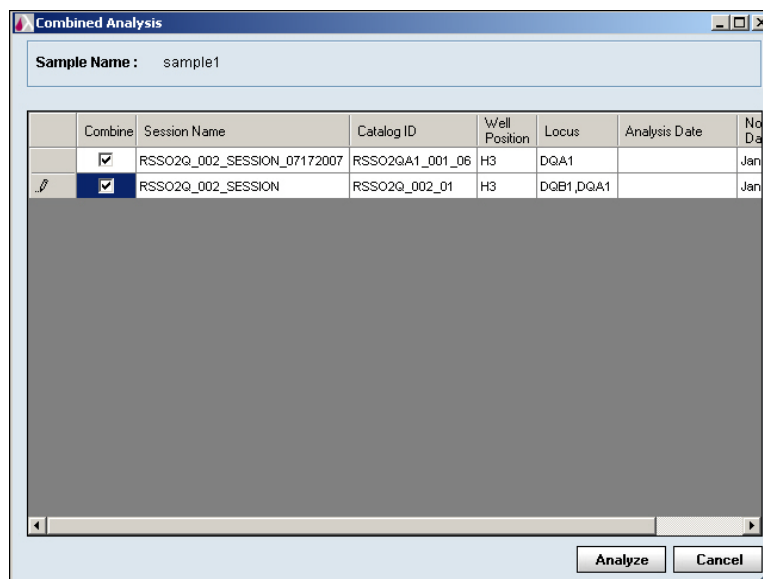
When a sample has a result with no false reactions (exact match result), the **Force 1** feature forces HLA Fusion™ *Research* to re-analyze the reaction to allow for one possible false reaction in any well. This feature is used to search for results that have close reactions to the actual reaction.

1. From the Analysis window, click **Force 1** to force the program to analyze the sample with one false reaction.
2. Click **Rxn Reset** to return to the default results.

Micro SSP Combined Analysis

HLA Fusion™ *Research* compares the sample IDs in the current session with sample IDs in existing sessions, and gives you the option to analyze the sample using readings for both Serology sessions. You can also combine sample readings from a LABType session with those from a Serology session as detailed below.

1. From the Analysis window, click on the **Analyze Combined** button. The next pop-up window displays previous session name to choose from.



2. To select the desired previous session(s), check the box next to it and click the **Analyze** button.

Note: You will notice that the **Analyze Combined** button in the Analysis window changes to **Reanalyze Combine** button. This is an indication that the selected sessions have been combined and reanalyzed.

To combine results for a sample, you need to start or continue a Micro SSP allele specific test and have a previously saved Micro SSP or LABType session to combine with it. After combining sessions, the possible typing assignments are displayed, and the reaction pattern table changes to reflect the reaction pattern of both trays. The reaction wells tray you combined with the current sample is marked with a * next to the well position.

Note: When running a combined analysis with a new sample/test, the user must first enter reactions and analyze sample, and then Analyze Combined can be performed.

Making Typing Assignments in Micro SSP Analysis

HLA Fusion™ *Research* provides computer-suggested allele pairs and coded assignments. Final typing assignments can only be made by the user.

From the Analysis window you can:

- Assign non-coded allele pairs
- Assign a coded allele pair

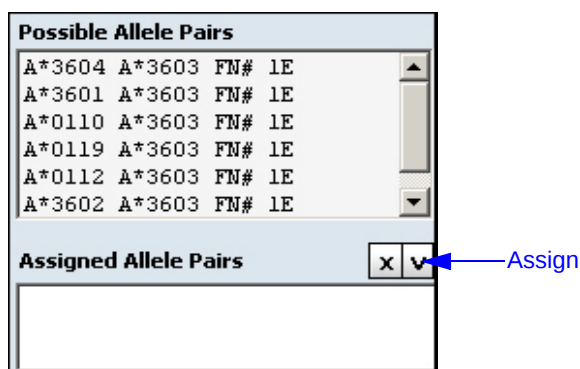
- Assign serological equivalents
- Make manual assignments
- Remove assignments
- Save and Confirm assignments

Possible Allele Pairs

The Possible Allele Pairs panel displays all possible typing assignments for the current sample. If there is only one coded allele pair typing assignment, you can assign it and move to the next sample with one button. Only the coded assignment is saved.

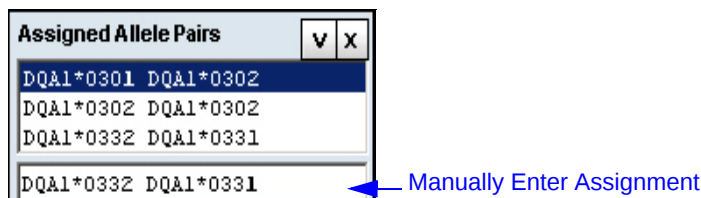
Allele Pair Assignments

1. Select an allele pair in the Possible Allele Pairs panel.
2. Click the **Assign** button next to **Assigned Allele Pairs** to add the assignment to the final assignment area. Alternatively, you can double click on the allele pair to assign it to the final assignment area.
3. To remove an assignment, highlight the assignment in the final assignments area and click on X.



Manual Allele Pair Assignment

Manual assignments must be entered in standard format (locus*four digits space locus*four digits).



1. Type an assignment into the text box right below **Assigned Allele Pairs**.
2. Click Enter and the typed allele is displayed in the **Assigned Allele Pairs** text box.

Allele Code Assignments

Possible Allele Code
DQA1*03XX1 DQA1*03XX1
XX1:=:01/02/03

Assigned Allele Code ☒ **Assign**
DQA1*03XX1 DQA1*03XX1

Manually Enter Assignment

The allele codes displayed in the **Possible Allele Code** text box are condensed ones that the system suggests from the list of possible allele pairs displayed.

- To assign an allele, select its code and click the **Assign** button.

Manual Allele Code Assignment

1. Type an assignment into the text box right below **Assigned Allele Code**.
2. Click Enter and the typed allele code would be appear in the **Assigned Allele Code** text box

Serology Assignment

Possible Serology
Sero Not Assigned

Assigned Serology ☒ ☐ **Assign** **X**
Manually Enter Assignment

Highlighting a serological typing pair displays all allele equivalent possibilities for the current sample. Serological equivalents are saved in addition to any allele or code assignments.

1. The **Possible Serology** panel displays serological equivalents for the current sample.
2. Highlight an assignment and click the Assign button to assign serology. It would be displayed under the **Assigned Serology** panel.
3. Click the X to remove typing assignment.

Bw4/Bw6 configuration results appear here.

Other Assignment

This tool allows non-formatted final assignment.

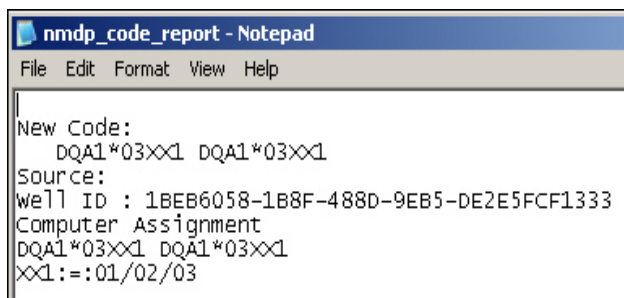
A small dialog box titled "Other Assignment" with a single text input field and a button.

Type an allele pair or allele code and click Enter. The typed allele would be assigned and included in the report.

Unknown Allele Codes

Unknown allele codes are marked with XX followed by a sequential number. The numbers are reset to 1 for each sample and locus. You can store these unknowns for later submission in a .txt file named nmdp_code_report.txt and located in the C:\Program Files\One Lambda\HLA Fusion\data folder. Code information is stored in the text file as it is added with the newest additions at the bottom.

1. From the Analysis window, click the XX code in the Possible Allele Code box to display the XX Code bar.
2. When you select an allele code under the **Possible Allele Code** text box, the **+Rpt/Close** button appears on top of the **More Test** button.
3. To add the code information to the .txt file, click **+Rpt**. Click **Close** to close the bar.
4. The allele code would be included in the text file, as shown below.

A screenshot of a Notepad window titled "nmdp_code_report - Notepad". The text inside the window is as follows:

```
New Code:
DQA1*03XX1 DQA1*03XX1
Source:
Well ID : 1BEB6058-1B8F-488D-9EB5-DE2E5FCF1333
Computer Assignment
DQA1*03XX1 DQA1*03XX1
XX1:=:01/02/03
```

Remove Assignments

You can select more than one specificity to remove by holding down the Ctrl key and clicking multiple specificities.

- From the Analysis window, highlight specificities in the Assignment boxes and click X to remove.

Sample Comments

Sample comments are displayed for that sample's results in the current analysis and reports in HLA Fusion™ *Research*.

-
- In the **Analysis** window, type sample comments into the Comment field below the Assignments area. Double clicking in this text box would invoke a new window to type comments in. Comments are saved with analysis.

A screenshot of a software interface showing a text input field. The field has a light blue header with the word 'Comment' in white. The main area of the field is white and is currently empty. To the right of the text area, there are two small, vertically stacked arrow buttons (up and down) for scrolling.

Flagging a Sample for Further Testing

This option flags a sample for further testing in the current analysis session and reports in HLA Fusion™ *Research*. More testing flag is saved with analysis.

1. In the Analysis window, check the **More Test** check box below the Assignments area.

Save Assignments

Lab Technicians and Supervisors can save analysis results for further review and approval. Samples are marked as “Ready”.

1. From the Analysis window, click **Save>>** to save analysis results and move to the next sample. Prior to confirming, a sample can be re-saved, if needed.

Confirm Assignments

When an analysis has been saved, lab Supervisors can review and confirm analysis results. Confirmed samples are marked as *Approved*. The Confirm button is gray when you view a saved but unconfirmed sample. The Confirm button is purple when you view an already confirmed sample. Samples may be reconfirmed.

1. From the **Analysis** window, click **Confirm>>** to confirm analysis results and move to the next sample.

Note: The application records two level analysis reviews—Save and Confirm. For re-saved and reconfirmed analysis, only the last user to save or confirm is recorded.

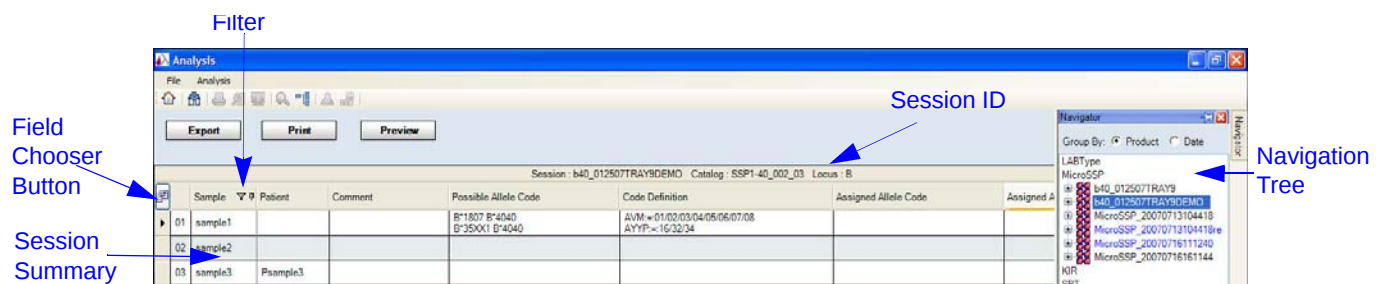
What is Session Summary?

The session summary table presents a pre-analysis of the results. It lists each sample in the session and their saved analysis results. This option allows you to quickly analyze a session in HLA Fusion™ *Research*, and save it for later review and final assignments. You can graphically view samples during batch analysis, but no final typing assignments are made. The summary table can simply be launched by clicking on a session in the Navigation tree.

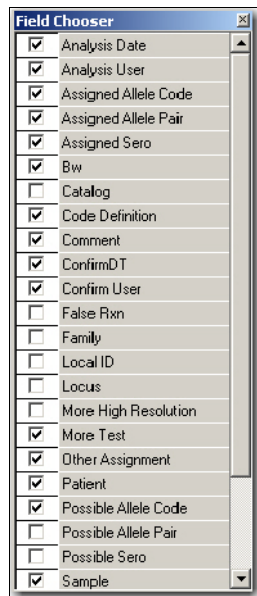
Note: You can return to a session summary from the Analysis Window any time by clicking the <<Summary link from the HLA Fusion™ <Emphasis>Research toolbar next to the sample/session ID.

Example Session Summary

The figure below displays the session summary displayed by clicking on a session. The summary table displays the analysis results for each sample in the selected session.



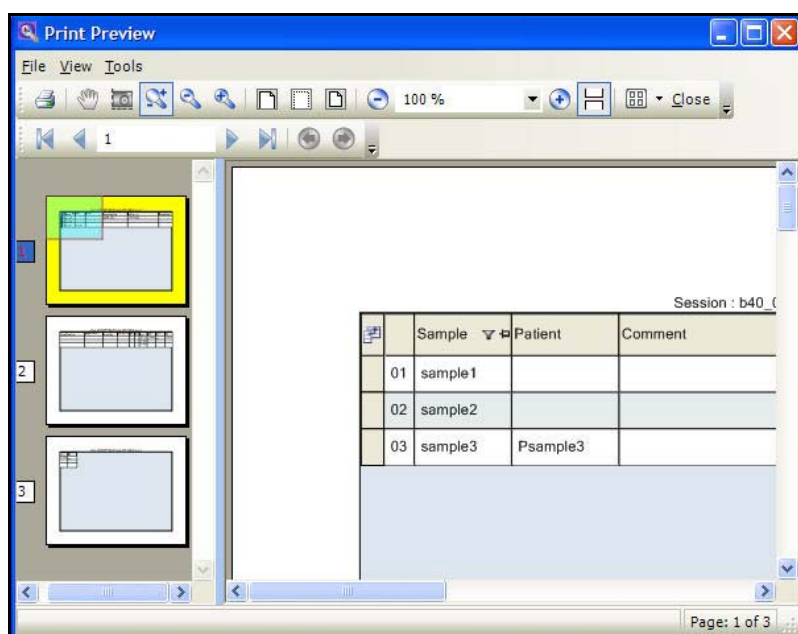
- Double-click a sample in the Summary Table or a data point to go directly to the analysis screen for this sample.
- Click on the **Field Chooser** button to the left of the table headings. The **Field Chooser** window is displayed. In this window, you can select or clear the check boxes next to column headings to add or remove those columns from the Summary Table. Checking or unchecking in this window instantly updates the table.



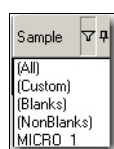
- Click on any column header of the Summary Table to sort the table by that column. The up or down arrows in the column header indicate the sorting order—up for ascending; down for descending.
- Click on the **Export** button to save the Summary Table on your computer or the network. The file will be saved in Excel (*.XLS) format.

	A	B	C	D	E	F
1	Well	Sample	Session	Catalog	Locus	Patient
2	01	sample1	b40_01250	SSP1-40_002	B	
3	02	sample2	b40_01250	SSP1-40_002	B	
4	03	sample3	b40_01250	SSP1-40_002	B	Psample3

- Click **Print** to print out a report of the Summary Table.
- Click **Preview** to view report of the Summary Table.



- In the print preview window, the slider on the left displays various sections of the comprehensive report.
- Double click on a sample in the Summary Table to go directly to the analysis screen for that sample.
- You can filter the samples by clicking the **Filter** button in the sample column header. This displays the filter-by options, as shown below.



The session name is displayed at the top of the Summary Table.

Session : b40_012507TRAY9DEMO Catalog : SSP1-40_002_03 Locus : B						
	Sample	Patient	Comment	Possible Allele Code	Code Definition	
01	sample1			B*1807 B*4040 B*35XX1 B*4040	AVM:=01/02/03/04/05/06/07/08 AYYP:=16/32/34	
02	sample2					
03	sample3	Psample3				

Creating and Managing Session Logs

HLA Fusion™ *Research* allows you the capability to create log files of your analysis sessions, which you can then print or archive.

See the following sections for procedures to create, manage, and print analysis session log files.

Creating a Session Log

1. Click the Main Menu option Data.
2. Provide all necessary session input information by using the drop-down menus and search buttons on the left side of the Data window.
3. Once a session is selected, its information is displayed on the right side of the window where you can add information.
4. Once you have all information you want to include in the log, click Save.

Managing Session Logs

1. Click the main menu option Data.
2. Provide all necessary session input information by using the drop-down menus and search buttons on the left side of the Data window in order to bring up the session you want.
3. Once you have displayed the session log you want, use the Archive, Active and Delete buttons at the bottom of the window to manage the log.

Printing Session Logs

1. Click the main menu option Data.
2. Provide all necessary session input information by using the drop-down menus and search buttons on the left side of the Data window in order to bring up the session you want.
3. Once you have displayed the session log you want, use the Print Session Log button at the bottom of the window to manage the log.

Chapter 7 Reports

HLA Fusion™ *Research* provides different report formats in which to output your analysis data and results. From the Reports menu you can do the following:

- Create, print and export reports for analysis data for all supported products
- Create custom reports for which you determine content type
- Create reports for electronic submission, such as NMDP HML reports
- Store as many as 18 reports in a My Favorites list for convenient access
- Modify the appearance of any report, such as fonts, formatting, and background colors (supervisors only)

Note: To view reports, your computer must have some form of printer driver installed. If you do not have a printer driver installed, you can download a free copy of PDF Distiller from Adobe.com, or Microsoft Office Document Image Writer from Microsoft.com.

In addition, you can print and export these reports from the analysis or batch summary window.

Using the Reports Window

The following sections describe how to create, save and print a report containing your analysis data. Here are the main steps you must take to create a report from this window:

1. Select a report type.
2. As needed, select criteria to refine report input, such as date range.
3. Select the sessions or samples to include in the report.
4. Select the **View Report** or the **Export Report** button

Accessing the Reports Window

- Access the Reports window in one of two ways:
 - From the home page, click **Create Reports**.
 - From the Fusion Research main menu options, select **Reports**.

The **Reports** window is displayed, with a list of any sessions that fall within the date range (based on the session date range set in the Find  dialog box). If no session are displayed, try modifying the date range.

Figure 7-1: Reports Window

Report types: Patient, Generic Typing, MicroSSP, SSO, Specialty, Statistical, Miscellaneous, My Favorite, Tools

Shortcuts to other Fusion Research menu options: Patient, Generic Typing, MicroSSP, SSO, Specialty, Statistical, Miscellaneous, My Favorite, Tools

Store and access up to 18 reports: My Favorite

Format reports & create data export templates: Tools

Close Reports window: Close

Separate report for each sample: 1 Sample Per Report

Export report data in CSV/XML/.txt: Export Report

Preview, print & export a report: View Report

Set order and sort criteria for report columns: Sort By: ASC, DESC, >, <, <<, >>

Select tab to view either by session or by sample: Sessions, Samples

List of sessions, filtered by report type & input criteria: Table with columns: Include, Session, Yes, Product Type, Operator, Session Status, Session Date

Date range for displayed sessions: Session Dates: 7/29/2009 ~ 5/10/2010

Click to filter sessions by selected criteria: Local ID, Catalog Type, Catalog ID, Locus, Test Type, Tech ID, Session Status

Criteria to refine report input (filters session display): Sample Profile: More Tests Needed, Notes/Remarks Added, Analysis Data Exists, Assignments Made, Generic Ambiguity Exists, False Reaction Exists, LBSW Generated

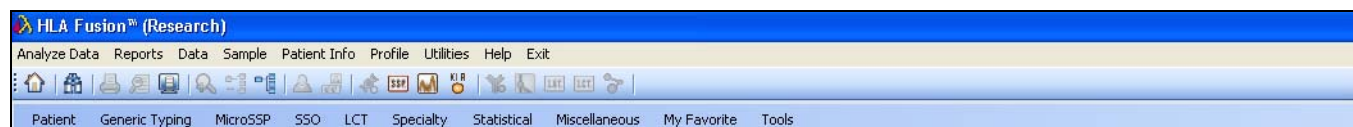
Required: Carefully review all HLA Typing and data in all reports for accuracy.

Include	Session	Yes	Product Type	Operator	Session Status	Session Date
☒	090717 15109 b_ID364	07/17/2009	LABType	é	PROCESSED	08/13/2009
☐	Batch:2009_09_17_12_38_ID21_HD	09/17/2009	LABType	1	PROCESSED	09/19/2009
☐	0406workshop_B_lot 9_ID403	04/11/2006	LABType	1	PROCESSED	05/03/2010
☐	121009 RUN 013_ID1721	12/10/2009	LABScreen	1	PROCESSED	12/11/2009
☐	121009 RUN 013_ID1721	12/10/2009	LABScreen	1	PROCESSED	10/09/2009
☐	121009 RUN 013_ID1721	12/10/2009	LABScreen	1	PROCESSED	12/09/2009
☐	12-3-09 RSSOH1B LOT 4_ID1784_HD	12/03/2009	LABType	1	PROCESSED	12/03/2009
☐	081309-4 C LOCUS_ID717	09/01/2009	LABType	1	PROCESSED	09/01/2009
☐	8-31-09 LS1PRA013-A40	12/18/2009	LABType	1	PROCESSED	12/18/2009
☐	0L1365_DR_L14_ID6247	08/13/2009	LABType	é	PROCESSED	08/14/2009
☐	BL04101409_ID1309_HD 131	10/14/2009	LABType	1	PROCESSED	10/30/2009
☐	8-31-09 LS1A04005-A28	08/31/2009	LABScreen	1	PROCESSED	08/31/2009
☐	8-31-09 LSM12015-A40	08/31/2009	LABScreen	1	PROCESSED	08/31/2009
☐	11-24-09 BERETTA-RSSD2Q005	11/24/2009	LABType	1	PROCESSED	11/30/2009
☐	5922-Zb-SJ_20091124_1737_ID201_HD	11/24/2009	LABType	1	PROCESSED	01/29/2010
☐	9-16-09 RSSOH2B1_004(120-165)_ID93_HD	09/16/2009	LABType	1	PROCESSED	09/19/2009
☐	SG24_1_A_L10_ID6428	09/24/2009	LABType	1	PROCESSED	11/30/2009
☐	DRB1_LOT9_nov2005	02/01/2005	LABType	2	PROCESSED	09/14/2009
☐	5941-Yb-SJ_20091201_1109_ID216_HD	12/01/2009	LABType	1	PROCESSED	01/29/2010
☐	120309 b345 lot 7	12/03/2009	LABType	1	PROCESSED	12/03/2009
☐	091127_SA1_5_kb_ID1880	11/27/2009	LABScreen	1	PROCESSED	11/30/2009
☐	0L1363_DR_L14_ID6229	11/08/2009	LABType	é	PROCESSED	08/13/2009
☐	5919-Wb-SJ_20091123_1950_ID192_HD_Ver27	11/23/2009	LABType	1	PROCESSED	01/29/2010

Select Report Type

- Select a report from the report type menu options displayed at the top of the **Reports** window. The list of sessions in the right pane of the Reports window is filtered to display only the ones related to the selected report type. For a list of reports you can generate, see [Report Types, p. 216](#).

Report Type Menu Options



Refine Report Input

- If needed, use the left panel of the **Reports** window, to further filter the sessions you want to include in your report. There are a number of criteria you can set:
 - Enter a Patient ID, Session or Sample ID fields, or browse for the information with the **Browse** button .
 - Adjust the date range. Use the drop-down calendars in the **Session Date** fields to select a different start and end date.

- Enter or browse for specific sample or session characteristics or status (see below).

The screenshot shows a filter panel for the Reports window. It contains the following fields and options:

- Patient ID:** Text input field with a search icon.
- Session:** Text input field with a search icon.
- Sample ID:** Text input field with a search icon.
- Session Dates:** Date range selector showing 5/28/2009 to 6/11/2009.
- ☐ Include all records for samples
- ☐ Include all combined samples
- Reset** and **Find** buttons.
- Local ID:** Text input field with a search icon.
- Catalog Type:** Text input field with a search icon.
- Catalog ID:** Text input field with a search icon.
- Locus:** Text input field with a search icon.
- Test Type:** Text input field with a search icon.
- Tech ID:** Text input field with a search icon.
- Session Status:** Dropdown menu.
- Sample Profile:**
 - More Tests Needed: ☐ Yes ☐ No ☒ All
 - Notes/Remarks Added: ☐ Yes ☐ No ☒ All
 - Analysis Data Exists: ☒ Yes ☐ No ☐ All
 - Assignments Made: ☐ Yes ☐ No ☒ All
 - Generic Ambiguity Exists: ☐ Yes ☐ No ☒ All
 - False Reaction Exists: ☐ Yes ☐ No ☒ All
 - LBSW Generated: ☐ Yes ☐ No ☒ All

Annotations in the image:

- A blue arrow points to the **Find** button with the text: "click to filter sessions by selected criteria".
- A blue box surrounds the filter criteria section (Local ID through Session Status and Sample Profile), with a blue arrow pointing to it from the text: "sample or session status or characteristics criteria".

- Once you set criteria and click the **Find** button on the left panel of the **Reports** window, the session list in the right panel of the window filters accordingly.

Session/Sample Selection

- In the sessions list, click the + sign next to any session to expand the display to show its samples.

Click tab to view samples—either all samples or only the selected ones

Session with some, but not all samples selected

Session with all samples selected

Samples

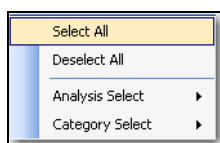
Include	Session	Test Date	Product Type	Operator	Session Status	Session Date
☐	980204_LS1A03_008_ID1466	02/04/2009	LABScreen	oli	PROCESSED	03/11/2010
☐	06-28-05 John Hopkins LS1_009_1	06/28/2005	LABScreen	oli	PROCESSED	03/12/2010
☐	06-28-05 John Hopkins LS2_009_2	06/28/2005	LABScreen	oli	PROCESSED	03/12/2010
☐	06-28-05 John Hopkins LSSingleAntigen	06/28/2005	LABScreen	oli	PROCESSED	03/12/2010
☒	06-28-05 John Hopkins LSSingleAntigen_A	06/28/2005	LABScreen	oli	PROCESSED	03/12/2010
☐	06-12-05_clsa123_15_ID62	12/06/2005	LABScreen	oli	PROCESSED	03/12/2010

Include	NB	NM	Mor	Sample	Well	Well Status	Catalog ID	Patient	Analyzed By	Analysis
☐	☐	☐	☐	neg control	1 (A3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	lab neg control	2 (B3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	4204493 campi	3 (C3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	4204143 eka	4 (D3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	4205137 adams	5 (E3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	4204454 clark	6 (F3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	4204468 bhula	7 (G3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	4203412 falema...	8 (H3)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	4205860 clark	9 (A4)	Batch Imported	LS1A04_002_00		oli	03/12/2010
☐	☐	☐	☐	ab7226837	10 (B4)	Batch Imported	LS1A04_002_00		oli	03/12/2010

- Select the check boxes next to each sample you want to include in a report. Select the check box next to a session ID to include all of its samples. (Deselect the check box of any sample or session you do not want to include in the report.)

If at least one sample has been selected for a session, the **Include** cell for that session is highlighted with grey. If all samples for a session are selected, there is a check box in the Include In cell.

- (Optional) To view all the samples available, or to view only the samples you have selected so far, click the **Samples** tab and select or deselect the check box for **Show selected samples**.
- Alternatively, you can right-click on a session and apply one of the following:

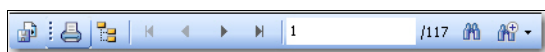


- **Select All:** select all sessions and samples for inclusion in the report.
- **Deselect All:** deselect all sessions and samples from inclusion in the report.
- **Analysis Select:** specify the analysis product report type (LABType, Micro SSP, LABScreen, etc.)
- **Category Select:** choose the report category—molecular or antibody.

Note: To create a separate report for each selected sample, select the check box next to **1 Sample per Report**.

View, Print or Export Reports

- Once you have the report type and all the samples selected, click **View Report**. The report is displayed in a separate window, the **Report Viewer**.
- The Report Viewer contains various toolbar buttons to allow you to export, print and navigate through your report. The functionality of these buttons is described in the following table.

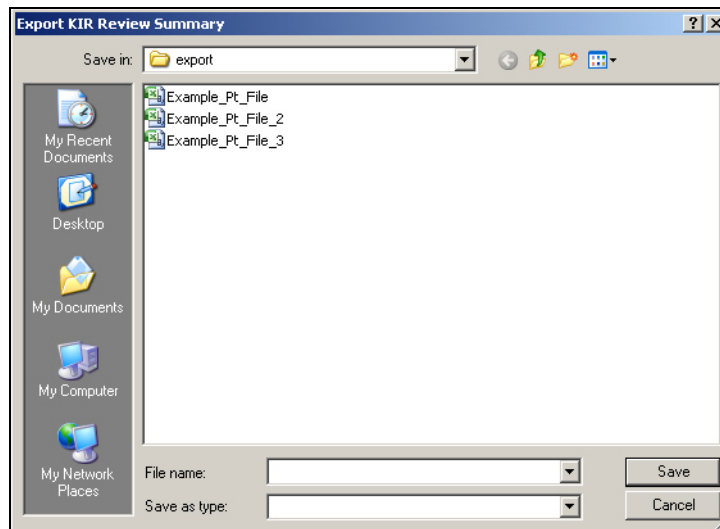


Toolbar Button	Function
	Export Report: exports reports in one of several available formats, including Crystal Report, Adobe PDF, and Microsoft Word.
	Print Report: prints the current report.
	Toggle Group Tree: opens a tree panel on the left, listing the samples included in the current report.
	Previous and Next Page: if the report has multiple pages, these buttons allow you to page back and forth in the report.
	Find Text: displays a dialog box that allows you to enter text to search for in the report.
	Zoom: select the magnification at which to display the current report by clicking on the drop-down list.

- To close the **Report Viewer** window, click the **Close** button  in upper right corner of the viewer.

Export Report

- Click the **Export Report** button  when you want to export a report in one of several standard formats. The **Select Output Directory and Save Type** dialog box is displayed.



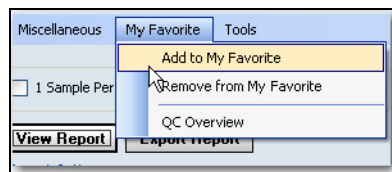
2. Enter a name for the current exported report, or browse for a report file to export. Select a format from the **Save as type** drop-down list (Excel, Acrobat, Word, or Rich Text format), and click **OK**. By default, the file is saved in C:\OLI Fusion\data\report). You can change where these files are saved by modifying the *Interface* path (see [Setting HLA Fusion Research Default URLs and Directory Paths](#), p. 132).

Accessing Reports from the My Favorite Menu

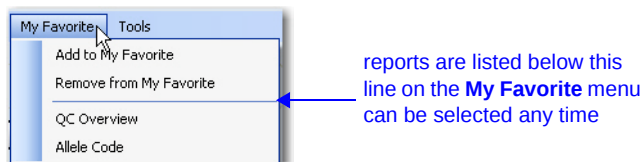
The **My Favorite** menu is a convenient way for you to access and generate the reports you use most. You can make as many as 18 report types available from the **My Favorite** drop-down, including custom reports. Adding to or deleting from the list is easy.

Adding Reports to My Favorite

1. Make sure you have selected the report you want to add to **My Favorite** (verify that its name is displayed in the **Report Options** section of the Reports window).
2. Select **My Favorite > Add to My Favorite**.

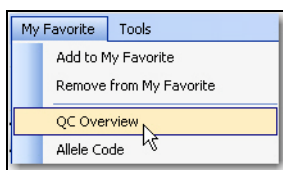


The current report name is added to your **My Favorite** menu. When you want to generate this report, just click on its name from the bottom portion of the **My Favorite** menu.

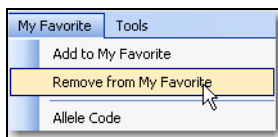


Removing Reports from My Favorite

1. Select **My Favorite**, and select the report you want to remove from the list of reports at the bottom of the menu. The **My Favorite** menu closes.



2. Select **My Favorite > Remove from My Favorite**. The report you selected in step 1 is no longer displayed at the bottom of the **My Favorite** menu.



Reports Tools

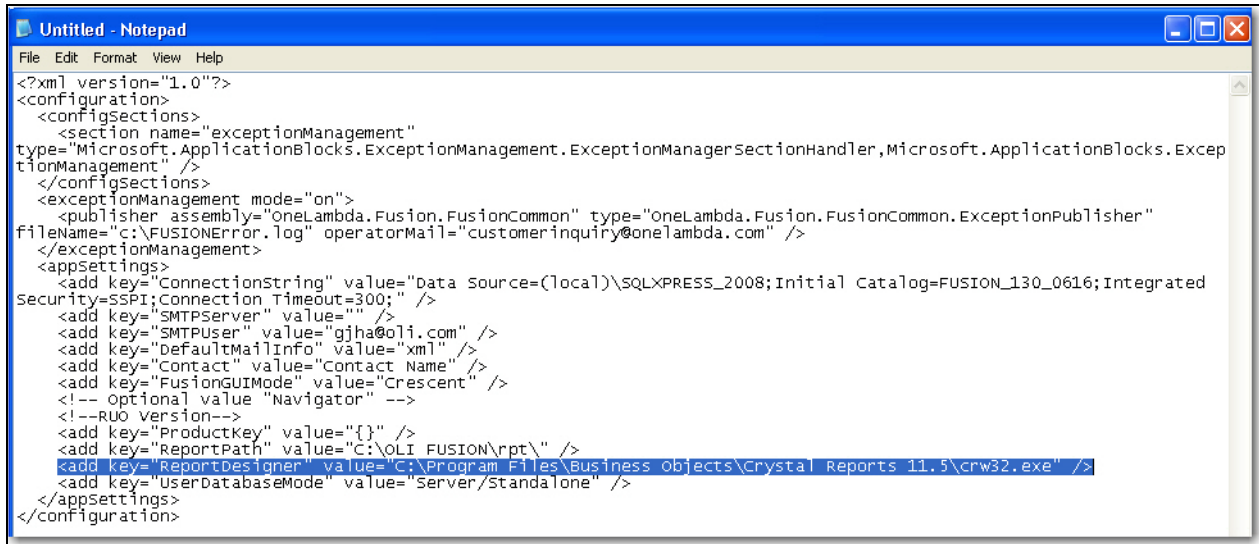
Customizing Report Appearance

Note: You must be a supervisor-level user in HLA Fusion *Research* and have Crystal Report Designer software installed on your computer to use this feature.

This feature allows you to format the appearance of HLA Fusion *Research* reports to meet your specific needs. For example, you can change font style, size and color as well as the location of text and data fields on the report.

- HLA Fusion *Research* automatically launches the report designer if it is installed in the default directory (C:\Program Files\Business Objects\BusinessObjects Enterprise 12.0\win32_x86\crw32.exe).

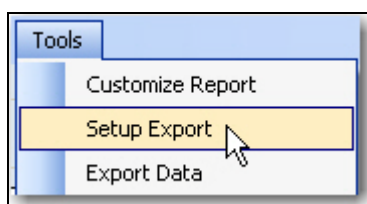
- Use Notepad to open the *OneLambda.Fusion.Interface.exe* file, located in C:\Program Files\One Lambda\HLAFusion\IVD. Make sure that Crystal Report Designer path name is entered on the following line of this file (see figure below): <add key="ReportDesigner" value="C:\Program Files\Business Objects\BusinessObjects Enterprise 12.0\win32_x86\crw32.exe" />



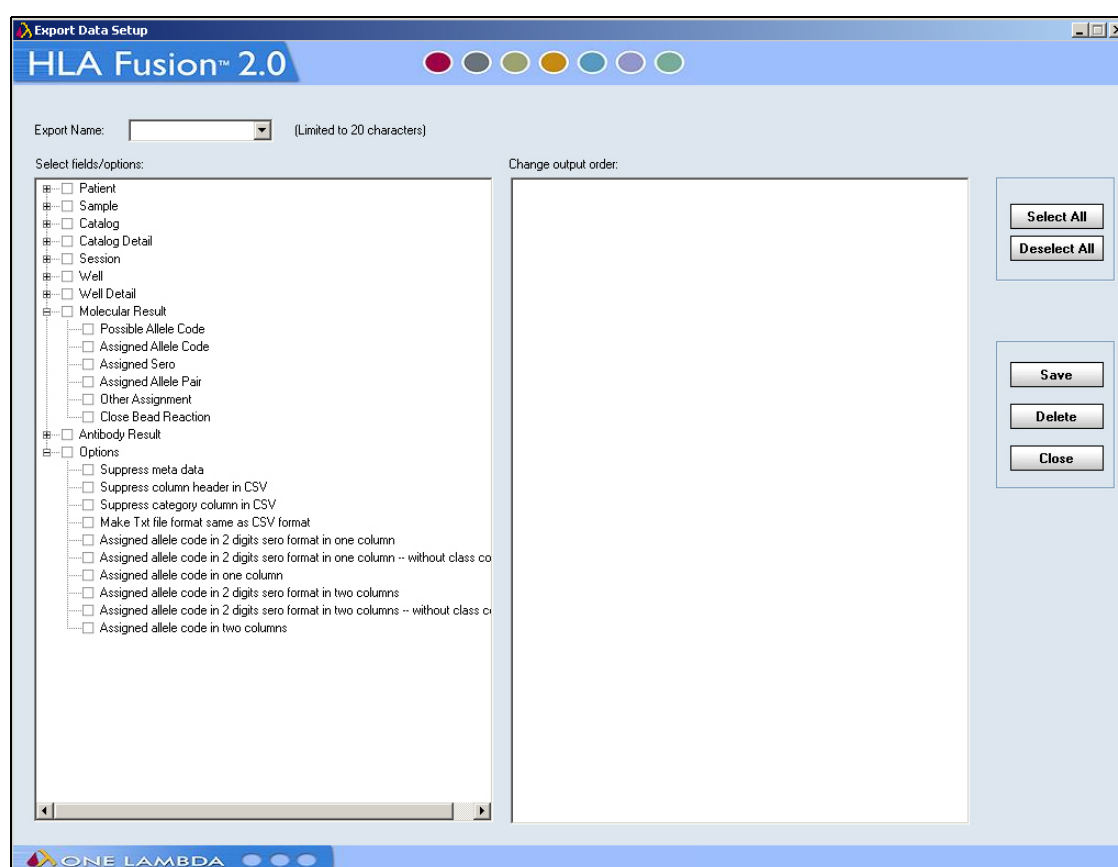
- Please note that all the report files used in HLA Fusion *Research* are installed in the directory C:\OLI Fusion\rpt, and they all have the extension of .rpt. These files can be moved anywhere for central access, but to do so, you must update *OneLambda.Fusion.Interface.exe* file to reflect the new location (see figure above).
 - When you open a report to customize it, a backup copy is automatically created with the timestamp as the suffix of the report name. This allows you to retrieve the original report format, if needed.
1. Select **Reports > Tools > Customize Report**.
 2. Use the Crystal Report Designer tools to modify the appearance of your report.
 3. Once you have made changes to the report format, save it. Make sure you do not change the name of the report file. Next time you run this report in HLA Fusion *Research*, the report will have the appearance you last saved in Crystal Report Designer.

Creating Custom Data Export Templates

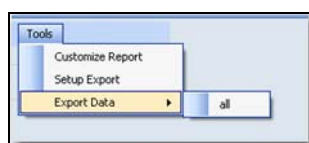
1. Select **Tools > Setup Export** to customize report data export by setting up templates that determine the type of report data (session, sample, patient, results, etc.) is exported when you select that template.



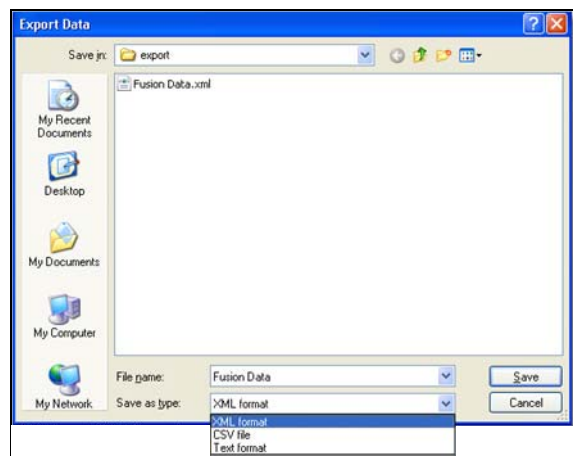
2. The **Export Data Setup** dialog box is displayed, allowing you to select the name of the export template, the fields and options to be included, and the field order you want for the template. Select check boxes on the left to select category, fields and options. On the right side of the dialog box, drag and drop the fields, or hold CTRL and press the Up/Down arrow keys to change the order.



3. When you are done, click the **Save** button. The new template is added to available export templates from the **Tools > Export Data** menu.



-
- When you are ready to export data, first select all the sessions you want to include from the available list. Then, select **Tools > Export Data**, and select one of the templates. The **Export Data** dialog box is displayed.



- Select the format for the exported data—XML, CSV or Text. The exported data file is saved by default in C:\OLI Fusion\data\export. You can change where these files are saved by modifying the *Interface* path (see [Setting HLA Fusion Research Default URLs and Directory Paths](#), p. 132).

Creating Custom Reports

Certain report types allow you to customize the types of fields to include.

Note: For Molecular Custom or Antibody Custom reports, you must make sure the *Free 3 of 9 Extended* font is installed on your computer—otherwise, the barcode is not recognized. If needed, you can download this font for free at <http://www.free-barcode-font.com/>.

- To create a custom report, select a report type containing the word “Custom” in its name (e.g., *Molecular Custom*, under the **Generic Typing** report type menu).
- Click the **Setup** button in the Report Option section of the window. The **Custom Report Setup** window is displayed, allowing you to customize report content by selecting from various categories and fields.

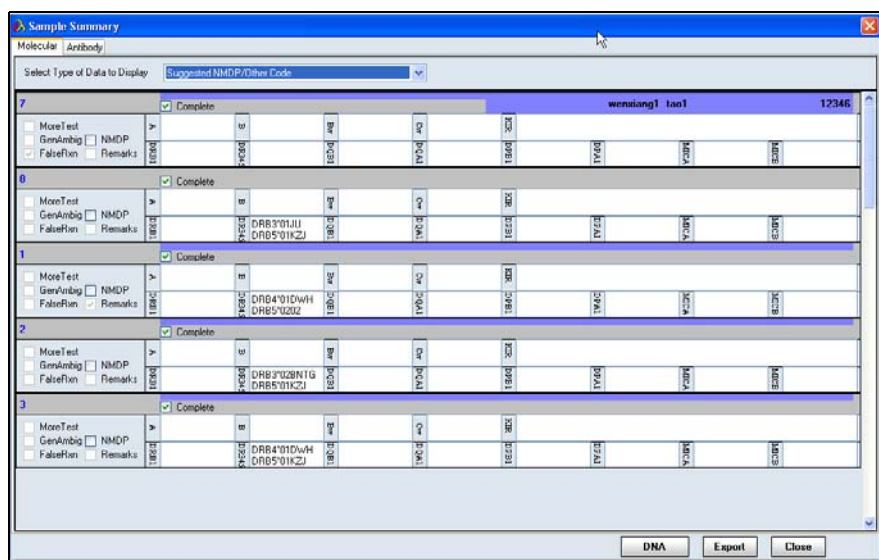


Molecular Typing Sample Summary

Selected antigen typing records are displayed on the Molecular tab of the Sample Summary screen. You can view typing information in a condensed format, as well as display more details for any sample.

1. Select samples using the **Reports** window.
2. Click the **Sample Summary**. The default tab is **Molecular**.
3. Select an option from the **Select Type of Data to Display** drop-down list.

The window displayed depends on the option selected.



4. Click the **Export** button to export the displayed data as an Excel file. Click the **DNA** button to export molecular specificities as an Excel file.
5. Click the **Close** button  in the upper right corner of the window to close and return to the **Reports** window.

Antibody Screening Sample Summary

Any selected antibody screening records are displayed on the Antibody tab of the Sample Summary screen. You can view screening information in a condensed format, as well as display more details for any sample.

1. Select samples using the **Reports** window.
2. Click the **Sample Summary** button .
3. Click the **Antibody** tab.

Sample Summary

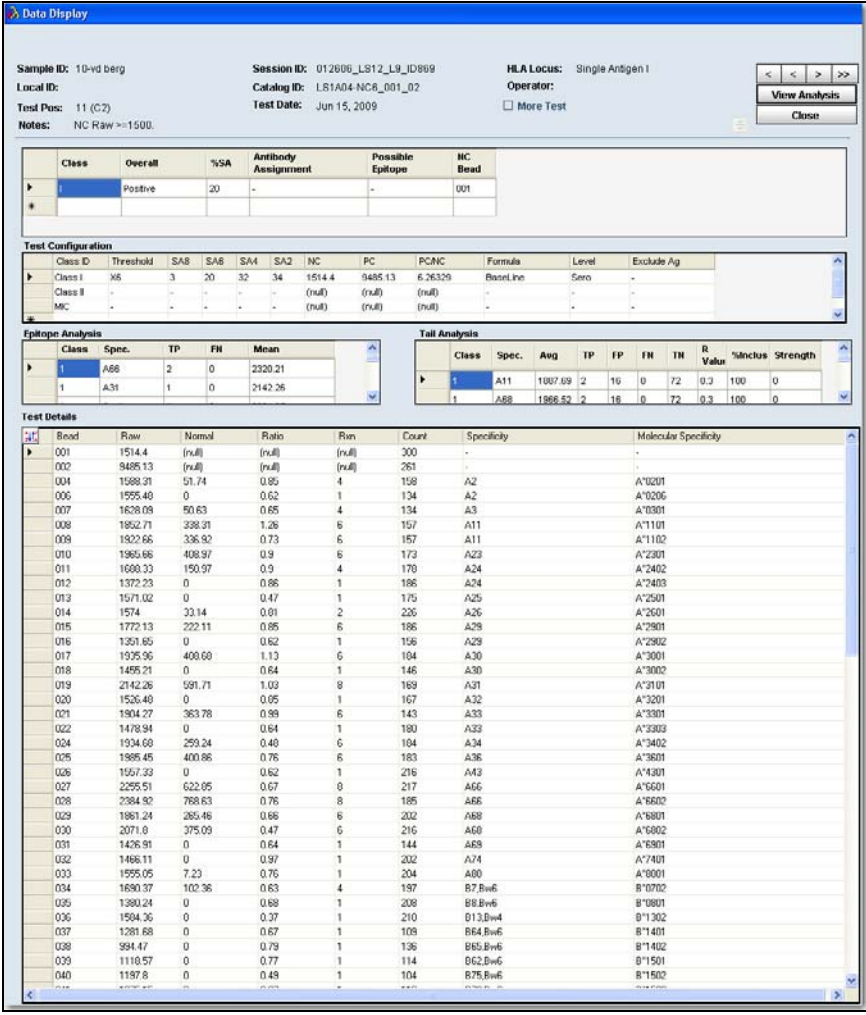
Molecular Antibody															
PatientID	Sample Name	More Test	TestDate	SessionID	CatalogID	Class I			Class II			MIC			Remarks
						+/	%	Specificity	+/	%	Specificity	+/	%	Specificity	
10-vdberg			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	20								NC Row >=1500
11-groen			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	13								Low NC Row Value
12-thorst			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	60								
13-vakman			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	11								Low NC Row Value
14-katcompag			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	28								
15-hedder (14-12)			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	53								
17-draeken			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Neg	0								Low NC Row Value
18-klomp (9-01-05)			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	94								
19-van Nijden			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	93								
20-brouwer			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	14								Low NC Row Value
26-p.brouwer			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	3								
21-veugelen			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Neg	0								
222001			06/03/2009	020401TGLFSPRA_007_1	LS2PRANCE_011				Pos	40					
222016			06/03/2009	020401TGLFSPRA_007_1	LS2PRANCE_011				Neg	0					NC Bead has a Row Value higher than all
222006			06/03/2009	020401TGLFSPRA_007_1	LS2PRANCE_011				Neg	0					
222011			06/03/2009	020401TGLFSPRA_007_1	LS2PRANCE_011				Pos	6					
222005			06/03/2009	020401TGLFSPRA_007_1	LS2PRANCE_011				Pos	31					
22-nuul			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	2								
23-klomp (9-12)			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	74								
24-bolstra			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	34								Low NC Row Value
25-krakz			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	94								
2-klomp			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	88								
2-akromm			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	1	B52.Cw6							
2-eggenman			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	26	A2A30.Cw10.A6							
2-ten haring			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	33	B8201.A28.Cw1							
2-hedder (9-12)			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	22								Low NC Row Value
2-nuulHuisen			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	72								Low NC Row Value
2-klomp1			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	33	Cw1.B8201.A31							Low Bead Count
2-klomp2			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	14	B51.B67.B55.Cw							Low Bead Count Low NC Row Value
2-klomp3			06/15/2009	012606_1212_19_ID469	LS1A04-NCE_001	Pos	52								Low Bead Count
LSNC			06/03/2009	012606_1212_19_ID469	LS1A04-NCE_001	Neg	0								
LSNC			06/03/2009	020206_1m11_ID380	LSH12_012_01	Neg			Neg						
LSNC			06/03/2009	020401TGLFSPRA_007_1	LS2PRANCE_011				Neg	0					
NZ			06/03/2009	020206_1m11_ID380	LSH12_012_01	Pos			Neg						Low Bead Count

4. Click the **Export** button to export the displayed data as an Excel file. Click the **DNA** button to export molecular specificities as an Excel file.
5. Click the **Close** button  in the upper-right of the window to close and return to the **Reports** window.

View Records

The View Records feature presents typing results and analysis details for each sample selected. Sample information is shown for one sample at a time. From the View Records menu, you can view screening and typing records individually.

1. Select data records using the **Reports** window.
2. Click the **View Records** button .
3. Use the arrow buttons to navigate through samples.



Data Display

Sample ID: 10-vd berg Session ID: 012606_LS12_L9_ID869 HLA Locus: Single Antigen I
Local ID: Catalog ID: LS1A04-NC8_001_02 Operator: ☐ More Test
Test Pos: 11 (C2) Test Date: Jun 15, 2009
Notes: NC Raw >= 1500.

Class Overall %SA Antibody Assignment Possible Epitope NC Bead

1	Positive	20	-	-	001
---	----------	----	---	---	-----

Test Configuration

Class ID	Threshold	SAB	SAB	SA1	SA2	NC	PC	PCNC	Formula	Level	Exclude Ag
Class I	35	3	20	32	34	1514.4	9485.13	6.26329	Baseline	Sero	-
Class II	-	-	-	-	-	(null)	(null)	(null)	-	-	-
MC	-	-	-	-	-	(null)	(null)	(null)	-	-	-

Epitope Analysis

Class	Spec.	TP	FN	Mean
1	A66	2	0	2320.21
1	A31	1	0	2142.26

Tail Analysis

Class	Spec.	Ang	TP	FP	FN	TN	R Value	%Inclus	Strength
1	A11	1007.69	2	16	0	72	0.3	100	0
1	A68	1968.52	2	16	0	72	0.3	100	0

Test Details

Bead	Raw	Norml	Ratio	Run	Count	Specificity	Molecular Specificity
001	1514.4	(null)	(null)	(null)	200	-	-
002	9485.13	(null)	(null)	(null)	261	-	-
004	1588.21	51.74	0.85	4	158	A2	A*0201
006	1595.40	0	0.62	1	134	A2	A*0206
007	1628.08	50.63	0.65	4	134	A3	A*0301
008	1852.71	338.31	1.26	6	157	A11	A*1101
009	1922.66	336.92	0.73	6	157	A11	A*1102
010	1965.66	408.97	0.9	6	173	A23	A*2301
011	1680.23	150.97	0.9	4	170	A24	A*2402
012	1372.23	0	0.86	1	186	A24	A*2403
013	1571.02	0	0.47	1	175	A25	A*2501
014	1574	33.14	0.01	2	226	A26	A*2601
015	1772.13	222.11	0.85	6	186	A29	A*2901
016	1261.65	0	0.62	1	156	A29	A*2902
017	1935.96	400.60	1.13	6	104	A30	A*3001
018	1495.21	0	0.64	1	146	A30	A*3002
019	2142.26	591.71	1.03	8	169	A31	A*3101
020	1526.40	0	0.05	1	167	A32	A*3201
021	1904.27	363.78	0.99	6	143	A33	A*3301
022	1478.94	0	0.64	1	180	A33	A*3303
024	1934.60	259.24	0.48	6	104	A34	A*3402
025	1985.45	400.86	0.76	6	183	A36	A*3601
026	1567.23	0	0.62	1	216	A43	A*4301
027	2295.51	622.05	0.67	0	217	A66	A*6601
028	2384.42	768.63	0.76	8	185	A66	A*6602
029	1861.24	265.46	0.66	6	202	A68	A*6801
030	2071.0	375.09	0.47	6	216	A68	A*6802
031	1426.91	0	0.64	1	144	A68	A*6801
032	1468.11	0	0.97	1	202	A74	A*7401
033	1595.05	7.23	0.76	1	204	A80	A*8001
034	1690.37	102.36	0.63	4	197	B7.Bw6	B*0702
025	1380.24	0	0.69	1	208	B8.Bw6	B*0801
026	1594.36	0	0.37	1	210	B13.Bw4	B*1302
037	1281.68	0	0.67	1	108	B64.Bw6	B*1401
038	994.47	0	0.79	1	136	B65.Bw6	B*1402
039	1110.57	0	0.77	1	114	B62.Bw6	B*1501
040	1197.8	0	0.48	1	104	B75.Bw6	B*1502

4. Use the arrow buttons to navigate through samples.

- Click the **View Analysis** button  to open the analysis window for the current sample. The analysis window can be resized.



- Click the **Close** button  to close the window and return to the **Reports** window.

Patient Info

You can view patient records associated with selected samples by clicking on the Patient Info tab. Patient information can also be viewed by patient ID using the Patient look up function of the Patient Management menu. From the **Patient Info** menu, you can view Patient/Donor records.

To view patient information, you must select a sample(s). You can view, but not edit the displayed information.

1. Select sessions or samples from the **Reports** window that have an associated Patient/Donor ID.
2. Click the **Patient Info** button . The Patient/Donor information card is displayed.



The screenshot shows the 'Patient Info' window with two tabs: 'General Info' (selected) and 'Test Info'. The window contains several sections of information:

- Patient/Donor Info:** Includes fields for Patient/Donor ID (1), Family ID (AIRLINES), First Name (PETER), Last Name (AIRLINES), Middle Name, Birthdate (2/18/1920), SSN (111-11-1212), Gender (Male), Ethnicity (American), Category/Gap (Human), Address (2089 PETER ROAD), City (PETER), Region (WESTERN), State/Province (CA), Postal Code (90010), Country (USA), Phone ((818) 555-1212), Email Address (PETER@AIRLINES.NET), Mobile ((818) 555-1212), Employer (AIRLINES), Work ((818) 555-1212), Fax ((818) 555-1212), Donor Center ID (DONOR 1), Disease (EXCELLENT), Division (DIVISION 1), BloodType (O), HospitalName (PATIENT HOSPITAL), and Rh (+).
- Spouse Info:** Includes Spouse Name (ANNA) and BloodType (O).
- Emergency Contact Info:** Includes Name (ANNA) and Phone ((818) 555-1212).

At the bottom of the window, there are navigation buttons (K, <, >, >I) and an 'Export' button.

3. Click the **Test Info** tab to see that information for the current patient/donor. If more than one information card is displayed, use the arrow buttons to navigate through the patient records.
4. Click the **Close** button  in the upper right corner to close and return to the **Reports** window.

Report Types

There are several report types available. Although most report types are listed in this section, please note that because new reports are sometimes added between updates to this user manual, you may see more reports listed in the software.

- **Patient** - (all patients in the Fusion Research database)
 - *Patient Summary* - (summary of both typing and antibody testing results associated with a patient ID)
 - *Patient Typing for Batch* - (typing summary report over different loci for a set of samples, based on a selected session)
 - *Patient Custom* - (you select the type of patient data to include for the selected samples)
- **Generic Typing** - (typing data from analyzed LABType and MicroSSP samples)
 - *Molecular Custom* - (you select the type of molecular data to include for a set of samples)
 - *Custom Typing Results by Sample* - (you select the type of molecular data to include for selected samples)
 - *Allele Summary* - (typing report of possible allele pairs and assigned allele code results for a set of samples)
 - *Allele Code* - (typing report of possible allele codes and assigned allele code results for a set of samples)
 - *Molecular Typing Summary* - (typing report of the possible allele code, assigned allele code, assigned allele pairs, assigned serology, and other assignments for a set of samples)
- **MicroSSP** - (data from analyzed Micro SSP samples)
 - *SSP Report* - (detailed typing report for Micro SSP™ tests that may be customized)
- **LCT** - (data from analyzed LCT samples)
 - *LCT Specificity* (test details of a single sample on an LCT analysis tray)

Sample management lets you to enter and export sample information to allow for faster analysis and data management. Sample information can exist in the database without any analysis data associated with it.

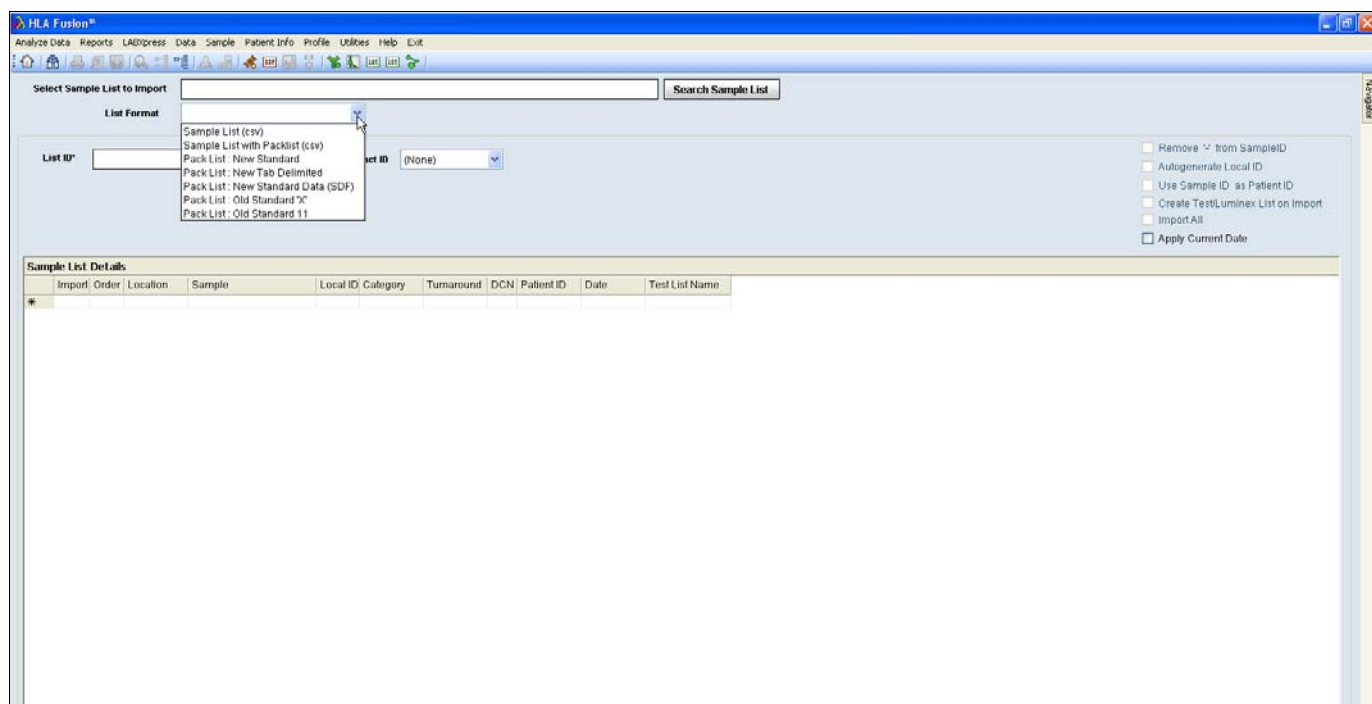
Sample Lists

In HLA Fusion™ *Research*, sample lists are an easy way to input a large list of sample IDs and other sample information into the database for use in analysis sessions. Sample lists may be in .xls, CSV or .txt file format. From the Sample List Import menu, you can import sample lists or edit sample lists prior to importation.

Importing Sample Lists

Sample lists are an easy way to input an extended list of sample ID's and other sample information into the database for use in analysis sessions. The information contained in the sample lists must be in one of the formats described in the section [Information Formats for Sample Lists, p. 91](#).

1. From the Main Menu, select **Sample > Import Sample List**.



2. Click the **Search Sample List** button; browse for the sample list to be imported; and click **Open**.
3. Type a name in the **List ID** field, and, if necessary, select a Lab code or **Contact ID** from the drop-down list.
4. Confirm sample information, and edit if needed. Click to clear the check boxes of any samples you do not want to import.
5. Click **Import List** to import the selected sample lists.
6. Click **Close** to return to the Main Menu.

Information Formats for Sample Lists

The information inside a sample list you import in to HLA Fusion *Research* must be in one of the following formats.

New packing list format

This file gives the fields (in this order):

ShipmentLoc (1 - 13), SampleIDName (0198-0398-0), SampleType (AB, DR or AB/DR),
TurnaroundTime (14, 21 or 14AB/21DR), DCN (3 digit).

example line:

1 - 13, 0198-0398-0, AB/DR, 14AB/21DR, 074

Pack list: Old Standard 'X' samples

This file gives the fields (in this order):

ShipmentLoc, SampleIDName, SampleType (1, 2, 3..., and an 'X' for AB/DR samples), DCN

example line:

```
1 - 12,0287-7867-8,X,074
```

Old packing list format, '11' for AB/DR samples

This file lists (in this order):

ShipmentLoc, SampleIDName, SampleType (1, 2, 3..., and an '11' for AB/DR samples), DCN

example line:

```
1 - 15,0287-0779-2,11,074
```

Comma delimited format

Each field is separated by commas. The use of quotes around a field is optional, and is required only if the contents of the field use a comma, which could confuse field separation. This file lists (in this order):

ShipmentLoc, SampleIDName, SampleType (AB, DR or AB/DR), TurnaroundTime (14, 21 or 14AB/21DR), DCN

example line:

```
"1", "12", "0287-7867-8", "AB/DR", "14AB/21DR", "074"
```

Tab delimited format

Each field is separated by a tab. This file lists (in this order):

ShipmentLoc, SampleIDName, SampleType (AB, DR or AB/DR), TurnaroundTime (14, 21 or 14AB/21DR), DCN

example line:

```
1      12      0287-7867-8      AB/DR      14AB/21DR      074
```

SDF format

Each field is separated by commas. This file lists (in this order):

BoxSlot, DonarID, SampleType (AB, DR or AB/DR), TurnaroundTime (14, 21 or 14AB/21DR), DonarCenter

example line:

```
1120287-7867-8AB,DR14,21074
```

Local/Sample/Patient ID Only

This file is a Microsoft Excel file. This file lists (in this order):

Row 1: Column Title "Local" and "Sample" and "Patient"

Column A: LocalID

Column B: SampleIDName (required)

Column C: PatientIDName

example:

	A	B	C
1	Local	Sample	Patient
2	local1	sample1	patient1
3	local2	sample2	patient2
4	local3	sample3	patient3
5	local4	sample4	patient4
6	local5	sample5	patient5
7	local6	sample6	patient6
8	local7	sample7	patient7
	local8	sample8	patient8

Viewing and Editing Sample Information

Sample information can be edited, but associated patient IDs cannot—only new patient IDs can be added.

1. From the Main Menu, select **Sample > Manage Sample Info.**

Figure 8-1: Manage Sample Window

Sample ID	Local	DCN	Category	Turnaround	Date	Location	Patient ID
-----------	-------	-----	----------	------------	------	----------	------------

2. Use the filters to find samples, and click **View Sample**.
3. Edit sample information.

Note: You can rename a sample by modifying the name in the Sample ID field. Sample IDs are listed alphanumerically, with all IDs beginning with numbers listed first.

4. Click **Save** to save. Or, click **Delete** to delete the sample.
5. Click **Close** to return to the Main Menu.

Note: You are not allowed to delete a sample that is part of a session that has already been analyzed.

Test Lists

A Test List is a list of Sample IDs that can be used repeatedly to automatically write the sample IDs into a session analysis that can be read by Luminex[®]. It is a useful tool when you have a group of samples to be run on multiple tests.

From the Test List menu you can:

- Create new Test Lists
- View and edit existing Test Lists
- Delete Test Lists
- Export Test Lists to a .txt file

Creating New Test Lists

Test Lists must be created in the order in which the samples are to be analyzed.

1. From the Main Menu, select **Samples > Manage Test List**.

Create/Edit Test List

Select Test List Or Enter new Test List Name: [Dropdown] [Continue >>] [Delete List] [Close]

Enter Sample Name: [Text Field]

Search Field: [Sample ID] Value: [Text Field] [Apply]

OR

Sample Name	Local ID	Patient ID
-------------	----------	------------

[Add >>] [Remove] [Remove All] [Move Up] [Move Down]

Test List Name: [Text Field]

[Save] [Export] [Refresh]

-
2. Type in a name for the new test list, and click **Continue>>**.
 3. Search for samples to add to the test list using the search fields, and click **Apply** to view search results.
 4. Highlight samples, and click **Add>>** to add them to the test list.
 5. Click **Save** to save the new test list.
 6. Click **Close** to return to the Main Menu.

Viewing and Editing Existing Test Lists

Test Lists can be viewed or edited at any time.

1. From the Main Menu, select **Manage Samples > Manage Test List**.
2. Use the drop-down list to select a test list, and click **Continue>>**.
3. Click **Delete List** to permanently delete the selected test list.
4. Click **Close** to return to the Main Menu.

Deleting Existing Test Lists

Deleting a test list removes the list from the database, but the sample IDs are not removed or changed in the database.

1. From the Main Menu, select **Manage Samples > Manage Test List**.
2. Use the pull-down menu to select a test list, and click **Continue>>**.
3. Add, remove or move samples as desired.
4. Click **Save** to save the new test list.
5. Click **Close** to return to the Main Menu.

Exporting Test Lists

Test lists can be exported for use outside of HLA Fusion *Research* only as a .txt files.

1. From the Main Menu, select **Manage Samples > Manage Test List**.
2. Use the pull-down menu to select a test list, and click **Continue>>**.
3. Click **Export** to export test list details to a .txt file.
4. If prompted to save the test list before export, click **Yes** to save and continue.
5. Select a location to save the test list and enter a file name for it.
6. Click **Save**.
7. When prompted to create a Luminex Patient List input, click **No**.
8. Click **Close** to close and return to the Main Menu.

Luminex Lists

HLA Fusion *Research* can create a Luminex List from a new or existing test list. You can use this list to quickly add information, such as sample ID, before you create a Luminex CSV output file. From the **Create/Edit Test List** window you can create a Luminex list

Creating Luminex Lists

Luminex List files can be edited after they are exported, but changes are not reflected in the test list from which they were created.

1. From the Main Menu, select **Samples > Manage Test List**.
2. Use the pull-down menu to select a test list, and click **Continue>>**.
3. Click **Export** to export.
4. Select a location to save the test list to and enter a file name.
5. Click **Save**.
6. When prompted to create Luminex List input, click **Yes**.
7. Click **OK** on the confirmation message to return to the **Test List** window.
8. Click **Close** to return to the Main Menu.

Create Sample Worklists

Note: The Sample Worklist feature is available *only* if you have SQL 2005 and above installed.

Sample Worklist functionality in HLA Fusion *Research* software gives you the flexibility to assign various tests to selected samples. This information is used in designing plates for Luminex processing.

sample search criteria

Sample Worklist

Search samples

Sample ID: Local ID: From: 4/19/2009 To: 5/19/2009 Location:

SampleID	LocalID	Date	Location
1			
1107			
2			
3			
324			
4			
5	clhlytuy		
6			
7			
8			
3068			
A*0108			
A*2603			
AP630			
ARA			
BCK			
bivdhd			
bivjs			

LABScreen Tests

☒ LSM

☒ PRA I ☒ PRA II ☐ PRA I+II

☒ LS SA I ☒ LS SA II

☒ LS Single I ☒ LS Single II

LABType Tests

☐ A ☐ B ☐ C

☐ DRB1 ☐ B*4 ☐ B7

☐ DQA ☐ DQB ☐ DQA/DQB

☐ DP ☐ DRB345

1. Select **Sample > Create Sample Worklist** from the Fusion Research main menu.
1. Use the search criteria to specify the samples that you would like to assign tests to, and click **Search**.
2. Select one session, or select multiple sessions (by holding and dragging the mouse). The selected samples are highlighted.
3. Now assign one or more tests by selecting the check boxes for the tests you want to run on the samples (listed under **LABScreen Tests** and/or **LABType Tests**).
4. Once you are done assigning tests to all the selected samples, click **Save** to save the worklist.

Create Plate Design

Note: The Plate Designer feature is available *only* if you have SQL 2005 and above installed.

Plate Designer functionality in HLA Fusion Research software gives you the flexibility to organize and to plan your samples in the plate format that is ready for processing through the Luminex device. You must first have created a sample worklist (see [Create Sample Worklists](#), p. 97).

1. Select **Sample > Create Plate Designer** from the Fusion Research main menu.
2. Select the **Assay type**.
3. Select the **New Plate** button option if you want to create a new plate; otherwise, select **Edit Plate** to change an existing plate.
4. Click **Go**.
5. For a new plate:
 - Enter an unique plate name
 - Use the following search criteria to search and select the samples you want to add to plate for testing:
 - Test name
 - Sample name
 - Sample collection date (From and To date)
6. Click **Search** to display a list of samples that match your criteria.
7. Select samples (one or many at a time), and use the left << button to assign these samples to a well in the plate. Repeat this until you have completed your plate design.
8. Click **Save** to save your plate design.
9. Click **Print** if you want to print your plate design.

Chapter 9 Patient Information

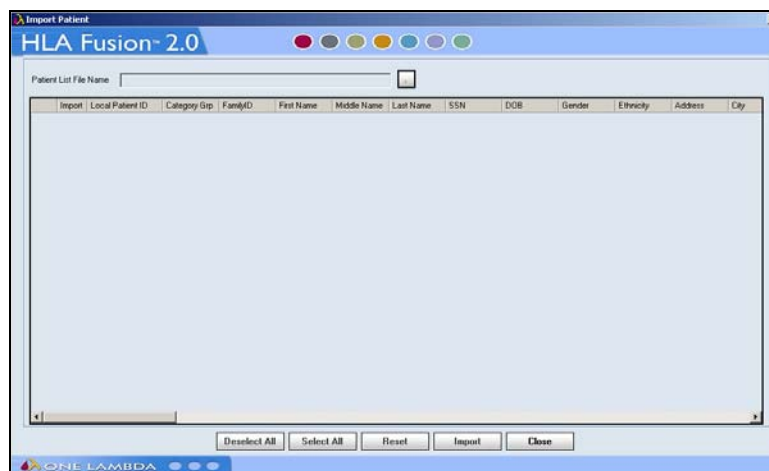
HLA Fusion™ *Research* can store patient information and associate sample IDs with patients and donors. You can store all typing and screening information in one location for each patient.

Note: Please verify all data you import as HLA Fusion Research performs minimal data validation upon import.

Importing Patient/Donor Lists

After creating a Patient/Donor List, you can import the information into HLA Fusion *Research*. (See [Creating Patient/Donor Lists](#), p. 106 for guidelines on creating a patient list.)

1. From the Main Menu, select **Patient Info > Import Patient List**.



2. Select the check box in the **Import** column for each patient you want to import.
3. Click the **Import** button to import checked patients.
4. Click **Close** to return to the main menu.

Note: The HLA Fusion Research system checks the patient/donor lists you attempt to import to verify that all characters contained in the data are supported by Fusion Research. If your list contains unsupported characters, a message is displayed to let you know, and the list is not imported. For a list of characters to avoid using, see [Special Characters to Avoid in Filenames, p. 136](#).

Newly imported patient records display alleles in the new nomenclature format. Existing patient records display alleles with the existing allele format.

Managing Patient/Donor Records

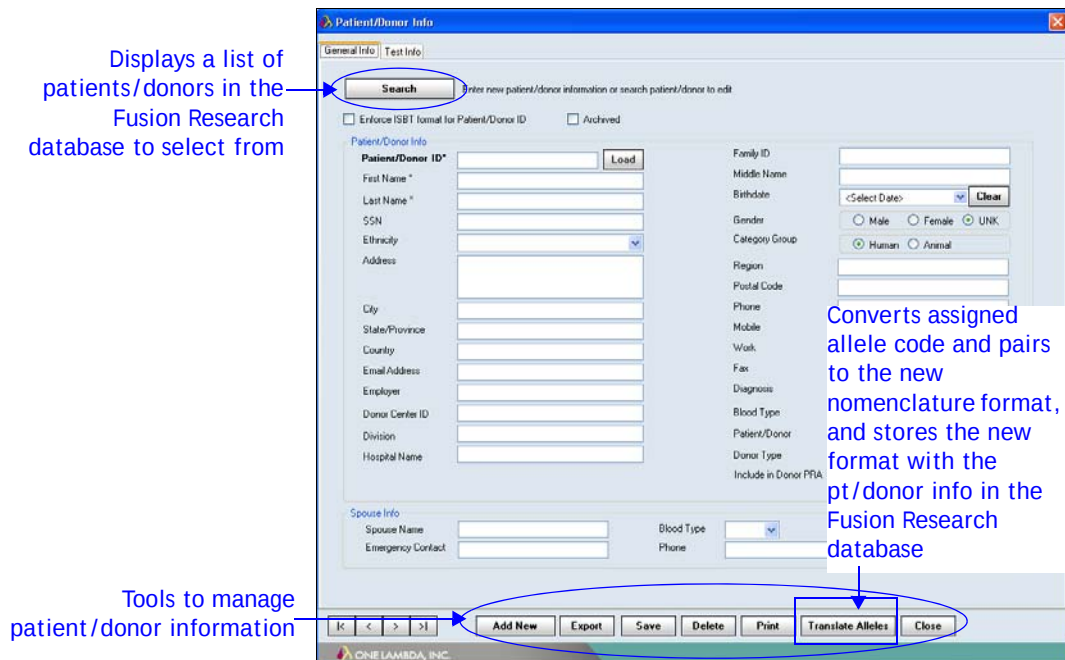
The Patient/Donor Management menu allows you to manage one record at a time. From the Patient/Donor Management menu you can:

- Add new patient/donor records
- Search existing patient/donor records
- Edit patient/donor records
- Associate patient/donor IDs with sample IDs
- Associate patient and donor records
- Print, export and archive patient records

Adding New Patient/Donor Records

You can add patient information using the Patient/Donor Information menu. This is the best option for adding a small number of patient records. To quickly add a large number of patient records to HLA Fusion Research, see [Creating Patient/Donor Lists](#), p. 106.

1. From the Main Menu, select **Patient Info > Manage Patient**.



2. Enter an ID in the **Patient/Donor** field.
3. Enter patient/donor information. Fields with an asterisk (*) are required.
4. Click **Save** to save the data.
5. Click **Close** to close and return to the main menu.

Lookup Patient/Donor Records

This option allows you to browse through records or search for specific ones.

1. From the Main Menu, select **Patient Info > Manage Patient**.
2. Enter a patient/donor ID and click **Load** to display patient information. Or, click **Select Patient** to browse patient records. Highlight a patient record and click **OK** to display.

Editing Patient/Donor Records

All patient/donor information (except patient/donor ID) can be edited.

1. From the Main Menu, select **Patient Info > Manage Patient**.
2. Select a patient/donor record.
3. Edit patient/donor information. Fields marked with an asterisk (*) are required.
4. Click **Save** to save data.
5. Click **Close** to return to the Main Menu.

Associating a Patient/Donor ID with Sample IDs

A Sample ID cannot be associated with more than one patient or donor record, but a patient or donor record can have more than one sample ID associated with it.

1. From the Main Menu, select **Patient Info > Manage Patient**.
2. Select a patient/donor record.
3. Click the **Test Info** tab.

The screenshot shows the 'Patient/Donor Info' window with the 'Test Info' tab selected. The window contains several sections for data entry:

- General Info:** Includes a 'Patient/Donor' text field, a 'View Sample Summary' button, and two buttons: 'Associate Sample IDs' and 'Associate Donor IDs'.
- HLA Assignments Molecular:** Contains two tables. 'Class I' has columns A, B, Bw, and C. 'Class II' has columns DRB1, DRB3, DRB4, DRB5, DQB1, DQA1, DPB1, and DPA1.
- HLA Assignments Serology:** Contains two tables. 'Class I' has columns A, B, and Cw. 'Class II' has columns DR, DR(51.52.53), DQ, and DP.
- Other:** Includes fields for MICA, MICB, and KIR.
- Antibody Assignments:** Includes fields for Class I Antibody Specificity, Class II Antibody Specificity, MIC Antibody Specificity, Unacceptable Antigens, and Acceptable Antigens.
- Notes:** A large text area for additional information.

At the bottom of the window are navigation buttons: '<', '<<', '>>', '>', 'Add', 'Export', 'Save', 'Print', and 'Close'.

4. Click the **Associate Sample IDs** button.
5. In the **Patient/Donor Sample Association** window, highlight a sample ID and click > to add it to the **Patient/Donor Sample List**. (Click < to remove a highlighted sample ID from the list.)

-
6. Click **Save** to save the data.
 7. Click **OK** to return to the patient record.
 8. Click **Close** to return to the main menu.

Associating Patient and Donor Records

A Patient ID can be associated with more than one donor record, and a donor ID can have more than one patient record associated with it.

1. From the Main Menu, select **Patient Info > Manage Patient**.
2. Click the **Test Info** tab.
3. Click the **Associate Donor IDs** button.
4. In the **Patient/Donor Sample Association** window, highlight a Donor ID and click > to add it to the **Patient/Donor Sample List**. (Click < to remove a highlighted Donor ID from the list.)
5. Click **Save** to save data.
6. Click **OK** to return to patient record.
7. Click **Close** to return to the Main Menu.

Printing Patient/Donor Records

HLA Fusion *Research* prints both Record Management tabs regardless of which tab is currently being viewed.

1. From the Main Menu, select **Manage Patient > Manage Patient**.
2. Select a patient/donor record.
3. Click **Print** to print.
4. Click **Close** to return to the Main Menu.

Exporting Patient/Donor Records

Patient/donor records can be exported individually to a CSV file. The file has the same format as a Patient List.

1. From the Main Menu, select **Manage Patient > Manage Patient**.
2. Select a patient/donor record.
3. Click **Export** to export.
4. Select a location to save the CSV file to and enter a file name.
5. Click **Save**.
6. Click **Close** to return to the Main Menu.

Archiving Patient/Donor Records

Archived patient/donor records are not available for reporting or associating. You can still view archived records and reactivate them by clearing the archive check box.

1. From the Main Menu, select **Manage Patient > Manage Patient**.
2. Click the **General Info** tab.
3. Select a patient/donor record.
4. From the **Patient/Donor List** window, select **Archive** from the drop-down **Active/Archive** list.
5. Click **Save** to save.
6. Click **Close** to return to the Main Menu.

Deleting Patient/Donor Records

Patient/donor records can be deleted through the Manage Patient menu option.

1. From the Main Menu, select **Manage Patient > Manage Patient**.
2. Click the **General Info** tab.
3. Select a patient/donor record Select a patient/donor record.
4. Click **Delete** to delete the patient/donor record from the Fusion Research database.
5. Click **Save**.

Creating Patient/Donor Lists

The following is an example of a patient list that can be created, and the guidelines for doing so. The patient list must be formatted for import via a program like Excel or Notepad, and saved as a Windows compatible CSV file (see [Importing Patient/Donor Lists, p. 100](#)). The first field/section must contain the names of the patient list fields, each separated by commas:

```
PatientIDName,CategoryGrp,FamilyID,FirstName,MiddleName,LastName,Ssn,Dob,Gender,Ethnicity,Address,City,State,Region,Country,ZipCode,Email,Phone,WkPhone,Cellular,Fax,Employer,SpouseName,SpouseBloodType,EmergencyContact,EmrgncyTel,DCN,HospitalName,Division,BloodType,Disease,RhBloodType
```

Subsequent lines must contain the actual patient information separated by commas. If there is no information for the patient in a particular field, that field still requires a comma as a placeholder. The following is an example of a patient list created in Notepad.

```
PatientIDName,CategoryGrp,FamilyID,FirstName,MiddleName,LastName,Ssn,Dob,Gender,Ethnicity,Address,City,State,Region,Country,ZipCode,Email,Phone,WkPhone,Cellular,Fax,Employer,SpouseName,SpouseBloodType,EmergencyContact,EmrgncyTel,DCN,HospitalName,Division,BloodType,Disease,RhBloodType,PatientDonorFlg,Associated SampleIDs,Associated DonorIDs,HLA1_A,HLA2_A,HLA1_B,HLA2_B,HLA1_BW,HLA2_BW,HLA1_C,HLA2_C,HLA1_DRB1,HLA2_DRB1,HLA1_DRB3,HLA2_DRB3,HLA1_DRB4,HLA2_DRB4,HLA1_DRB5,HLA2_DRB5,HLA1_DQB1,HLA2_DQB1,HLA1_DQA1,HLA2_DQA1,HLA1_DPB1,HLA2_DPB1,HLA3,HLA1_DRB4,HLA2_DRB4,HLA1_DRB5,HLA2_DRB5,HLA1_DQB1,HLA2_DQB1,HLA1_DQA1,HLA2_DQA1,HLA1_DPB1,HLA2_DPB1,HLA1_DPA1,HLA2_DPA1,HLA1_MICA,HLA2_MICA,HLA1_MICB,HLA2_MICB,HLA_KIR,ClassI_AbSpec,ClassII_AbSpec,MIC_AbSpec,UnacceptableAntigens,AcceptableAntigens,Notes,SHLA1_A,SHLA2_A,SHLA1_B,SHLA2_B,SHLA1_Cw,SHLA2_Cw,SHLA1_DR,SHLA2_DR,SHLA1_DR345,SHLA2_DR345,SHLA1_DQ,SHLA2_DQ,SHLA1_DP,SHLA2_DP,DonorType,IncludeInDonorPRA
```

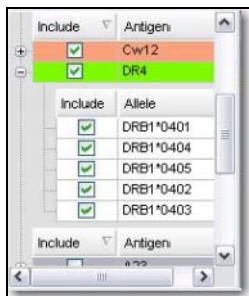
Patient Antibody Tracking

You can track molecular and antibody typing information for each patient over a period of time. The information tracked is taken from the typing data stored in their Patient/Donor Info card and the antibody data in their analysis samples (LABScreen Single Antigen and LABScreen Singles) for the specified date range. Take the following steps to display graphs and data that track a patient's antibody data.

1. Make sure you have patient and donor information entered into HLA Fusion *Research*. If not, you can import it from a patient list and/or manually enter the data on the **Test Info** tab of the Patient/Donor Info card. Patient and donor records must be associated (see [Associating a Patient/Donor ID with Sample IDs](#), p. 104).
2. Select **Patient Info > Ab Tracking**. The Antibody Tracking window is displayed:

Note: To add final assignments to a sample, double-click in the **Final Assignment** column for the sample to display the analysis window and add the assignment. Also, only samples with a date can be included in this tracking. If the Sample Date column is empty for a sample, click on the empty Sample Date cell and use the pull-down date-finder to add a date.

6. Select the check box in the **Include** column for the sample(s) you want to include in the Ab tracking graphs and data. The graphs are displayed (to display a specific type of graph, click on the associated tab).
7. Select the check box for the antigen(s) you want to include in the tracking.

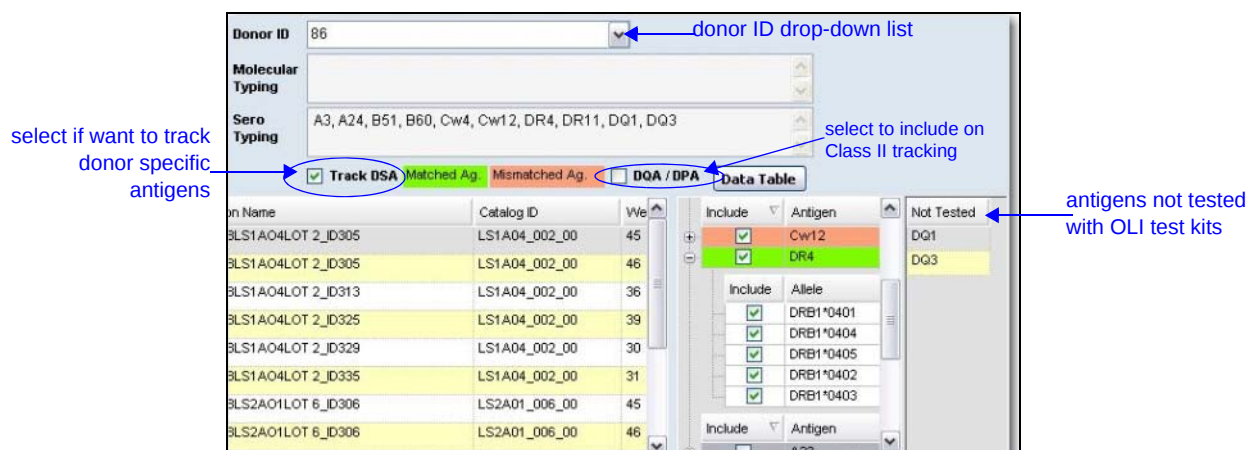


8. Select the formula to use for the graphs by clicking the drop down arrow in the **Formula** field (Default versus Raw). The formula can also be changed after the graphs are displayed if you want to compare the tracking with different formulas.



Note: You can double-click on a graph to expand it, and there are right-click options available from each graph (see graphic above).

- (Optional) You can add donor data, if desired, by using the drop-down arrow next to the Donor ID field to select from a list of donors in your Fusion Research database.



10. (Optional) Select the check box next to **Track DSA** to track donor specific antigens. If this is selected and there are donor specific antigens that are not tested with OLI product kits, these are listed.
11. (Optional) Select the DQA/DPA check box to include these in Class II tracking.
12. Click the **Data Table** button to display a raw data table CSV file with the patient antigen signal over a period of time. The table can be printed or exported.

Antibody Tracking Information

Patient Information

Patient ID :

12345

Molecular Typing :

A*0101, A*01, B*405, Cw*07, DRB1*01, DQB1*01

Sero Typing :

Donor ID :

patient1

Molecular Typing :

A*0101, A*0102, B*1010, B*3040, Cw*202, Cw*01010, DRB1*3040, DRB1*0102, DRB3*3333, DRB3*3334, DRB4*0101, DRB4*0120, DRB5*2020, DRB5*0606, DQA1*101,

Sero Typing :

Data Type : Raw Data

☐ DSA

Export

Close

Class I

Class II

Sample Index	Sample Date	Sample ID	A*0201 (A2)	A*0203 (A2)	A*0206 (A2)	A*3301 (A33)	A*3303 (A33)	B*5701 (B57)	B*5703 (B57)	A*3001 (A30)	A*3002 (A30)	A*6601 (A66)	A*6602 (A66)
1	3/20/2009	1	4856.24	9741.2	7692.91	6011.08	9292.97	4925.3	2323.28	10958	9312.46	3938.43	24

Chapter 10 Profile Management

HLA Fusion™ *Research* tracks all changes to analysis data made by users and allows added data security with a two level analysis result confirmation (Save and Confirm). HLA Fusion *Research* also stores general laboratory information to be used on reports including multiple contract lab codes.

User Management

From the Profile main menu you can:

- Add new users
- Edit existing user profiles
- Change passwords
- Reset passwords
- Archive users

HLA Fusion *Research* uses two user levels for added security and control of typing and screening results:

Supervisor can...	Lab Technician can...
Modify all product configuration settings	Modify all product configuration settings—except to enable Auto Accept All and Computer Generated Serology for LABType and Micro SSP products
Save and Confirm analysis results	Analyze data and save analysis results

Supervisor can...	Lab Technician can...
Update reference files, such as catalogs and NMDP codes	<i>(Only if authorized by the supervisor)</i> - Update reference files, such as catalogs and NMDP codes
Archive catalogs	Archive catalogs
Modify and delete session and sample data	<i>(Only if authorized by the supervisor)</i> - Modify and delete session and sample data
Modify own & other user accounts	Modify own account only
Change the Lab Profile	Manage sample and patient information

Viewing the User List

The List User option displays a list of all users currently in the database, both active and retired. You can look up and select user profiles.

1. From the Main Menu, select **Profile > List User**.
2. Type in a name and click **Search** to search for current users.
3. Double click to the left of a user entry to view the profile.
4. Click **Close** to return to the main menu.

Adding New Users

Supervisors can add new supervisor or technician level users. Technicians cannot add new users. Fields marked with an (*) are required.

1. From the Main Menu, select **Profile > List User**.
2. Click **Add User** to add a new user.
3. Enter new user information. Select the **Active** check box under the Role field to activate the user account.

Note: If this is a lab tech profile and you want to allow reference file update and/or data management privileges for this user, select the appropriate check boxes.

4. Click **Save** to save the new user information and return to the main menu or click **Close** to discard changes and return to the main menu without saving.

Editing User Profiles

Supervisors can edit the user profile of any user. Technicians can only edit their own profiles. Fields marked with an asterisk (*) are required.

1. To edit your own profile, select **Profile > My Profile**. To select from a list of users to edit, select **Profile > List User** and double-click to the left of a user to select that profile.
2. Edit user information.
3. Click **Save** to save user information and return to the Main Menu.

or

Click **Close** to discard changes and return to the Main Menu without saving.

Changing Passwords

Supervisors can change passwords for any user, but they must have the user's old password. Technicians can change only their own passwords.

1. From the Main Menu, select **Profile > My Profile**.
2. In the user profile, click the **Change Password** button.
3. Enter the current and new passwords.
4. Click the **Save Password** button to change the password. Or, click **Close** to close and return to the main menu without changing the password.

Resetting Passwords

If a users lose or forget their password, HLA Fusion *Research* can reset the password. The new password is the same as the user's user name. Only Supervisors can reset a user's password.

1. From the Main Menu, select **Profile> List User** and select a user.
2. In the user profile, click the **Reset Password** button.
3. Click **Close** to return to the main menu.

Changing User Privileges

Only Supervisors can modify a user's privilege level.

1. From the main menu, select **Profile> List User** and double-click to the left of a user to open their profile.
2. In the user profile, select the check box next to either **Manage Data** or **Update Reference Files**, or both, to give the selected user privileges for those activities within the Fusion Research application.
3. Click **Close** to return to the Main Menu.

Inactivating Users

Supervisors can inactivate users who are no longer using HLA Fusion *Research*. User information is still stored in the database, but the user is not able to log into the program.

1. From the Main Menu, select **Profiles > List User** and select a user to edit.
2. Clear the **Active** check box to deactivate the user.
3. Click **Save** to save user information and return to the main menu, or click **Close** to discard changes and return to the Main Menu without saving.

Lab Profile

The Lab Profile menu displays the contact information for your lab, network information used by HLA Fusion *Research*, and NMDP contract lab codes. Most of this information is entered during installation, but can be updated at any time. Only supervisors can change the Lab Profile.

From the Lab Profile menu you can:

- Edit the Lab Profile
- Add, edit and remove Lab Codes
- Change the Network Path
- Change the Email Server Name

Editing the Lab Profile

Laboratory information displays on most reports, and includes contact information for your lab. This information is initially entered during installation, and can be edited any time from the Lab Profile menu. Fields marked with an asterisk (*) are required.

1. From the main menu, select **Profile > Lab Profile**.
2. Edit lab profile information.
3. Click **Save** to save changes and return to the main menu, or click **Cancel** to return to the main menu without saving any changes.

Managing Lab Codes

Lab codes are used on NMDP reports to identify contract labs. Multiple lab codes may be entered and stored in HLA Fusion *Research*. You can select the lab code you wish to use when creating an NMDP report. Only the first three digits of a lab Code are used on NMDP reports; lab code descriptions are not included on reports.

1. From the main menu, select **Profile > Lab Profile**.
2. Add, edit or delete Lab codes:
 - Click **Add Lab Code** to add a new lab code. Enter information into the new row.

-
- Highlight a lab code to be edited. Click **Edit Lab Code** to edit the lab code.
3. Edit lab code information.
 - Highlight a lab code to be deleted. Click **Delete Lab Code** to delete the lab code.
 4. Click **Save** to save changes and return to the main menu, or click **Cancel** to discard changes and return to the main menu without saving.

Chapter 11 Utilities

HLA Fusion™ *Research* uses a variety of reference files and configurations for data analysis that need to be updated for new products, lots and revisions. You can also change many global product settings to customize analysis for your lab, and you can modify default system settings to reflect your personal or network file system.

Warning: Always use the latest reference files for analysis. Otherwise, analysis results may not be accurate.

Managing Catalog Reference Files

Catalog reference files contain all of the reaction-specific information needed for analysis: bead and well specificities, QC information, cut-off values, bead and primer information, etc. Each new lot or revision of a product needs its own catalog file for analysis results to be accurate.

Updating Catalog Files from a Local or Network Drive

Lab supervisors can input new catalog files for use in analysis when new products, lots, or updates become available. Catalog files are also available on the One Lambda download site (see [Updating Catalog Files from the One Lambda Download Site, p. 119](#)).

1. From the Main Menu, select **Utilities > Update Reference > Update Reference File**.



2. Make sure the **Catalog** option is selected.
3. Using the file directory tree on the left, locate catalog files to be imported.

Option	What Displays
In Fusion Research DB	Catalogs in your current database
Updates/Revisions	Catalogs that need to be updated
Not in Fusion Research DB	Available catalogs not yet in current database
All Catalogs	All available catalogs

List of available catalogs, per display criteria selected below

Expand to see catalog information

Downloads all associated documents, such as worksheets, probe/primer sheets & datasheets

Note: To determine which catalog is the most recent available, HLA Fusion Research looks first at the lot number and then the revision number. A updated lot number gets flagged as the most

recent version of a catalog, even if there is also an update to the revision number of the previous lot since you last downloaded catalogs.

4. Highlight the files you want to import, or click **Select All** to select all files listed.
5. Click **Import** to import the selected catalog files.
6. A confirmation dialog box displays import results, click **Close**.
7. Click **Close** to return to the Update Reference menu.

Imported catalog files can be used without restarting Fusion Research.

Updating Catalog Files from the One Lambda Download Site

Product catalog files are available on the One Lambda download site (<http://download.onelambda.com>).

1. From the Main Menu, select **Utilities > Update Reference > Update Reference File**.
2. Click **Auto Update** to open the One Lambda **Catalog Updates Selection** window.
3. Select the check box next to the files you want to import. Click the plus or minus signs on the file directory tree, to locate the catalog files for each product. You can also click **Select All** or **Deselect All** to select or clear all the check boxes at once.
4. Click **Import** to import the selected catalog files.
5. When the confirmation dialog box displays import results, click **Ok**.
6. Click **Close** and then **Yes** to return to the Update Reference menu.

Imported catalog files can be used without restarting Fusion Research.

Note: You can also click **Go to OLI**, click the links for the products and catalog files you want to import, and follow the download instructions.

If Auto Update does not respond, verify your network connectivity and that the URL you set for One Lambda in **Utilities > URLs & Paths** is correct.

Updating Molecular Typing Reference Files

Reference files contain allele code and serology equivalent information used in analysis. It is important to update them regularly for accurate allele code and serology assignments.

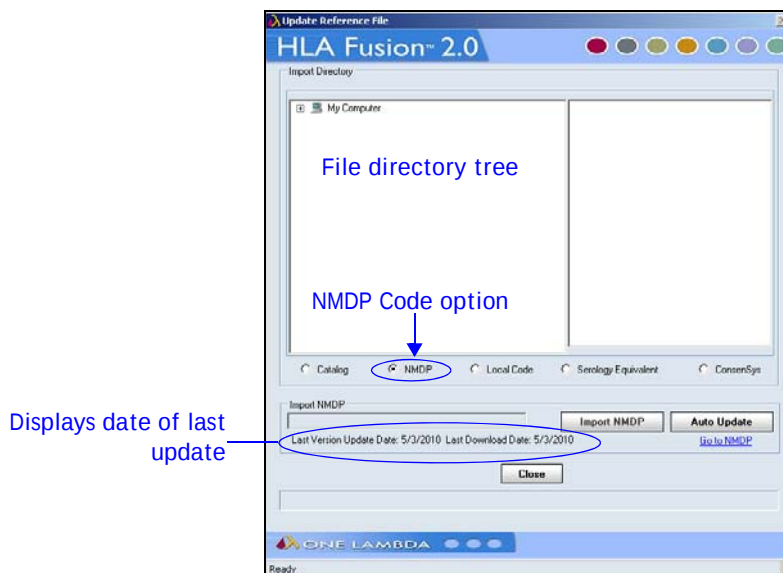
From the Update Reference menu you can

- Update NMDP codes
- Create and update Local codes
- Update Serology Equivalent files

Updating NMDP Codes from a Local or Network Drive

The National Marrow Donor Program (NMDP) provides a list of allele codes that can be used in molecular typing analysis. If you have a current list stored on your local or network drive, use this procedure to import it so HLA Fusion Research can access it. The most current NMDP code file is available on the NMDP download site (see [Updating NMDP Files from the NMDP Web Site](#), p. 120).

1. From the Main Menu, select **Utilities > Update Reference > Update Reference File**.
2. Select the **NMDP** option.



3. Navigate to the NMDP file on a local or network drive, using the **Import Directory** tree.
4. Click **Import NMDP** to import the selected file.
5. Click **Close** to return to the Update Reference menu.

Updating NMDP Files from the NMDP Web Site

Follow this procedure to import the NMDP list from the NMDP web site.

1. From the Main Menu, select **Utilities > Update Reference > Update Reference File**.
2. Select the **NMDP** option.
3. Click **Auto Update**, which automatically imports the current NMDP file for use with HLA Fusion Research. Or, click **Go to NMDP** and follow the instructions for downloading an NMDP file from the website.

Note: If Auto Update does not respond, verify your network connectivity and that the URL you set for NMDP in **Utilities > URLs & Paths** is correct.

Creating a Local Code File

Local code files are created by individual labs; local codes are created to make ambiguous typing assignments easier to store and read. For example, ambiguities, such as B*1501/1501N/1502, can be condensed with a code to B*15AB for simpler record keeping.

1. Copy the local code template from the HLA Fusion *Research* CD to a local drive.
2. Use a text editor to edit the template and add code definitions. Follow the example format, using a **Tab** to separate each field, and a slash to separate multiple values within a field:

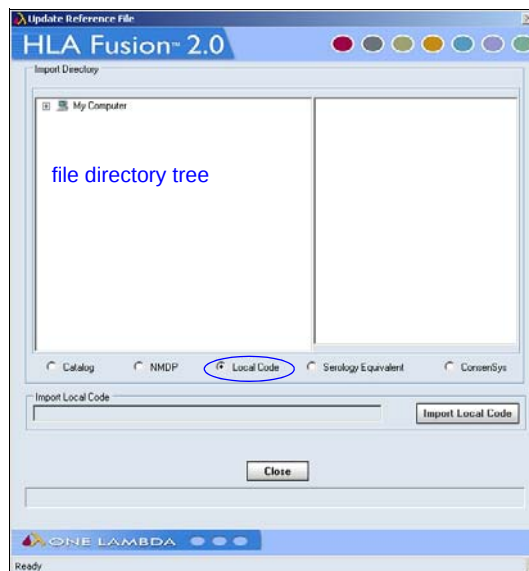
```
letter code <tab> numeric allele extension to which the code applies
```

3. Save the file as `local_code.txt`
4. See the next section, *Updating the Local Code File*, to import the file.

Updating the Local Code File

After a Local Code file has been created, it must to be updated in HLA Fusion *Research*. To use the codes in analysis, see [Changing Molecular Product Configuration](#), p. 129.

1. From the Main Menu, select **Utilities > Update Reference > Update Reference File**.

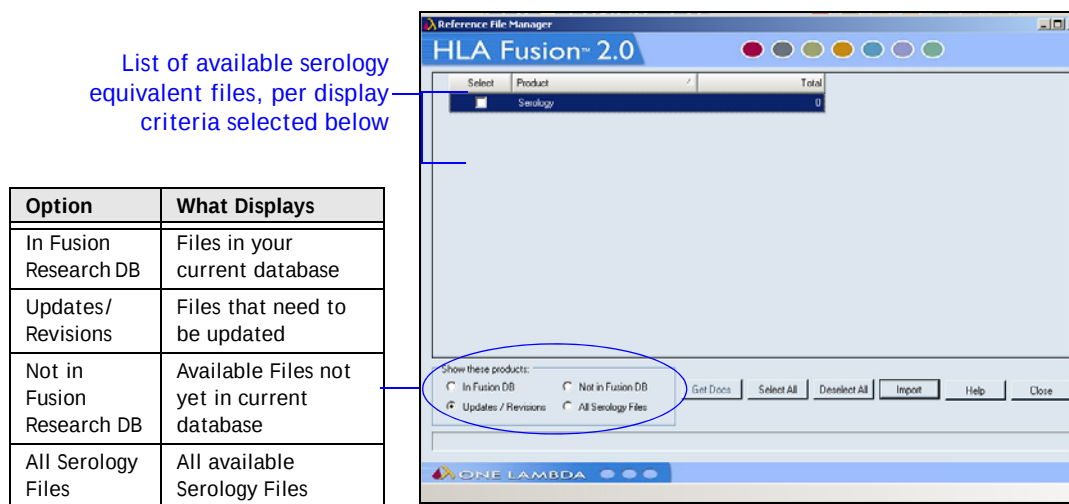


2. Select the **Local Code** option.
3. Use the **Import Directory** tree to locate and select the Local code file to be imported.
4. Click **Import Local Code** to import the selected file(s).
5. Click **Close** to return to the **Update Reference** menu.

Updating Serology Equivalent Code File from the One Lambda Web Site

The Serology Equivalent file can be auto updated from the One Lambda download site (<http://download.onelambda.com>).

1. From the Main Menu, select **Utilities > Update Reference > Update Reference File**.



2. Select the **Serology Equivalent** option.
3. Click **Auto Update** to open the One Lambda **Catalog Updates Selection** window.
4. Select the check box next to all files you want to import.
5. Click **Import** to import the selected files. Catalog files are ready for use without restarting HLA Fusion Research.
6. A confirmation dialog box displays import results, click **Ok**.
7. Click **Close** and then **Yes** to return to the Update Reference menu.

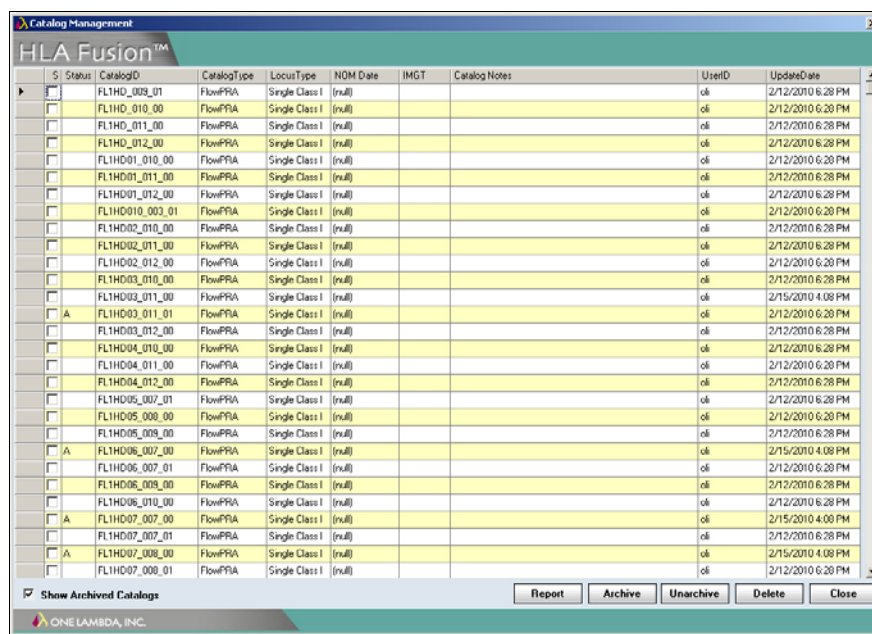
Note: If Auto Update does not respond, verify your network connectivity and that the URL you set for Serological in **Utilities > URLs & Paths** is correct.

Archiving Catalog Files

Archive Catalogs

You can archive catalog files that are no longer used. The catalog information still exists in the database, but is not included in the list of available catalog files for analysis. Catalog files can also be restored for use in analysis.

1. From the Main Menu, select **Utilities > Update Reference > Archive Catalog**.

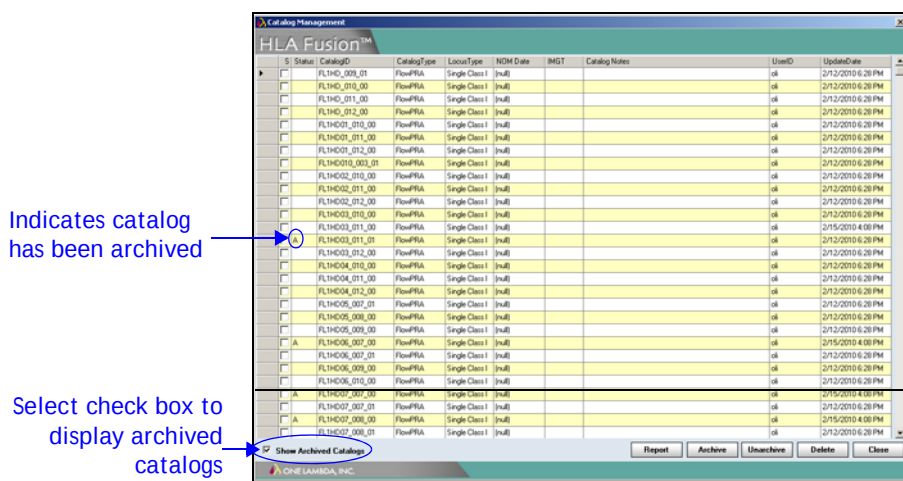


2. Select the **Archive** check box for the catalog files you want to archive.
3. Click **Save** to save changes and return to the **Update Reference** menu.
4. Click **Close** to return to the **Update Reference** menu without saving.

Note: When you import a new version of a catalog file, the system auto-archives the previous version.

Un-Archive Files

Archived catalog files are highlighted in grey when you view the catalog list. The most recently archived catalog files are displayed at the bottom of the list.



- From the **Archive Catalog** window, clear the **Archive** check boxes for catalog files you want to restore to active use, and click **Save**.

Viewing Catalog File Information

You can view information about a catalog file and generate a report from the **Catalog Information** menu. Catalog files displayed with a shaded line have been archived.

- From the Main Menu, select **Utilities > Update Reference > Catalog Information**.
- Click a column header if you want to sort the catalog file list.
- Click **Report** to display a printable, exportable report of the currently displayed catalog information.
- Click **Close** to return to the Update Reference menu.

Associating Product Catalog Files and Luminex Templates

You can associate a catalog file with the Luminex template name used for a specific product. HLA Fusion *Research* automatically associates catalog ID and template names the first time you run the analysis for the product. After an association has been made, HLA Fusion *Research* automatically selects the catalog file associated with the template used in the CSV file when you start analysis. You can also manually add, remove, or change associations.

- From the Main Menu, select **Utilities > Catalog Template Association**.
- Add, remove or modify an association:
 - Add a New Association

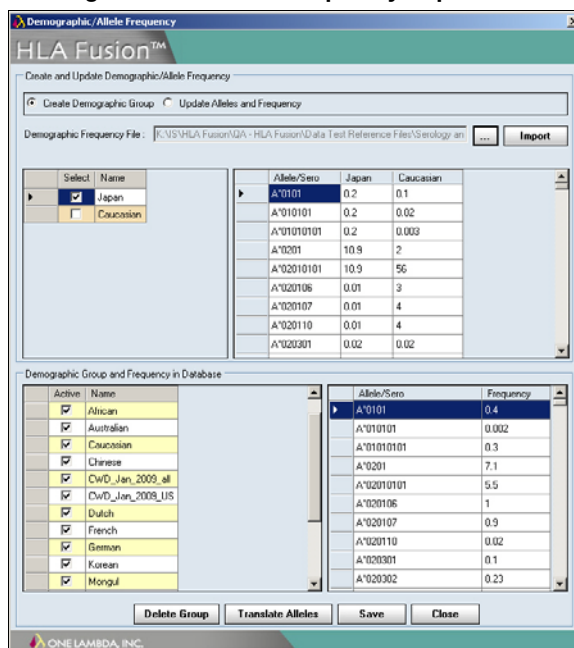
- Select a catalog file.
 - Type in a new template name, or click **Browse** to select a Luminex template file (.lxt format) to associate with the filename.
- b. Remove an Association
- Select a catalog file.
 - Select a template name and click **Remove**.
- c. Modify an Association
- Select a catalog file.
 - Edit existing template name(s).
3. Click **Save** to save changes.
4. Click **Close** to return to the Main Menu

Importing Allele Frequency Files (Demographic Frequency)

You can import allele frequency files to use in analysis based on demographics.

1. From the Main Menu, select **Utilities > Update Reference Allele Frequency**.

Figure 11-1: Allele Frequency Import



2. Select the **Create Demographic Group** option.
3. Click the browse  button and locate Allele Frequency files.

4. Click **Import**.

When an Allele Frequency file is successfully imported, the groups it contains are listed in **Demographic Group and Frequency in Database**.

5. Click **Save**.

Note: If the header for the column of any allele frequency file you import is empty, the entire column is not imported into Fusion Research, regardless of any other data it contains. If columns are duplicated, Fusion Research gives you an error message and does not import the allele frequency file.

The data contained in the Allele Frequency file look similar to [Figure 11-2](#).

Figure 11-2: Example Allele Frequency File Data

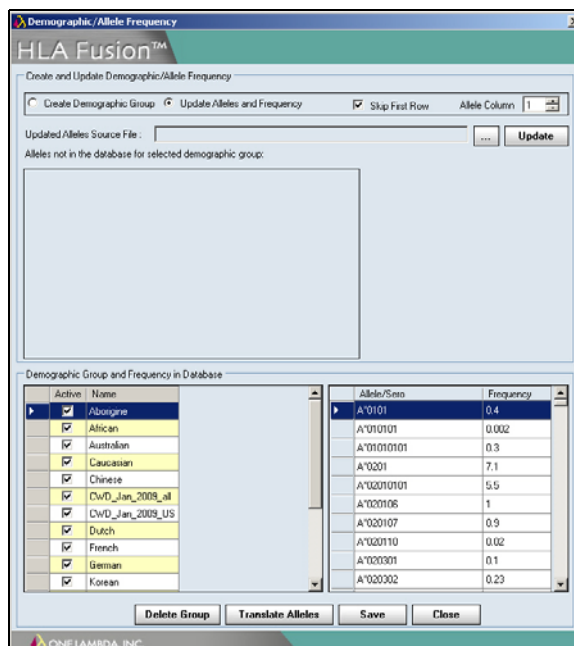
	A	B	C	D
1	Official Name	Japan	Caucasian	oli2
2	A*0101	0.2	0.1	0.2
3	A*010101	0.2	0.02	0.2
4	A*01010101	0.2	0.003	0.2
5	A*0201	10.9	2	
6	A*02010101	10.9	56	
7	A*020106	0.01	3	
8	A*020107	0.01	4	
9	A*020110	0.01	4	
10	A*020301	0.02	0.02	
11	A*020302	0.01	0.01	
12	A*020601	10.4	10.4	
13	A*020602	0.01		
14	A*0207	3.4	3.4	
15	A*0210	0.1	0.1	
16	A*0215N	0.01		
17	A*0218	0.02	0.02	
18	A*0228	0.02	0.02	
19	A*0242	0.01		
20	A*0251	0.01	0.01	
21	A*0253N	0.01	0.01	
22	A*0259	0.01		
23	A*0270	0.01	0.01	
24	A*0271	0.01	0.01	
25	A*0272	0.01		
26	A*0301	0.8	0.8	
27	A*03010101	0.8	0.8	
28	A*0302	0.02	0.02	
29	A*1101	8.1	8.1	
30	A*110101	8.1		
31	A*1102	0.1		
32	A*110201	0.1	0.1	0.1
33	A*24020101	35.6	35.6	35.6
34	A*24021	35.6	35.6	35.6
35	A*2404	0.02	0.02	0.02
36	A*2408	0.02	0.02	0.02
37	A*2420	0.02	0.02	0.02
38	A*2425	0.01	0.01	0.01
39	A*2443	0.01	0.01	
40	A*2601	9.8	9.8	
41	A*260101	9.8	9.8	
42	A*2602	2.2	2.2	
43	A*2603	2.1	2.1	
44	A*2604	0.01		
45	A*2605	0.02		
46	A*2606	0.02		
47	A*2611N	0.01		

Updating Allele Frequency Files (Demographic Frequency)

You can modify allele frequency files before using them in analysis based on demographics.

1. From the Main Menu, select **Utilities > Update Reference Allele Frequency**.

Figure 11-3: Allele Frequency Import



2. Select the **Update Alleles and Frequencies** option.
3. Click the browse button and locate the Allele Frequency file you want to update.
4. Double-click on the file, or click **Open** in the browser window.
5. Do any or all of the following to modify the file:
 - Add/delete alleles
 - Delete existing demographics
 - Change the allele frequencies
 - Convert allele format (click **Translate Alleles**)
6. Click **Update**.
7. Click **Close**.

Changing Product Configuration Settings

Changes to product analysis settings apply only to samples not previously analyzed. Previously analyzed samples must be re-analyzed for the changes to be applied.

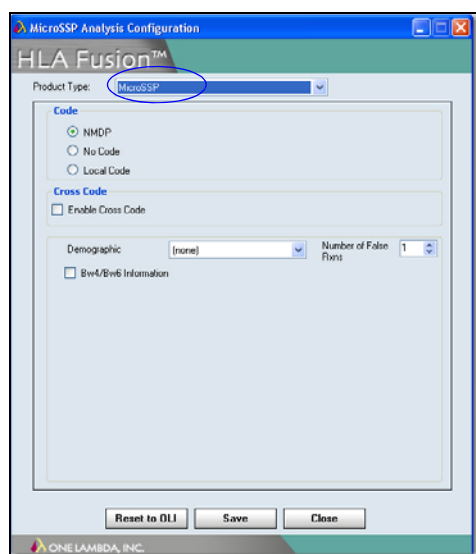
From the Product Configuration menu you can

- Change Micro SSP product configuration
- Change Ab1 file name configuration

Changing Molecular Product Configuration

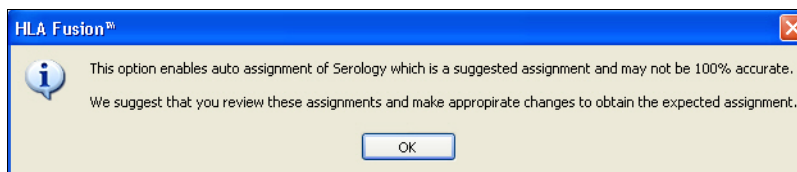
Changes Micro SSP analysis settings apply only to samples that have not yet been saved or confirmed. To change analysis settings for previously saved or confirmed samples, you must change the settings from the product analysis window and re-analyze the sample.

1. From the Main Menu, select **Utilities > Molecular Product Configuration > Molecular Analysis Configuration**.
2. Select **Micro SSP** from the Product Type drop-down menu.



3. Change configuration values as needed.
 - **Allow Auto-Accept All** can only be selected by someone with Supervisor user privileges, and allows you to select a button on LABType session summary to accept the batch analysis results for all samples.

- **Computer Assigned Serology** can only be selected by someone with Supervisor user privileges, and automatically populates Micro SSP analysis serology assignment fields. If this is selected, the following warning message is displayed as a reminder that the assignments are estimates, and should not be accepted without verification:



4. Click **Save** to save changes.
5. Click **Close** to return to the Update Reference menu.

Changing Ab1 Filename Configuration

You can modify the way Ab1 filenames are configured.

1. From the Main Menu, select **Utilities > Molecular Ab1 Filename Configuration**.

A	B	Cw	DRB1	DRB345	KIR
A	B	Cw	DRB1	DRB345	KIR
DPB1	DPA1	DQB1	DQA1	MICA	MICB
DPB1	DPA1	DQB1	DQA1	MICA	MICB

2. Make the format changes you want, and click **Save**.
3. Click **Close** to return the the HLA Fusion Research home page.

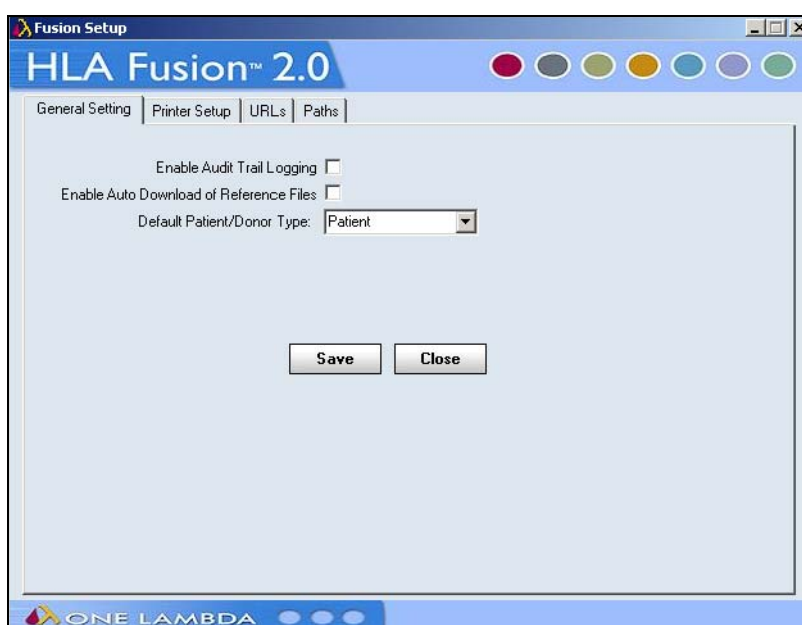
General System Settings

Several HLA Fusion Research system settings can be set through this menu option under Utilities.

General Settings

For enabling certain system options, use this tab on the Fusion Settings window.

1. Select **Utilities > General Settings**. The **Fusion Setup** dialog box is displayed.

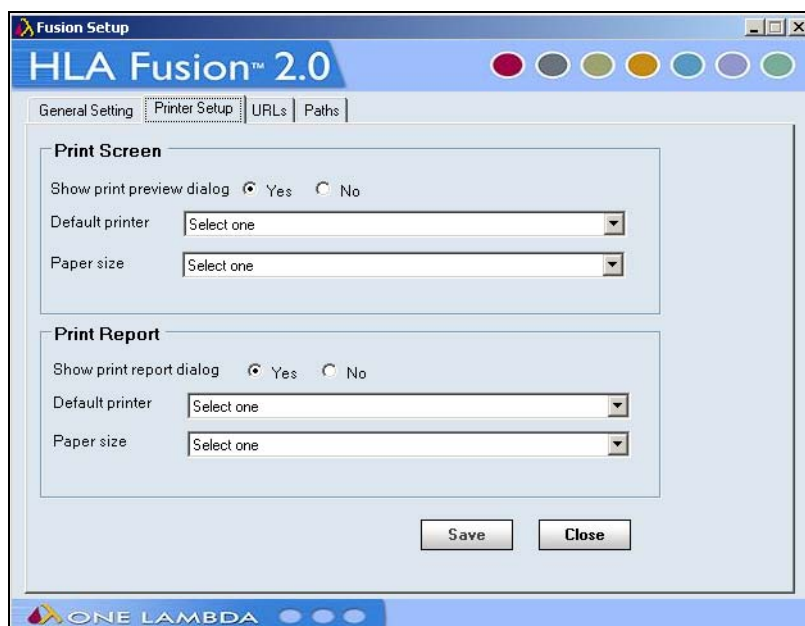


2. Select check boxes and from the drop down menu as desired to modify the current Fusion Research settings.
3. Click **Save** and then **Close** to save your changes and exit to the main Fusion Research application.

Choosing Default Printer Settings

You can set printer defaults for printing HLA Fusion *Research* screens or reports—whether you want to select a printer and settings each time you print, or whether you want screens or reports to be automatically sent to the specified printer with the specified settings.

1. Select **Utilities > General Settings** and select the **Printer Setup** tab. The Printer Setup dialog box is displayed.



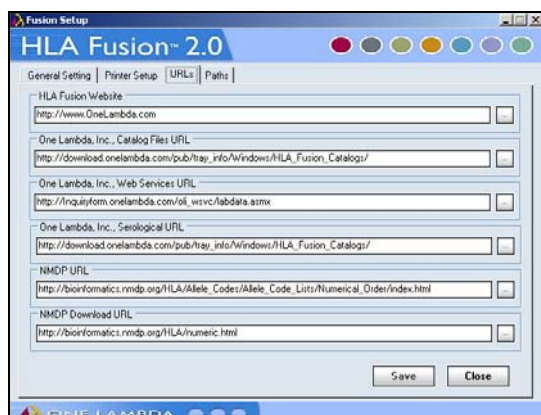
2. Select from the following options for both the **Print Screen** and **Print Report** panels of the dialog box:
 - If you want to select a printer and have the option of setting other printer settings each time you print, make sure the **Yes** option is selected.
 - If you do not want to select a printer each time you print, select **No**, and select the default printer and paper size from the drop-down menus.

Note: This default printer configuration may be overwritten by the specific page properties of certain reports.

Setting HLA Fusion *Research* Default URLs and Directory Paths

The **URLs & Paths** option under the Utilities menu allows you to set the default URLs for OLI and NMDP web sites to download reference and catalog files, and product updates. This option also allows you to set the directory path where HLA Fusion *Research*, by default, stores catalogs, session/batch files, reports, etc. Modifying URLs or paths ahead of time allows you to avoid having to browse for files each time you need them.

1. From the Main Menu, select **Utilities > General Settings** and select the **URLs** or the **Paths** tab.



URL tab



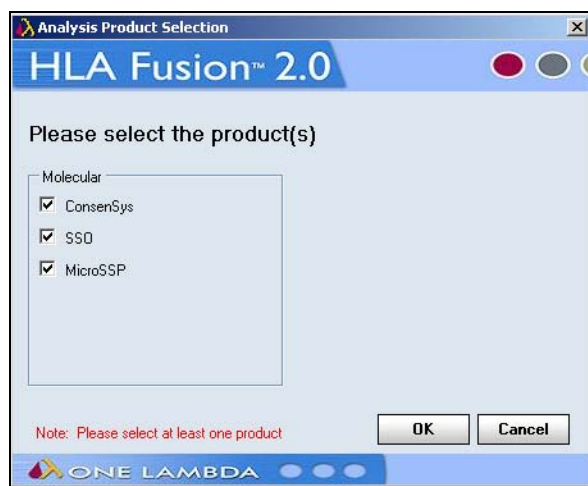
Paths tab

2. Click the **URLs** or the **Paths** tab.
3. Enter a URL and verify it works by clicking . For paths, use the browse button  to locate the directory you want to use for the specified purpose.
4. Click **Save**.

Activating Products

The Products Selection option on the Utilities menu allows you to activate or de-activate the various OLI analysis products that may be used with HLA Fusion *Research*.

1. From the Main Menu, select **Utilities > Products Selection**.



2. Select or clear the check box next to the product(s) you wish to activate or de-activate.
3. Click **Ok**.

Software Validation

The HLA Fusion *Research* software has functionality to help with the validation process required by Labs, Clinics, and hospitals seeking to comply with GCP, GLP and GMP. Validation of the HLA Fusion *Research* software for your lab environment for regulatory or performance reasons, can be automated by using the **IQ** (Installation Qualification) and **OQ** (Operational Qualification) options from the **Utilities > Validation** menu. Your lab may choose to run these as a standard regulatory validation process, to help troubleshoot issues, or to provide information to prepare for a software upgrade.

IQ (Installation Qualification)

The IQ process assists you with installation qualification of HLA Fusion *Research* software by providing a built-in function. Once the Installation qualification completes, a results report is generated, which you can save, print or export to Excel.

Note: If your IQ results concern you, export them to an Excel file and e-mail the file to OLI customer support (see [Technical Support, p. 3](#)).

1. From the Main Menu, select **Utilities > Validation > IQ**. The validation test runs. When it is complete, a report is displayed, with the following categories of data:
 - Systems Information (e.g., operating system)
 - Environment (e.g., directory path where the HLA Fusion *Research* program files are stored)
 - URLs (e.g., the URL for the catalog download site)
 - Database Information (e.g., name of the database)
 - Number and types of files installed (e.g., dll)
 - Lab Information (e.g., name and address of your lab)
 - Analysis Configuration for each product (e.g., low bead count for LABType)
2. Choose to save the report, preview it, print it, or export it to Excel.

IQ Type		
Installation Qualification (IQ) Summary		
Description	Value	Status
Performed By	One Lambda Inc.	
Performed on	Thursday, March 27, 2008 1:37 PM	
Number of tests performed	148	
Passed	148	
Failed	0	
N/A	0	
IQ Type		
Systems Information		
Description	Value	Status
Operating System	Windows XP	
Service Pack	Service Pack 2	
Region	United States	
Language	English (United States)	
IQ Type		
Environment		
Description	Value	Status
Program Path	C:\Program Files\One Lambda\HLA\Fusion\WD	Passed
Configuration Files	C:\Program Files\One Lambda\HLA\Fusion\WD	Passed
Catalog Files	c:\OUI\Fusion\data\catalog	Passed
Session/Batch	c:\OUI\Fusion\data\session	Passed
Reports	c:\OUI\Fusion\data\report	Passed
Interface (Import/Export) Files	c:\OUI\Fusion\data\report	Passed
Temp Files	c:\OUI\Fusion\data\temp	Passed
IQ Type		
URLs		
Description	Value	Status
OUI Catalog URL	http://download.onelambda.com/pub/tray_info/Windows/HLA/Visual	Passed

Example page from an IQ report

Special Characters to Avoid in Filenames

Some file formats that HLA Fusion Research imports use special characters as field separators. Therefore, it is recommended that you not use the following special characters when you name sessions or other files within Fusion Research.

Character	Name
,	comma
;	semi-colon
:	colon
.	period
/	slash
\	backslash
?	question mark
%	percent sign
*	asterisk
	vertical bar
"	double-quotation mark

'	single-quotation mark or apostrophe
<	less than
>	greater than

Chapter 12 LABXpress

This chapter describes how to create sample worklists, plate designs and custom runs for the LABXpress system.

Note: *Only use these procedures if you have access to and plan to use the LABXpress system (including pipetting machine) for automated sample processing.*

You should make sure you also have access to and have reviewed the LABXpress™ User Manual.

Managing Sample Information

Sample management in HLA Fusion *Research* software allows you to manage sample information before adding samples to a sample worklist. Sample information can exist in the database without any analysis data associated with it.

1. Select **LABXpress > Sample > Sample Manager**

Use Filter to Search for Sample Information

Search Criteria

Sample ID Local DCN Category TurnAround Date Location Sample List

* * * * * 2/14/2008 * *

Reset Filter View Sample

View/Edit Sample Information

SampleID	Local ID	DCN	Category	TurnAround	Date	Location	Patient ID
*							

2. Use the filters to find samples, and click **View Sample**.

Note: It is not recommended that you search by Sample ID—this may lead to a lengthy search, especially with larger databases.

3. Edit sample information.
4. Click **Save Changes** to save the sample information.
5. Click **Close** to return to the Fusion *Research* main menu.

Managing Test Lists

A Test List is a list of Sample IDs that can be used repeatedly to automatically write the sample IDs into a session analysis that can be read by the Luminex[®] system. It is a useful tool when you have a group of samples to be run on multiple tests.

From the Test List menu you can:

- Create new Test Lists
- View and edit existing Test Lists
- Delete Test Lists
- Export Test Lists to a .txt file

Creating New Test Lists

Test Lists must be created in the order in which the samples are to be analyzed.

1. From the main HLA Fusion *Research* menu, select **Sample > Manage Test List**.

2. Type in a name for the new test list, and click **Continue>>**.
3. Search for samples to add to the test list using the search fields, and click **Apply** to view search results.
4. Highlight samples, and click **Add>>** to add them to the test list.
5. Click **Save** to save the new test list.
6. Click **Close** to return to the Main Menu.

Viewing and Editing Existing Test Lists

Test Lists can be viewed or edited at any time.

1. From the main HLA Fusion *Research* menu, select **Sample > Manage Test List**.
2. Use the drop-down list to select a test list, and click **Continue>>**.
3. Click **Delete List** to permanently delete the selected test list.
4. Click **Close** to return to the Main Menu.

Deleting Existing Test Lists

Deleting a test list removes the list from the database, but the sample IDs are not removed or changed in the database.

1. From the main HLA Fusion *Research* menu, select **Sample > Manage Test List**.
2. Use the pull-down menu to select a test list, and click **Continue>>**.
3. Add, remove or move samples as desired.
4. Click **Save** to save the new test list.
5. Click **Close** to return to the Main Menu.

Exporting Test Lists

Test lists can be exported as .txt files for use outside of HLA Fusion.

1. From the main HLA Fusion *Research* menu, select **Sample > Manage Test List**.
2. Use the pull-down menu to select a test list, and click **Continue>>**.
3. Click **Export** to export test list details to a .txt file.
4. If prompted to save the test list before export, click **Yes** to save and continue.
5. Select a location to save the test list and enter a file name for it.
6. Click **Save**.
7. When prompted to create a Luminex Patient List input, click **No**.
8. Click **Close** to close and return to the Main Menu.

Creating Luminex Lists

HLA Fusion can create a Luminex List from a new or existing test list. You can use this list to quickly add information, such as sample ID, before you create a Luminex CSV output file. From the **Create/Edit Test List** window, you can create a Luminex list

Luminex List files can be edited after they are exported, but changes are not reflected in the test list from which they were created.

1. From the main HLA Fusion *Research* menu, select **Sample > Manage Test List**.
2. Use the pull-down menu to select a test list, and click **Continue>>**.
3. Click **Export** to export.
4. Select a location to save the test list to and enter a file name.
5. Click **Save**.
6. When prompted to create Luminex List input, click **Yes**.
7. Click **OK** on the confirmation message to return to the **Test List** window.
8. Click **Close** to return to the Main Menu.

Creating Sample Worklists

Note: The Sample Worklist feature is available *only* if you have SQL 2005 and above installed.

Sample Worklist functionality in HLA Fusion *Research* software gives you the flexibility to assign various tests to selected samples. This information is used in designing plates for Luminex processing.

Sample search criteria

Sample Worklist

Search by sample | Search by test list

Sample ID: * Local ID: * Sample date between: From: 2/25/2010 To: 3/25/2010 ☒ Show empty date Location: * **Clear Filter** **Search**

	SampleID	LocalID	Date	Location
*				

LABType Tests **LABScreen Tests**

☐ A ☐ B ☐ C
☐ DRB1 ☐ Bw4 ☐ B7
☐ DQA ☐ DQB ☐ DQA/DQB
☐ DP ☐ DRB345
☐ A-HD ☐ B-HD ☐ C-HD
☐ DRB1-HD

Save **Close**

1. Select **Sample > Sample Worklist** from the HLA Fusion *Research* main menu.
1. Use the search criteria to specify the samples that you would like to assign tests to, and click **Search**.
2. Select one sample, or select multiple samples (by holding and dragging the mouse). The selected samples are highlighted.
3. Now assign one or more tests by selecting the check boxes for the tests you want to run on the samples (listed under **LABScreen Tests** and/or **LABType Tests**).
4. Once you are done assigning tests to all the selected samples, click **Save** to save the worklist.

Creating a Plate Design

Note: The Plate Designer feature is available *only* if you have SQL 2005 and above installed.

Plate Designer functionality in HLA Fusion *Research* software gives you the flexibility to organize and plan your samples in a plate format that is ready for processing through the Luminex system. You must first create a sample worklist (see [Creating Sample Worklists](#), p. 142).

SampleID	Date
1107	5/19/2009 4:40 PM
2	5/19/2009 4:40 PM
3	5/19/2009 4:40 PM
324	5/19/2009 4:40 PM
4	5/19/2009 4:40 PM
5	5/19/2009 4:40 PM
6	5/19/2009 4:40 PM
7	5/19/2009 4:40 PM
8	5/19/2009 4:40 PM
9068	5/19/2009 4:40 PM
A*0108	5/19/2009 4:40 PM
A*2603	5/19/2009 4:40 PM
AP630	5/19/2009 4:40 PM
ARA	5/19/2009 4:40 PM
BCK	5/19/2009 4:40 PM
biobdd	5/19/2009 4:40 PM

1. Select **LABXpress > Plate Designer** from the main HLA Fusion *Research* menu.
2. Select the **Assay type**.
3. Select the **New Plate** button option if you want to create a new plate; otherwise, select **Edit Plate** to change an existing plate.
4. Click **Go**.
5. For a new plate:
 - Enter a unique plate name
 - Use the following search criteria to search and select the samples you want to add to plate for testing:
 - Test name

-
- Sample name
 - Sample collection date (From and To date)

To edit a plate, modify the data in the fields listed above.

6. Click **Search** to display a list of samples that match your criteria.
7. Select samples (one or many at a time), and use the left << button to assign these samples to a well in the plate. Repeat this until you have completed your plate design.
8. Click **Save** to save your plate design.
9. Click **Print** if you want to print your plate design.

Creating a Run Design

If you have not yet created a plate design, see [Creating a Plate Design, p. 143](#).

1. Select **LABXpress > Run Designer** from the main HLA Fusion Research menu.
2. Select the **Run Assay Type**.
3. Select the **New Run** button option if you want to create a new plate; otherwise, select **Edit Run** to change an existing run.
4. Click **Go**.
5. For a new run:
 - Enter a unique run name
 - Use the following search criteria to search and select the samples you want to add to plate for testing:
 - Plate design name
 - Plate design creation date (From and To date)

To edit a run, modify the data in the fields listed above.

6. Click **Search** to display a list of plate designs that match your search criteria.
7. Select the check boxes in the **IsUsed** column for each plate design you want to include, and click the **assign** button ☐ to add all the selected designs to the run.

Note: You can select a maximum of 8 plate designs per run design.

The bottom portion of the screen displays the resources and volumes required to make this run on LABXpress.

To remove a plate from the Run, select the check box in the **IsExists** column for that plate, and click the Remove button

8. When you complete the run design, click **Save**.

Determining the Run Type

The following table lists the types of LABXpress runs you can select for each assay:

Run Type	Definition
LABScreen Plate Driven Custom	You select a run from the <i>plate-based</i> run designs you have created for this assay type in HLA Fusion Research LABXpress Run Designer (see Creating a Plate Design , p. 143).
LABScreen Plate Driven Express	You create a run on the fly, using pre configured plates. This requires you to supply a barcode for each plate you include.

Run Type	Definition
LABScreen Sample Driven Custom	You select a run from the <i>sample-based</i> run designs you have created for this assay type in HLA Fusion Research LABXpress Run Designer (see Creating a Plate Design, p. 143).
LABScreen Sample Driven Express	You create a sample-based run on the fly, using pre configured plates. This requires you to supply a barcode for each plate you include.
LABType Plate Driven Custom	You select a run from the <i>plate-based</i> run designs you have created for this assay type in HLA Fusion Research LABXpress Run Designer (see Creating a Plate Design, p. 143).
LABType Plate Driven Express	You create a run on the fly, using pre configured plates. This requires you to supply a barcode for each plate you include.

Starting and Monitoring a Run

For step-by-step instructions on starting and monitoring a run through LABXpress to process samples automatically, refer to the *LABXpress™ User Manual*.

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