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HLA Fusion™ Version 3.0

FUSPGR

For In Vitro Diagnostic Use.

DESIGNATED USERS

All users of HLA Fusion™ Software. This software applies to LABScreen®

, LAT™

, LCT™, FlowPRA®

, LABType®

,

and Micro SSP™

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RELEASE CONTENTS
The HLA Fusion™

3.0 package includes the following items:
1. HLA Fusion™

3.0 CD

2. HLA Fusion™

3.0 User Manual

3. HLA Fusion™

3.0 Installation Guide

4. HLA Fusion™

3.0 Release Notes

5. HLA Fusion™

3.0 Database Utility User Manual

MINIMUM SOFTWARE REQUIRED
• One of the following operating systems:
 Microsoft® Windows® 7
 Microsoft® Windows® XP (minimum Service Pack 2 or 3) (only 32 bit)
• For Windows XP systems, Microsoft® Windows® Installer 3.1
• Microsoft® .NET Framework Version 3.5 (Service Pack 1)*
• Visual JSharp (version must match the .NET Framework version you are using)*
• Microsoft® SQL Server 2005 Express*, Microsoft® SQL Server 2005 Enterprise, Microsoft® SQL Server 2008
Express, Microsoft® SQL Server 2008 Enterprise version
Note: Before you upgrade to a new Service Pack from third party vendor such as Microsoft, contact your One
Lambda representative to verify that HLA Fusion supports it. If you are missing some of the Microsoft requirements listed, see the Microsoft.com Web site.

MINIMUM HARDWARE REQUIRED
• 1 GHz Pentium Processor
• 32-bit (x86) or 64-bit (x64) microprocessor
• 1 GB hard disk space (more may be required for large databases)
Note: Regardless of where you install HLA Fusion, as much as 400MB of space on your local hard drive may
be required for temporary installation files as well as any programs you may need.

• 512MB RAM
• 8-bit graphics adapter and display (for 256 simultaneous colors)
• VGA display with minimum of 1280 x 768 resolution
• Mouse or other Windows® compatible pointing device; mouse with wheel required for certain products
• A Windows® compatible printer driver, (PDF Distiller or Microsoft Document Image Writer are available for free)
* Included with HLA Fusion installation.

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WHAT HAS CHANGED
The following changes were made to HLA Fusion™ Software since version 2.0 and its related Service Packs: Enhancements

• The system now has overlapped bead separation algorithm support for all LABType® HD products, using
existing RSSOH1C logic.
• The system now has support for FJ correction to single-antigen Class II, similar to W632 for Class I.
• Users can now select a default Home Page to start with when they log in to HLA Fusion.
• The system now enables users to set or view the path for LABType HD conversion output. This path will be
used to store converted CSV files for LABType HD kits.
• The system now provides A1, B2, A1B, and A2B blood type choices on the patient form.
• The system has additional tutorial and "Show Me" features in the online help.
• The system now has a field for the LABType HD Output file path. The file path will be used to store converted
CSV files for LABType HD kits.
• The system has improved Bw4/Bw6 coloring in LABScreen to distinguish the specificity.
• The probes in the Reaction Table in LABType Analysis are now colored based on the exon region to better
distinguish the probes.
• The system now uses a new Bead naming convention (Analyte).The system now includes a Luminex Device
field and a Software Version field on the import and batch summary screens and in the custom reports. These fields appear only for LABType and LABScreen products.
• Users can now reconfigure any HLA Fusion database to increase the maximum database size.
• Users can now merge HLA Fusion audit log databases.
• The system now enables users to send software feedback and reports by e-mail from within the HLA Fusion
application.
• The HLA Fusion database is optimized for space and indexing.
• Users can now search and sort for all samples assigned with a given specificity.
• Typing results are now available in the tool tip when the user hovers over a sample in the QC histogram in the
first quadrant of LABType analysis.
• A user-designed cutoffs feature is now available for LABScreen PRA products.
• Bead ID, Raw Data, and Specificities are now available in the Data Export setup.
• Users can now include more lab information in custom reports.
• In the Patient Ab Tracking module, users can now choose to track only antibodies that meet a user-defined
cutoff.
• Exports and printouts of the Column (Spec) graph now include a legend that shows the Sample ID’s that
correspond with each Sample Index. This feature enables users to identify which bar graph belongs to which Sample ID.
• The Haplo tab in LABType now groups according to the true haplotype organization.
• LABScreen analysis now displays the match/mismatch information for Donor Specific Antibodies (DSAs).
• The Antibody custom report now displays the match/mismatch information for DSA. The information is
displayed as a table containing the donor IDs, DSA, raw data for the test, and highlights indicating match/mismatch or group by match/mismatch.

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• The system now enables the user to make a single allele final assignment. Also, when a homozygous result
has been confirmed by family study, the user can activate a "Homozygous Assignment Confirmed" notation
for reporting purposes in addition to the attachment of related records.

• The Custom Antibody report now includes a graph that shows specificity (serological, at minimum) and bead
ID plotted against the normalized Mean Fluorescent Intensity (MFI) values.

• Control (NC & PC) values are now displayed in the data table for each sample in the Antibody Tracking
module.

• A report/export is now available, resembling a Microsoft® Excel worksheet, where the first column includes all
the sample names, each row belonging to a different sample, and the rest of the columns across from left to right are the bead IDs, with the raw data associated with each sample.

• The “%SA” field is now a part of the Field Chooser, so that users can remove it from their summary reports.

• In the Epitope Analysis results in the LABScreen analysis and the corresponding reports, the Mean (raw) of
positives has been replaced with the Mean (normal) of positives.

• The MFI and normalized values are now displayed as whole numbers.

• In the HLA Assignments Serology section of the Manage Patient module, users can now assign Bw4/6 and
then track Bw4/6 in the Ab Tracking module.

• Users can now export LABType product information that resembles the temporary files that were used to
import product information in HLA Visual.

• The Find Antigen function in LABScreen Mixed analysis now works similarly to its counterpart in LABScreen
PRA/SA analysis, where broad antigens can be searched and its split antigens are circled. For example, if a broad antigen, A9, is searched, the split antigens, A23 and A24, are circled.

• The system now has a Donor PRA function, similar to the one used in LABScreen analysis for Patient Ab
Tracking, where the percentage is calculated for both Class I and II of a chosen serum.

• The specificities in the test details section of the Custom Antibody report are now sorted alphanumerically
where the locus is treated as an alphabetic character and the number portion is treated as numeric
characters.

• The DQA and DPA alleles are considered In the Tail and Epitope Analysis for Class II Single Antigen.

• Cutoff values for each of the individual tests are now included in the list below the tray grid in the LAT-Mixed
Raw Data Report. Also, a column for each Cutoff location has been added.

• The LABType analysis page is now enhanced to include details of all of the results for each locus. As results
are saved for each locus, either the serology result or allele code for each locus fills this "all loci" section.

• Titles on custom reports (such as Molecular Custom) are now limited to 50 characters.

• Session ID and Sample ID search in modules such as Manage Data and Reporter now support Chinese
characters.

• The system now recognizes the ELISA reader from COM ports other than COM 1.

• Micro SSP Analysis now ignores the first well (1H) when determining whether to analyze non-amp wells with
a positive and negative score.

• The specificities in the Reaction Score section of the Custom Antibody report are now ordered the way UNOS
sorts the specificities, which is by locus (A, B, BW, DR, DQAB) and within each locus, sorted numerically. In addition, within each reaction group, each specificity is listed only once as opposed to listing it for each bead.

• The Combined Sample report in the Reporter module now has an option to display the Assigned Allele Pairs
in the Corrected Typing field instead of the Assigned Allele Codes field.

• The system now provides clarification that LAT analysis configuration settings do not apply to LATM analysis.

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• The system now enables users to update existing NMDP codes. The system overwrites existing NMDP codes
each time there is an update.
• The Manage Data module now includes a patient filter.
• Wildcard searches are now available for the Sample ID filter in the Manage Data module.
• The Test Date field on the Custom SSP Report is now the sample analysis date and not the session date.
• The Test Details section of the Custom SSP report no longer abbreviates allele specificities.
• The User defined Cutoffs feature is now expanded for use with the LABScreen PRA products.
• Users can now enter reactions in SSP analysis using the number keys on the keyboard.
• The LABType assignments text box is now larger so that all the assignments can be viewed without having to
use the scrollbar.
• Users can now make a single allele final assignment. Also, when a homozygous result has been confirmed
by family study, users can now activate a "homozygous assignment confirmed" notation for reporting.
• The specificities in the Final Assignment list are now color coded to differentiate specificities assigned in the
Tail and Epitope Analysis results and manual assignments that have been assigned.
• Donor PRA has been added to the batch summary.
• The system now provides the option to group sessions by test date instead of session date in the navigator.
• Users can now assign donors to groups and then calculate Donor PRA based on the donors in the selected
group instead of all the donors in the database.
• The system now provides a configuration setting so that the user can choose not to see the warning message
about requiring a certain screen resolution, and is not forced to change the screen resolution.
• The system now provides the option of hiding the CREG Bar in the analysis from within the Antibody Analysis
Configuration Settings. This feature enables the full graph and specificities to be viewed on computers with smaller monitors.
• Donor PRA calculation now includes DQA1*. This means that the software takes into consideration the
molecular assignments made to the patient card to calculate the Donor PRA.
• The system now indicates whether the active NMDP code is v2 or v3.
• After selecting More Tests, users now have the option to specify which tests they want to run. Samples for
which tests are selected are added to a cumulative sample/test list based on the specified tests.
• The different levels of DSA strength are now emphasized in Pt Ab Tracking-giving different colors to the Ab
specificities in the Antigen Table by their strength.
• The system now enables switching users without the need to exit the application and then start again with a
different login.
• The system now displays Serology and NMDP updates on the molecular products home pages.
• Users can now select Auto Accept All to save all the suggested results for all samples of an LAT Mixed
session.
• The system now enables analysis of G and P groups during LABType analysis.
• The specificities listed in the Rxn Score section of the Custom Antibody report now match the specificities in
the Test Details section.
• Users can now edit session-level comments for the LABType Session Summary, Control Value, and Bead
Analysis tabs.
• The system now provides a feature to prevent the overwriting of existing patient information in the Manage
Patients module.

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• The sample date is now displayed during analysis.
• Session ID, patient ID, well ID, and test date are now included in the raw data reports from the analyses
windows.
• Users can now set configuration options such as Default Threshold (e.g., 2X).
• For the Antibody Custom report, each specificity is now separated into separate cells in the Rxn Score
section.
• A new report is available under Statistical reports to that includes a listing of all LABType control values and
such statistical information as average number of samples, min and max values.
• The size of SSP gel image in the Custom SSP report is now larger than 700 pixels.
• Users can now rotate and zoom in/out of gel images attached to the analysis.
• Users can now include a graph in the Custom Antibody report that has MFI values on the y-axis and antigens
on the x-axis, sorted by descending MFI value.
• For the final assignments in antibody analysis, the sorting is now alphanumeric.
• The LABType (BMT) report now includes a column for Comments and a column for Other Assignment.
• The system now appends the Donor PRA and then the Allelic Specificities (MFI) of the Final Assignments to
the end of the BMT - LABScreen report. The allelic specificities are sorted in alphanumeric order.
• Users can now stay on the current sample after a Save or Confirm without moving to the next sample.
• The Assigned Allele Code in the BML report has been replaced with Assigned Allele Pairs.
• The system now provides an additional field on import in which to enter and the secondary attribute that was
used. This also enables the tracking of Secondary Ab.
• Users can now filter the samples by the secondary attributes during Ab Tracking.
• The system now provides separate fields for comments-one for system status messages and one for user-
entered comments.
• When a global cutoff adjustment is made, the system now records it in the comments for only those samples
affected by the cutoff. For example, if a global cutoff adjustment is made and only 5 samples out of 96 samples are affected, then the global cutoff status comment is recorded for those five samples only.
• The columns in the UMC-Utrecht report labeled A1_1 Result and A1_2 Result now have 4-digit results,
excluding the Locus letter (e.g., 03:01).
• The initial date in Ab Tracking now defaults to the sample date of the sample associated with the patient ID.
• Users can now create a multi-batch of patient lists by applying the individual patient lists from a Luminex®
patient list through the Plate Designer.
• Users can now import a batch of Micro SSP sessions, including the ability to browse for files.
• Users can now add comments to graphs in Ab Tracking, and print out the graphs with the comments.
• Users can now navigate to the Ab Tracking window from analysis and back to analysis once the Ab Tracking
window is closed.
• The timelines for Ab Tracking graphs can now be configured to be, for example, total days represented by
sample set, actual sample dates, etc.
• Graphs from Ab Tracking now include the patient's name (first and last name).
• Users can now search for a patient by sample ID, local ID, and other patient information.
• Users can now use patient name rather than patient ID in Ab Tracking.

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• Users can now add a donor and donor information, and link it to the current patient in Ab Tracking.
• The system now does not split HLA specificities across rows. This applies particularly to the Antibody
Assignment field in the Test Results section of the Antibody Custom and Antibody Screening/ID reports.
• The system now displays the patient name to be displayed in the Ab Tracking module.
• Users can now search for a patient ID by entering part of the ID and selecting from the list displayed in Ab
Tracking.
• Users can now enter Creatinine levels for various dates that will be plotted alongside the antigens in Ab
Tracking.
• The graphs on Ab Tracking now contain a button to expand and contract the graphs.
• Users can now search for records by patient ID, and then move, archive or delete that patient's records as
needed.
• Users can now generate the Catalog Information Report in the old format.
• Users can now set a minimum scale for the graphs in Ab Tracking.
• A fourth graph has been be added to Patient Ab Tracking, which tracks sample dilution, with dilution factor on
the x-axis and raw data on the y-axis.
• Users can now configure LABScreen Single Antigen to default to W632 normalization.
• Users can now apply W6-32 normalization to imported sessions.
• Users can now compare W632 normalized data with data not normalized by W632 in the Raw Data table.
• The system now automatically calculates Donor PRA upon saving/confirming a sample analysis.
• The same chart for comparing different antigens across different LABScreen kits is now available for samples
that have already been tested.
• The system now separates the two columns of alleles in Forced Rxn so they are separately sortable.
• The system now supports a bead exclusion report that shows a summary of how many times each bead was
excluded for a selected catalog.
• The first quadrant of the LABType analysis window now has a tab that shows a histogram of the user's
cumulative data. It displays the normalized values for all the samples this user has ever run for the product (same lot), and serves as a user-created QC graph. The graph is continually updated as the user uses the product over time.
• The sample search now enables users to enter alleles and a catalog ID. The system then displays all
analyzed samples with the entered catalog ID and entered alleles in the Allele Pair window or Assigned Allele window.
• Users can now customize the Combined Sample Report to include serological results and Other
Assignments.
• The system now provides a field for the type of transplant the patient will or has received, with a drop-down
list [e.g., SPK (simultaneous pancreas kidney transplantation), KTA (kidney transplant alone), LDKT (living donor kidney transplantation), SPLK (pancreas living-donor kidney), and Other]. There is another drop-down field for patient status (e.g., C0 = in assessment, C1 = active listings, C2 = pending, C3 = transplanted, and
C9 = deceased).
• The session (batch) summary screen now supports the display of DONOR PRA percentages and enables
them to be reported from here.
• In the third quadrant of the LABType analysis window, users can now set a configuration default to always
show the Delta view first.

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• Users can now enter and save LAT test information (sample IDs, tray info, etc.), and then perform the tray
reading with the software at a later time.
• Users can now name exported Ab Tracking graphs, and to select the export destination.
• The system now displays the same bead information when the user selects the Bead Analysis tab for
sessions as it does when the user selects the Bead Info tab during sample analysis.
• Users can now keep the Raw Data table open, and make assignments from the table.
• With the LABType HD products when there are false reactions, the system now indicates which probes, and
their allelic representation, are relevant for the false reactions.
• The Thai Export and Thai Export V3 reports have been modified to expand the export of results for LABType
and LABScreen.
• The system now supports the bulk collection of allele codes with XX code into a properly formatted Excel file
to examine and to send to NMDP.
• Users can now translate allelic final assignments from V2 to V3 nomenclature using the Data module.
• Users can now enter the sample date during LAT analysis.
• The system now provides a Catalog Import Date column in the Catalog Management module.
• All Updates Available links for Product Catalogs now display the nomenclature date and revision notes.
• The LSM Detail report now displays patient ID, patient name, and local ID at the top of the report.
• A new report has been added that shows the historical performance of a LABScreen product by displaying the
MFI values for every bead of all samples that have been tested.
• The Molecular Custom report now contains match reactions.
• Users can now import packing lists that use the new format from NMDP.
• If the user selects the Update Previously Downloaded Documents check box next to Get Docs (from the auto
update page in Update References), the latest version of documents will be imported, even if older versions were imported previously.
• A new report has been added, similar to the Cutoff Adjustment summary report. The new report shows, for a
given catalog, the number of samples that used that catalog, what percentage of those samples had a low positive control value, and what percentage had low bead counts.
• An new statistical report has been added for LABScreen catalogs, listing such statistics as:
• Total number of samples using the catalog
• Number of samples with a low bead count
• Number of samples with high negative control values
• Number of samples with low positive control values
• The BmT LABType report has been expanded to include SSP tests. It uses the same format as the current
BmT LABType report but exports SSP results into that format.
• The system now automatically detects if there is a software update/patch and informs users of available
updates. The software update "Upgrade" feature is only available to HLA Fusion supervisor level users with
MS Windows admin rights.
• The BmT LABScreen report now has a donor PRA field.
• Manual entry for LCT analysis now resembles the one for Micro SSP, where multiple sessions can be entered
with different catalogs and/or samples.

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• The allele specificity of the Antibody Custom report is now displayed in individual columns for each locus,
where each allele is displayed in its corresponding locus column.
• A graph is now included in the Custom Antibody report that shows antigens and bead ID plotted against the
normalized MFI values in descending order. It resembles the LABScreen analysis graph.
• The LABScreen PRA/Single Antigen Summary is now a report accessed through the Report tab in the
session summary. The report includes patient ID.
• Users can now sort DQA and DPA specificities in the histogram during LABScreen SA analysis.
• In the Antibody Assignment field in the Test Results section of the Antibody Custom and Antibody
Screening/ID report, users now have the option not to split specificities when they extend past the row.
• Users can now edit the Patient ID field in the Manage Sample Info to change an existing patient ID or add a
patient.
• The system now has a computer-assigned serology function in Micro SSP analysis similar to the one that has
been available for LABType analysis.
• When starting a new Micro SSP session, users can now add a locus filter for narrowing down the number of
SSP catalogs that appear in the drop-down list, and more importantly, show only the catalogs that test the selected locus.
• LABType analysis now performs faster when moving from one sample to another by abbreviating the
suggested allele pairs list instead of showing the full list each time.
• The sample ID information is now displayed for every result in the Custom Molecular report even when it is for
the same sample ID within the same session.
• A report has been added that groups all the assigned allele codes in a simple format and includes serology
assignments, close bead reactions, and comments.
• A section has been added to the Molecular Custom report just for PC and NC results, near the session
information section.
• A virtual Crossmatch function has been added that enables users to record and search for class I and II
antibodies of the patient against donor typing.
• The system now indicates whether a patient or donor is from another facility and that facility name using the
Manage Patient module. That information appears in reports.
• The system now supports transplant history for a given patient.
• The system now supports patient CDC, CDC/AHG and VX Crossmatching in the patient management
system.
• Users can now perform auto and manual as well auto import of P and G groups from the IMGT site.
• The system now supports auto serology assignment in SSP module.
• The system now logs database maintenance processes by user.
• Users can now change the database from within HLA Fusion without exiting the software.
• Users can now customize EPITOPE tables. Users can choose to use their own EPITOPE table from one they
created within the HLA Fusion system. The system allows only uppercase letters as Antigen names, and
allows the use of existing tables as templates in the creation of new EPITOPE tables.
• Users can now circle antigens on the analysis screen based on the selected EPITOPE group/table.
• The LAB Profile should has been updated to include distributors' names and e-mail addresses. The e-mail
addresses must be semicolon (;) or comma (,) separated.
• The Reporting module now supports the transmission of selected reports using e-mail. The e-mail button will
be activated only when the e-mail has been configured in the user profile. An internet connection is required.

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• The user profile now supports e-mail configuration to allow the use of Microsoft® Outlook, Hotmail, Yahoo,
AOL, and Google e-mail transport.
• Please note that HLA Fusion will use provide the e-mail ID and e-mail provider. The HLA Fusion neither
guarantees the accuracy of the e-mail addresses nor the delivery of the e-mail. It is up to the user to verify
and confirm the accuracy of the e-mail addresses and to confirm the delivery of the e-mail with recipient.
• HLA Fusion is using the e-mail transport provider published protocol and configuration as of Dec. 2011 which
is subject to change from time to time. HLA Fusion will enhance the configuration in the following release if there are any changes in the e-mail transport provider configuration and protocol.
• The system now supports NKR (National Kidney Registry) data export using patient and date range for
LABScreen SA products.
• For RSSOH2B1 (LABType HD DRB1 SSO DNA Typing Test)) lot 7B and later, the system distinguishes and
separates the signals from regular and overlapping magnetic beads. The requirement for this change is specific to DRB1 HD kit lot 07B and later only.
• The system now uses the original Luminex bead for low bead count warning messages for HD kits.
• Users can now choose to display or to not display the computed HD bead count in the raw data table as part
of the Molecular Analysis configuration.
• The system can now indicate the type and cause of ambiguity with regards to the High Definition analysis.
• Users can now analyze multiple samples using different SSP products under one session.
• Users can now choose not to create database backup sets for the Schedule Backup function.
• Users can now sort the LAT-Mixed report by well position.
• Users can now include possible allele pairs in the Export Data function.
• The system now provides a report that tracks the number of Samples excluded on each bead per catalog ID.
• Users can now create custom reports for LAT, LCT, and Flow tests.
• Users can now mark a sample for More Test and then is then given the option to specify additional tests to
run.

• Users can now configure the wells in the gel representation in SSP analysis to be numbered.
• Users can now see the sample date in the sample selection window for side by side analysis during analysis.
• The system now displays the full software version information (including SP version) in reports.
• The system now has an Australia report in HLA Fusion for LABType (LABType - Australia).
• The system now supports an export similar to the report from legacy LAT software.
• The fields, Class I Antibody Specificity, Class II Antibody Specificity, MIC Antibody Specificity, Unacceptable
Antigens, and Acceptable Antigens box, in the Antibody tab of the Patient Sample Summary, are now larger
so the users can see all the information without having to scroll through each field.
• In the custom reports (Molecular, Antibody, Patient, SSP, etc.), users can now select and include any/all of
the patient data that is available in the Patient/Donor Info, including birthdate, ethnicity, diagnosis, blood type, etc.
• The system has enhancements to the Exon 4+ combined analysis.

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Bug Fixes
• The ability to exclude exon 3 from analysis for SSP, and RSSO samples referring to DQ and DP products.
• When a cut-off is made in a DRB345 kit, different results, such as DR52 and DR53, are not mapped correctly.
• Reaction pattern table is now presented in alphanumerical order. The force tab now consistently list the
alleles in the proper order meaning the lower of the two alleles are listed on the left side.
• Bw4 Bw6 assignment has been corrected to be at the allelic level instead of the serological group level.
Recognition site control updated to recognize negative values in rrecognition site location..
• Samples now remain on the plate when assigning two test lists which have the same sample ID with the
same test assigned on a plate.
• Updates to the search functions.
• Installation issue on x64 bit platform. The supported platform section has been updated and only Win XP 32
and Win 7 (32 and 64 bit) platforms are supported.
• The system only allows users with sysadmin role to upgrade the database and all other users will not be able
to perform DB related tasks.
• Exception errors caused by combining LABType HD samples with Exon 4-7 samples due to low positive
control has been corrected.
• The NC and PC columns are now included in the data export.
• The LAT analysis results were improved in cases when all beads are negative the DR51/52/53 will not be
suggested as a result.
• The issues with database name that caused the auto schedule backup to throw exception has been fixed.
• "Show matches with all testing" option include C locus test results has been addressed.
• In some unique situation the system will allowed the user to associate a template name to multiple catalogs.
This has been changed so that users will not be allowed to do that.
• The sorting of serological and/or allelic specificities under the final assignment field has been addressed.
• The soring order now defaults back to system sort and does not persist from previous sample sort order for
the Antibody analysis.
• In Custom SSP report setup, Nomenclature date and NMDP/Local code update now displays in the report.

LIMITATIONS AND RISK MITIGATION
• HLA Fusion Software has a limitation when utilizing cross loci wells in the Micro SSP analysis
module. When viewing the software suggested assignment, be sure to verify any final assignments
when a cross loci well is part of the reaction pattern. Mitigation: Use manual analysis in these cases.

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INSTRUCTIONS

Updating Databases from Prior Versions of HLA Fusion™
Upgrading a Prior Version of an HLA Fusion Database after a New Installation
For users of previous versions of HLA Fusion:
1. After you have followed the HLA Fusion Installation Guide to install version 3.0 of HLA Fusion, open the
Fusion Database Utility by double-clicking the shortcut on your computer desktop.
2. Choose the Upgrade prior versions of HLA Fusion database to 3.0 function from the Fusion Database
Utility.
3. Select the database you want to update, and specify a location in which you want to store a backup copy.
4. Click the ‘Upgrade’ button.
5. Choose the ‘Select Database’ function from the Fusion Database Utility.
6. Select the database you upgraded in step 3, and click the ‘Set’ button.

REVISION HISTORY
Revision Date Revision Description
0 12/20/2012 Original release
1 02/2014 Per CR#130079 (CAPA #493), adding Limitation statement to release
notes regarding cross loci wells.