TypeStream Visual NGS Analysis Software

User Manual

Version 3.x.x

Catalog Number: TSVPGR

For Research Use Only in US and Canada. Not for use in diagnostic procedures

IVD In Vitro Diagnostic Medical Device

CE

EC REP

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TypeStream Visual NGS Analysis Software

Introduction

Intended Use: TypeStream™ Visual NGS Analysis Software is an accessory for the evaluation of test results from One Lambda, Inc Next Generation Sequencing (NGS) products for molecular typing.

It is a standalone software solution that supports the analysis of both single read and paired-end sequencing data produced using NGS assays manufactured by One Lambda, Inc.

Upon completion of sequencing, TypeStream Visual (TSV) aligns unmapped barcode sequences to the IMGT reference library to generate individual genotype assignments. It uses kmer seeded alignment along with smith-waterman alignment for refinement. In addition to genotyping, TypeStream Visual provides the analyst with a wide range of analytical tools, run statistics and

> **NOTE:** Make sure you have downloaded the most up to date Nomenclature and/or Serology Equivalent files before you import catalogs or attempt to analyze sessions/samples.

quality metrics to facilitate examination and reinforce decision making.

Upon successful installation of TypeStream Visual 3.0 , two icons are created on the desktop.

TypeStream Visual now leverages multi-processor CPU, effectively cutting in half, or better,

your analysis time for any session with more than two samples. Engine and logical processor use is as follows:

Total logical processors 8-23: 2 engines
Total logical processors 24-31: 3 engines
If the total logical processors >= 32: threads per engine 6, engine # = total processors / 6 – 1

Sessions with only single samples will not be able to take advantage of this increase in analysis speed.

Program Updates

You may also obtain updates of TypeStream Visual 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 TypeStream Visual are available through your One Lambda Inc. representative, or from the One Lambda website:

- TypeStream™ Visual NGS Analysis Software

Supported Products

All One Lambda software products are designed to assist personnel experienced in analysis by suggesting typing results. However, results must be carefully reviewed by a person qualified in 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.

Catalog selection needs to match the SKU name for the assay used. For AllType NGS Amplification reagents, use catalog beginning with 'ALL.' Refer to the table below when analyzing using TypeStream Visual NGS Analysis Software (Cat. No. TSVPGR)

Product Description	Catalog Number	Assay Regulatory Status
AllType NGS 11 Loci Amplification Kit	ALL-11L	CE-IVD
AllType NGS 11 Loci Amplification Kit	ALL-11LX	For Research Use Only. Not for use in diagnostic procedures.
AllType NGS 9 Loci Amplification Kit	ALL-9LX	For Research Use Only. Not for use in diagnostic procedures.
AllType NGS 8 Loci Amplification Kit	ALL-8LX	For Research Use Only. Not for use in diagnostic procedures.
AllType FASTplex NGS 11 Loci Kit for Illumina	ALL-FAST11LFX	For Research Use Only. Not for use in diagnostic procedures.
AllType FASTplex NGS 11 Loci Kit for Ion	ALL-FAST11LX	For Research Use Only. Not for use in diagnostic procedures.
AllType FASTplex NGS 11 Loci Kit for Illumina	ALL-FAST11LF	CE-IVD
AllType FASTplex NGS 11 Loci Kit for Ion	ALL-FAST11L	CE-IVD

Technical Support

For technical questions, customer support, and to report software cyber security vulnerabilities please contact us at:

One Lambda Technical Support
North America: + 1 747-494-1000 Option #2 (PST)
North America Toll Free: +1 800-822-8824 Option #2 (PST)
International: +49 3302883-426 (CET)
International Toll Free: 00800 6200 0000 (CET)

Web: www.onelambda.com Email: 1lambda-TechSupport@thermofisher.com

Precautions

- TypeStream Visual NGS Analysis Software is intended for Professional Use by technologist or laboratory director trained in histocompatibility testing. This software is intended for use in accredited laboratories ASHI, EFI, CLIA.
- Clinical laboratories are governed by ASHI, CLIA, and EFI guidelines mandating laboratories to make clinical decisions based on multiple sources. Solid organ transplants require confirmatory testing derived from multiple sources to determine donor suitability. A transplant decision will not be made solely on the results of the test in question being either positive or negative.
- The Lab Director or the Technical Lab Supervisor should reviews and approves final reports for reliability and accuracy of test results.
- The laboratory must have an ongoing process to ensure that all computer assisted analysis are accurate and validated for accuracy.
- When updating the IMGT, users should also update serology equivalents, P code, and G codes to latest released version.
- Only Authorized Users with training and credentials should assign the final test results to the samples.
- Users should review the reports generated by the software and compare against analysis screen for accuracy prior to signing off.
- Cybersecurity vulnerabilities were tested for this software and required design update recommendations have been implemented. All Laboratories and users are suggested to follow their security policies for running and installing regular software patches.
- Loss of data may occur, users should establish their own data backup procedure based on their data protection guidelines.
- TypeStream Visual Software does not save / transmit any patient data to One Lambda, Inc. servers. All analysis data generated by software is saved by users and are suggested to establish and follow their security policies for patient medical and personal data protections.

Limitations

- Software was verified and validated with current IMGT v.3.46 Updates in IMGT may impact assigned test results.
- Software analysis files exported from sequencers should be in .fastq/ .bam format. Performance of sequencer, sequencer reagents, and biases on sequencing

accuracy due to specific HLA gene motifs such as homopolymers and repeat base(s) is critical for optimal performance of the next-generation sequencing workflow. Users should refer to sequencer user manuals for any sequencer-related limitations.

- Software analysis is based on the primer information included in the catalog file are lot specific, refer to resolution limitation document for ambiguities list document for known limitations.

  Note: The limitation documents only lists ambiguities due to the primer positions but not the ambiguities due to genotype phasing.

- When upgrading from previous database version to new, certain configurations may return to default settings.
- Refer to software generated warning / system messages for trouble shooting.
- Users can use CWD or CIWD. Users should update to latest serological equivalent file Jan 2022 or later, to reflect CIWD database updates.

Warnings

- LRS (long read sequencing) and LRP (long read primer) analysis is not supported by an assay manufactured by One Lambda Inc. Analysis is for Research Use only, should not be used for diagnosis of assigning results to patient samples.
- Users should utilize most updated software version published for optimum performance and enhanced user experience.
- The user manual only provides instructions related to navigating the software.
- This user manual does not provide guidance on the clinical interpretation of results.

Scope of this Manual

This manual provides information on how to import raw data, make changes to configuration and control adjustments as necessary for analysis. It is very important to recognize that the defaults set in this program are based on One Lambda's experience with the product in a tightly controlled research and development environment. A laboratory performing typing in another environment may need to reset parameters to meet specific laboratory requirements.

From the Main Menu of TypeStream Visual, you can access the four major components of the program:

- Analyze Data
- Create Reports
- Manage Records
- Manage Database

System Requirements

The minimum system requirements are as follows:

- Microsoft® Windows® 10.0, 64-bit OS
- 4-Core processor with 8 threads, 16 GB RAM
- 8-bit graphic adapter and display with 1920 x 1080 screen resolution
- Microsoft .NET 4.8.1 Framework (included in installation package)

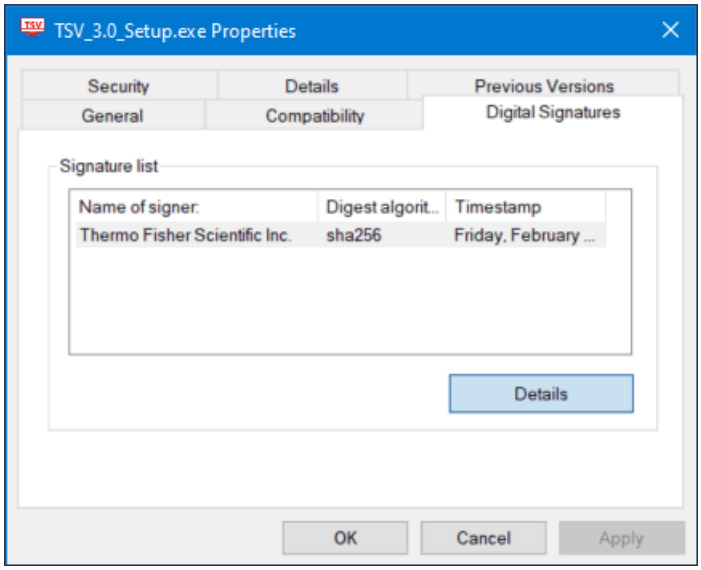
- Microsoft Visual C++ 2019 SP1 Redistributable package (included in installation package)
- Microsoft SQL Express 2014 (included in installation package)
- Crystal Reports 13.0.17 Runtime for .Net 4.6.1 64-bit (included in installation package)
- WinZip (not included in installation package)

New in v3.0

Software Signing

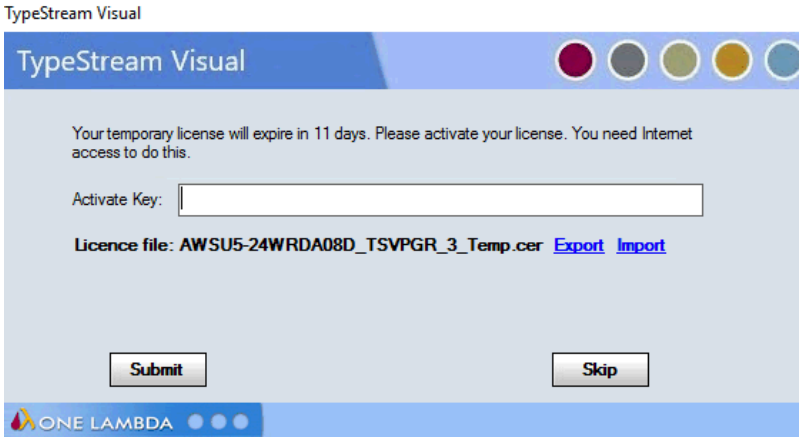
Software signing, also known as code signing, offers important protections. Software signing verifies the identity of the publisher via a third party, which helps users ensure they're installing software from a publisher they trust. The process also helps to prevent tampering and insertion/distribution of malicious code.

TSV_3.0_Setup.exe is code signed and will have a Digital Signature tab. The algorithm used for signing is sha256. Right-clicking on the file and clicking the Digital Signatures tab reveals the digital signature information:



Software Activation

IMPORTANT: When you first install TypeStream Visual, you will receive this message. The software will expire in 11 days if you do not activate your license.



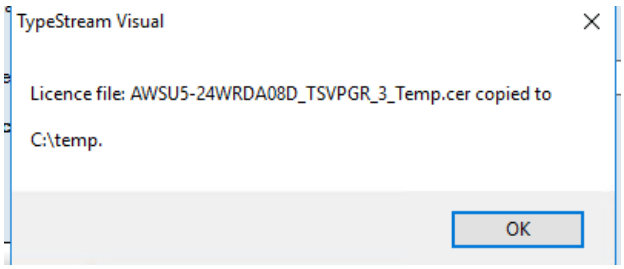
License Key Activation

TypeStream Visual requires a license key to run the application. A temporary license is provided for the first 11 days of usage, after which the software will cease to function unless a permanent license is obtained. After the permanent license is activated, the software will display a warning message at 30 days before expiration of this license. Your license information for TypeStream Visual is stored in a certificate file on your local computer

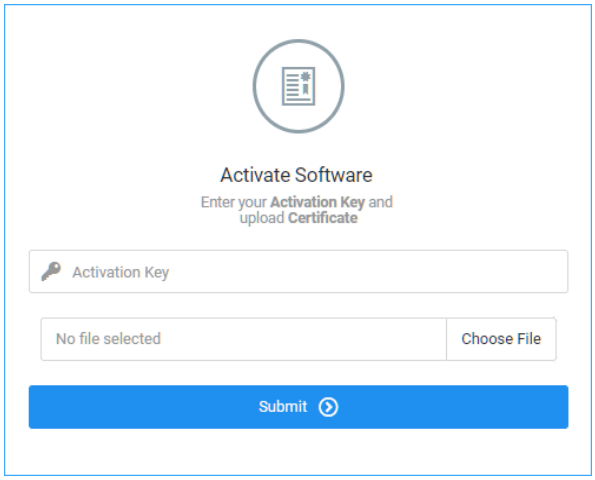
Please convert your temporary license into a permanent license as soon as possible to avoid interruption of software operation. To convert your temporary license into a permanent software license, please do the following:

1. After the initial installation, when TypeStream Visual starts up, an 11-day license reminder screen will be displayed as shown above.
2. If you do not yet have a license key, you can click Skip to ignore the warning and continue to operate the software; however, please convert your license at the earliest opportunity to avoid interrupted software operation.
3. At the reminder screen, type in your Activation key and press Submit. Your activation key can be found on your order confirmation.
4. If the activation of your license fails by using the Activate Key facility, proceed with the rest of these steps.
5. Export your certificate file to disk using the Export link. The Export for Folder box will appear and allow you to save the certificate file on your computer. Press OK when ready to save the file:

6. A message will then appear confirming successful saving of the file.

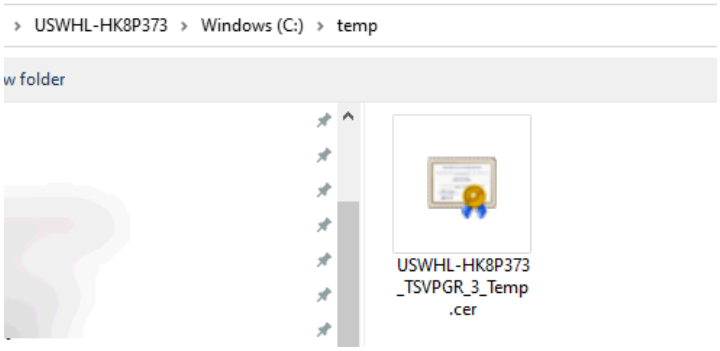


7. On a computer with Internet access, navigate to the **OLI License Renewal website** and do the following:
   a. In a web browser, go to https://forms.onelambda.com/software/activation

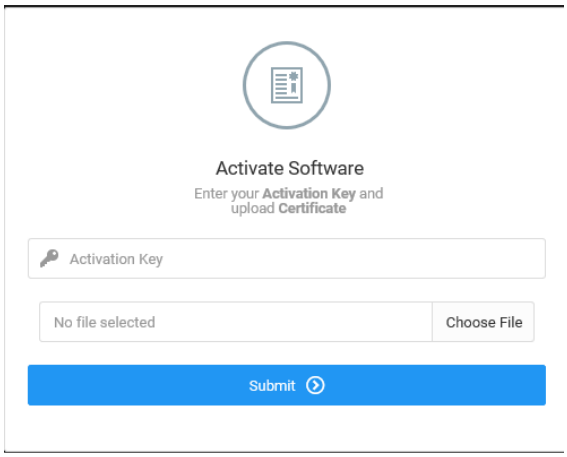


   b. Copy your certificate from Step 4 to a folder on this computer.
   c. Enter your activation key in the **Activation Key** box shown above, then click the

Choose File button (your certificate file name and location will vary from the example shown).



d. Click on the certificate file you previously saved and click **Open** (above).
e. The certificate file will be displayed in grey on the web form (shown below).

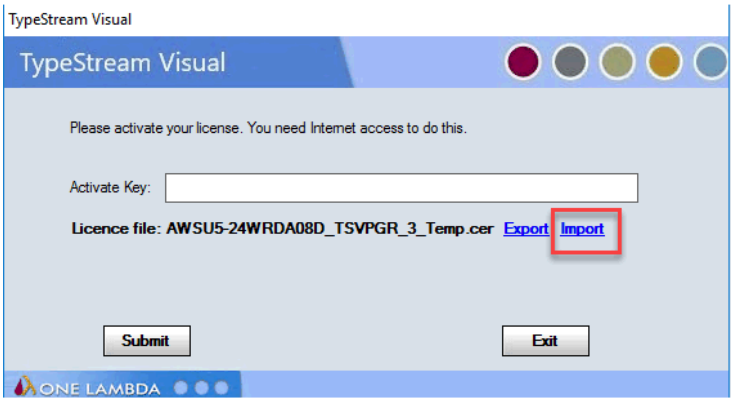


Click the blue Submit button, and observe the results:

If the operation was successful, your order information will be updated for TypeStream Visual and it will convert your temporary license into a permanent license.
Click on the Download button to download your certificate with your permanent license.
Copy your certificate file with your permanent license, back to that the computer you are attempting to activate TypeStream Visual.

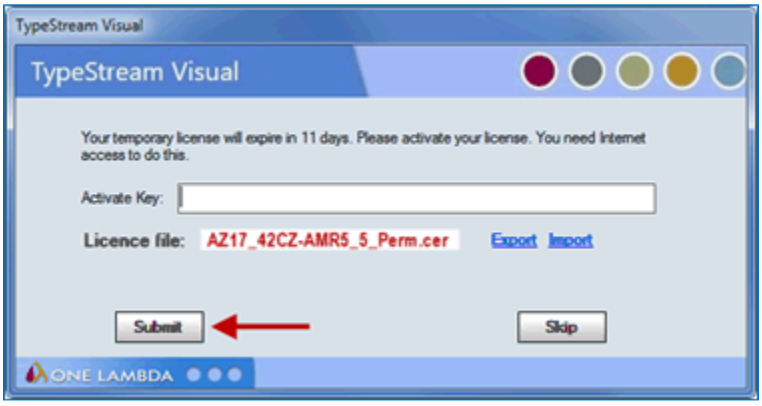
8. Startup TypeStream Visual. If the program runs successfully, you are finished with the licensing procedure. Skip to Step 9.

9. Click the **Import link** on the reminder screen to install the certificate with permanent license that you obtained from the website:



10. A selection box will appear and allow you to choose the certificate file to import into TypeStream Visual:

11. Once the new certificate file has been selected, it will be displayed in the **License file field.** At this point, click **Submit:**



Installation

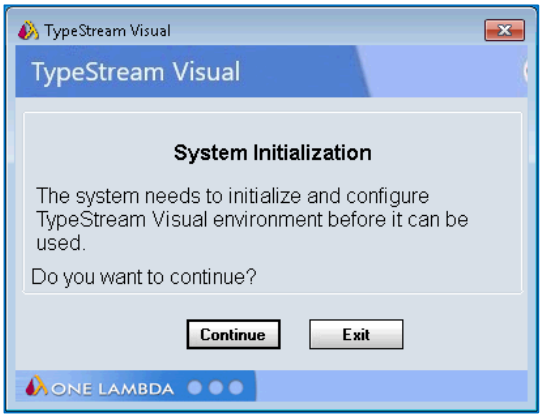
Proceed with the installation as described in the Installation Guide.

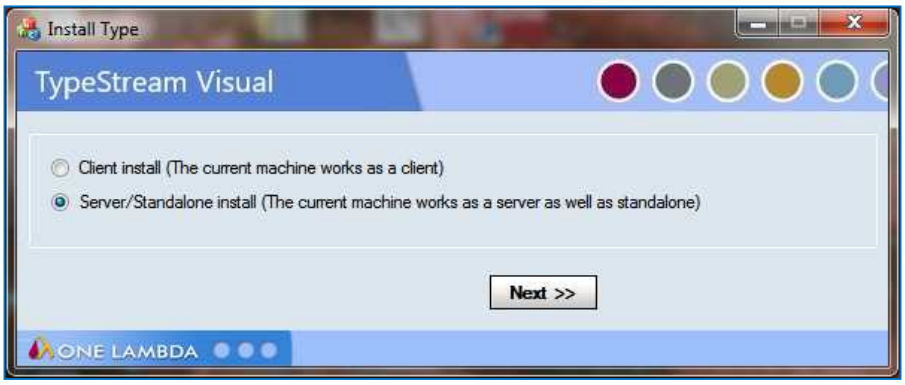
Launch Application

When installation is complete, select the check box for Launch TypeStream Visual 3.0, and then click the Finish button.

The installer automatically launches the TypeStream Visual application (This may take a few moments.) If TypeStream Visual does not start, double-click the TSV 3.0 icon on your computer desktop

If the TypeStream Visual database connection is not yet set up when the program is launched, (as is the case the very first time it is launched) a System Initialization message is displayed to indicate this. Click the Continue button.





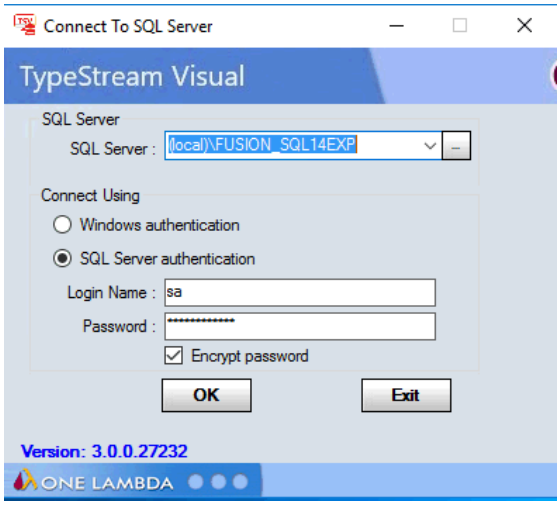
Select Server/Standalone installation type from the TypeStream Visual Database Utility window that displays after TypeStream Visual has been installed.

Connect to a SQL Server

New in v3.0

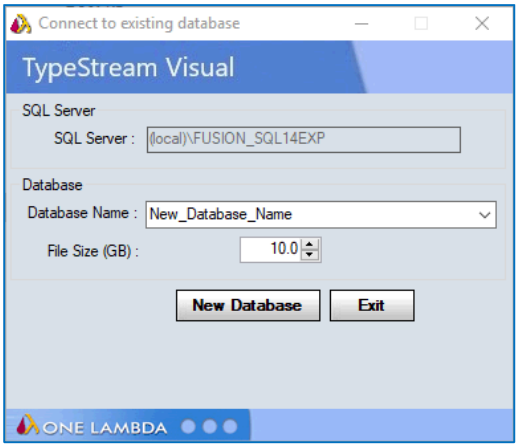
In TSV 3.0, security has been enhanced. TSV provides an option for users to encrypt password. Choosing the option, will encrypt the database server password in the application config file.

Note: You can also now use all editions of Microsoft SQL 2019.



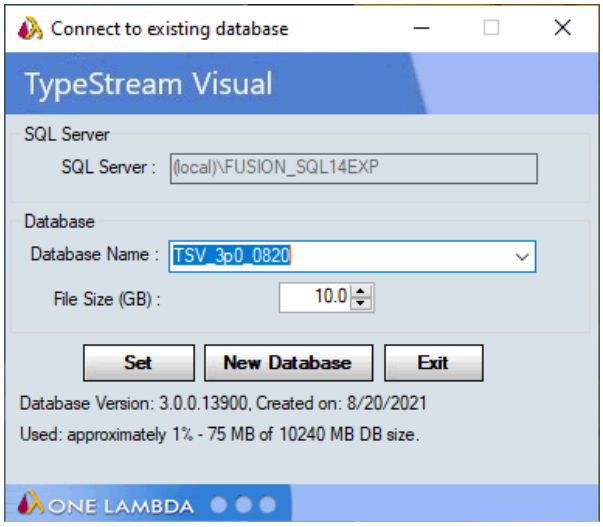
Make sure your SQL Server information is correct and click the OK button. The Database Utility Main Window is displayed.

12. Select a SQL Server by doing one of the following:
    a. Type in the full path, directory, and server name.
    b. Click the drop-down arrow in the SQL Server field to display a list of local SQL Servers.
    c. Click the Browse button ... to display a list of SQL Servers available from your network.
13. Select a security connection type. SQL Server authentication is recommended.
14. For SQL Server authentication, enter Login Name and Password, (Windows authentication usually requires configuration by administrator).
15. Click the OK button.

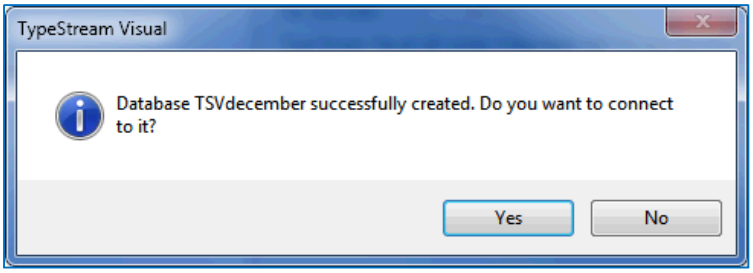


Connect to a Database

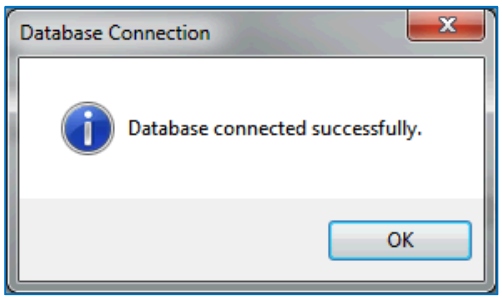
16. Create a new database and/or connect to an existing one
    a. Instructions for connecting to an existing database
        i. Select existing database from dropdown menu.
        ii. Click the Set button.



    b. Instructions for creating a new database
        i. To create a new database, enter a unique name for the new database, and click the New Database button.
        ii. It is highly recommended that database names contain no spaces or dashes.
        iii. After the database has been created, click the Set button (above).



A confirmation message is displayed when you have successfully connected to a database:

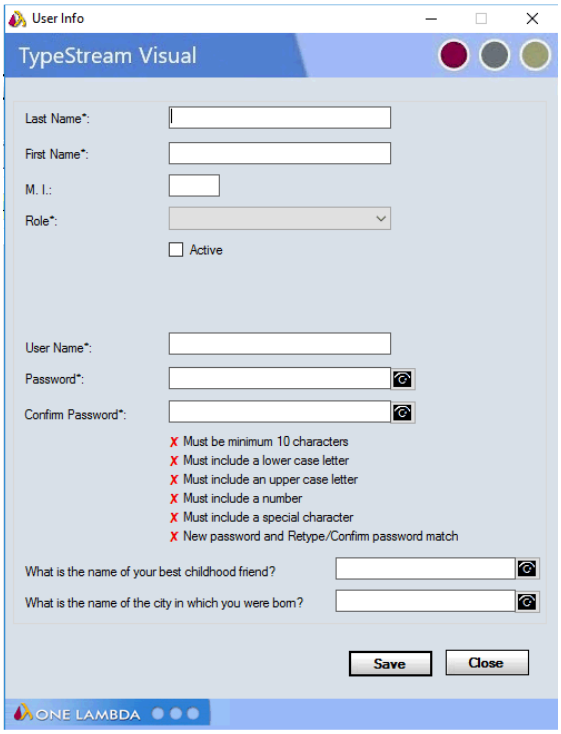


Click the OK button. The TypeStream Visual application should automatically launch. If it does not, double-click the TSV 3.0 icon located on your computer desktop.

When the database connection is set the password to the server is encrypted and saved in the config file if the Encrypt Password option is selected.

17. Set Up the first user profile and lab information

    When the software launches with a connection to a new database, the User Info Screen appears. Fill in all required fields, (denoted with an asterisk*****) to set up a User Profile and click the Next button.

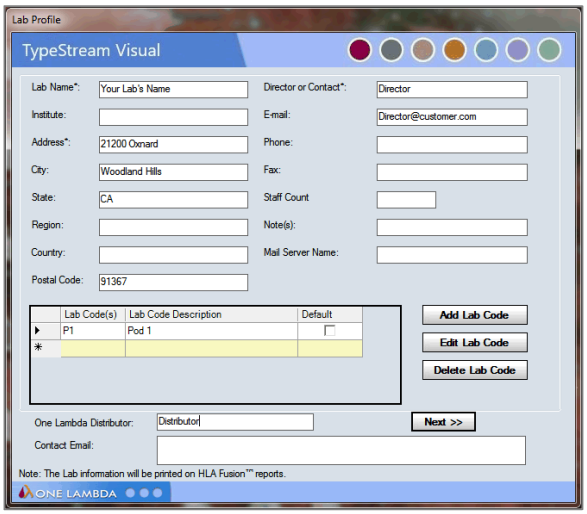


Enter all necessary information on the Lab Profile Screen (an asterisk * denotes required fields)

Click the Next button. *(See next chapter for more information.)*

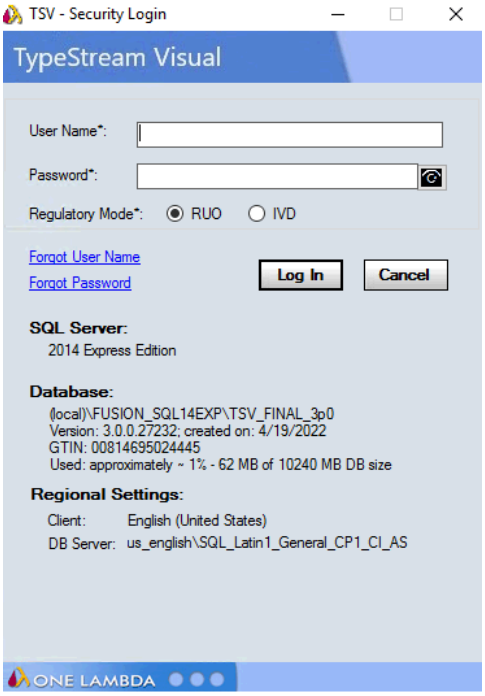
NOTE: The first user is always set to the Lab Supervisor Role. See more detail about Supervisor vs. Technician roles and permissions under "User Profile" in Chapter 2. Lab name , contact information and regulatory mode will be displayed in the footer section of the TypeStream Visual reports.

NOTE: If you will be using TypeStream Visual to generate NMDP code reports, add a Lab Code to the Lab Profile.



Log in

Log in to TypeStream Visual using the credentials entered during installation/configuration.

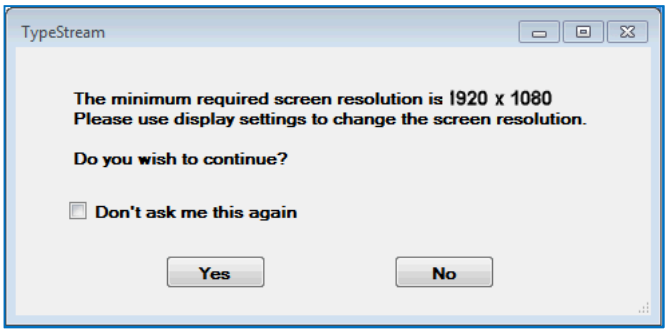


1. IVD and RUO mode - No mode is selected for new database. Once a selection is made, the software will default the selection to the last used mode. When in IVD mode, only IVD SKU's can be used for analysis and data generated from IVD SKU's are available for reporting. When in RUO mode, only RUO SKU's can be used for analysis and data generated from RUO SKU's are available for reporting. Analysis of datafiles generated from Long-Read Sequencing (LRS) and Long-Read Processing (LRP) platforms are only available in RUO mode.
2. Version of SQL server used
3. Database which is currently active in TypeStream Visual
4. GTIN number: a number established in the GS1 database for Unique Device Identification (UDI).
5. Database Collation

Key System Settings

Screen Resolution

TypeStream Visual software requires a minimum screen resolution of 1920 x 1080. The software displays a message if your current resolution is less than the expected generals.



You can select 'Yes' to continue to start the application or No to exit the program.

In addition, if your computer is running Microsoft® Windows 10®, the text display size setting must be set to "Smaller - 100% (default)." Take these steps if you need to adjust this setting:

1. Right-click on the computer desktop. Select the Screen Resolution option.
2. Select Smaller sized text.

Software may not resize for full view of graphic user interface if the window is not maximized. This truncated view is eliminated by maximizing the screen.

File Permissions

All TypeStream Visual users must have read and write permissions to the following directories and files:

- C:\Program Files (x86)\One Lambda\
- OneLambda.Fusion.Interface.exe.config
- ReportMap.xml
- C:\OLI TSV\ (and all the sub directories and the files in these directories)
- C:\ProgramData\One Lambda folder (Note: C:\ProgramData is a hidden folder)

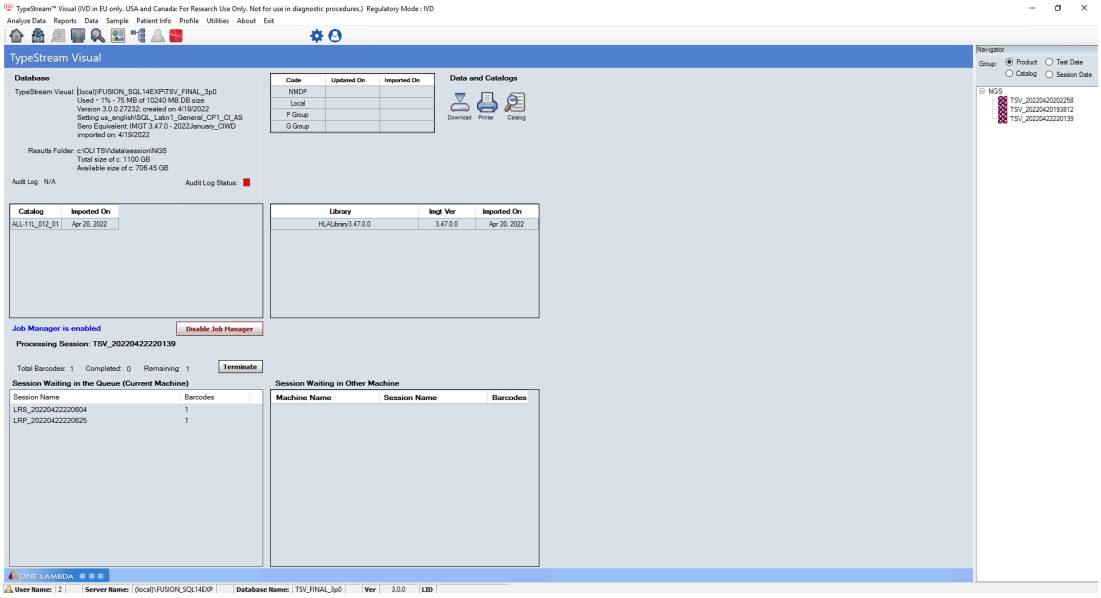
2

Application Setup

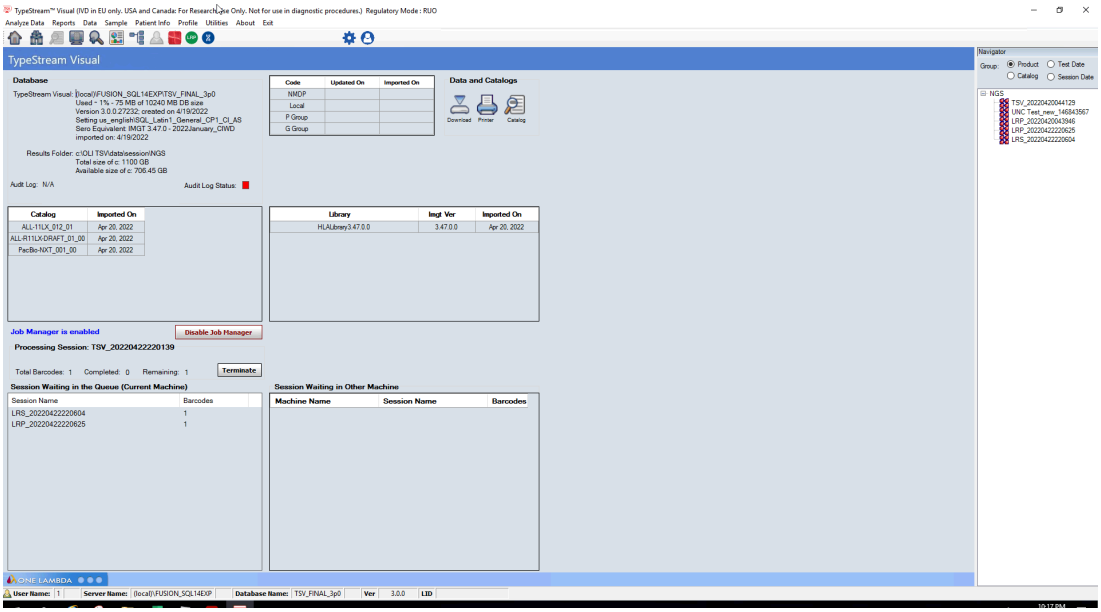
Home Page

Login will take you to the home page.

IVD mode



RUO mode



The window title displays the mode that the user is logged into the application.

> **Important:** TypeStream Visual is optimized for use with Microsoft Windows when set to 100% zoom.

Home page contains information on the following:

- Database status
- Active catalogs
- Active library
- Reference files
- Job Manager - which session is currently on the engine and what is waiting in the queue
- Toolbar and Menu Options

See the following chapter for more information on these topics.

Profile Management

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

User Profile

From the Profile main menu, you can:

- Add new users
- Edit existing user profiles

Change passwords
Reset passwords
Archive users

TypeStream Visual uses two user levels for added security and control of typing and screening results.

Supervisor	Technician, if given specific permission
Modify all product configuration settings	Modify all product configuration settings—except to enable Auto Accept All
Save and Confirm analysis results	Analyze data and save analysis results
Update reference files, such as catalogs and NMDP codes	*(Only if authorized by the supervisor)* - Update reference files, such as catalogs and NMDP codes
Archive catalogs	Archive catalogs
Modify and delete session and sample data	(*Only if authorized by the supervisor*) - 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.

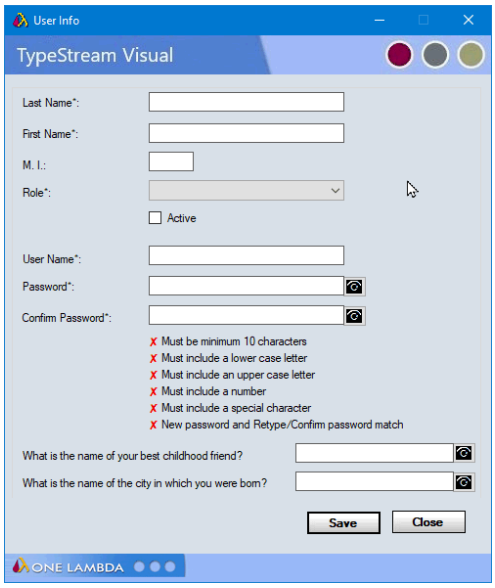
1. From the Main Menu, select Profile > List User.
2. Click Add User to add a new user.
3. Enter new user information.
4. Select the Active check box under the Role field to activate the user account.
5. Click Save to save the new user information and return to the main menu or click Close to discard changes and return to the main menu without saving.

NOTE: If this is a lab tech profile and you want to allow reference file update, configuration update and/or data management privileges for this user, select the appropriate check boxes. Lab technicians are unable to save any updates made in the Analysis parameters, exclude region and health metrics option if their profile to update configuration is disabled.

New in v3.0

The "eye" control allows the user to temporarily view sensitive fields (user password and security answers when entering the data.

In addition, there are new rules for password complexity, as listed in the screen. The software will not allow you to continue until all listed conditions (those with a red X by them) are satisfied in the new password:



When saving New User profiles, the answers to the security questions are encrypted in the database.

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.
2. 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.
3. Edit user information.
4. Click Save to save user information and return to the Main Menu.
5. Click Close to discard changes and return to the Main Menu without saving.
6. You will not be able to modify a username.

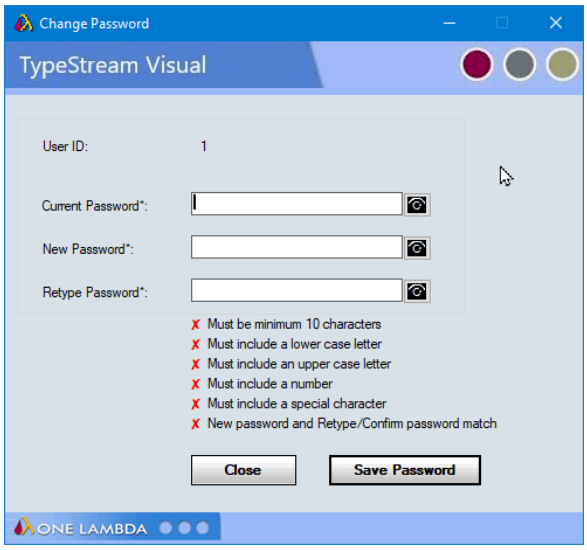
Changing Passwords

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.

New in v3.0

When changing a password, password fields are hidden from view for security. The "eye" control allows you to temporarily view them when entering. Also, password complexity rules have been added. The software will not allow you to continue until all listed conditions (those with a red X by them) are satisfied in the new password:

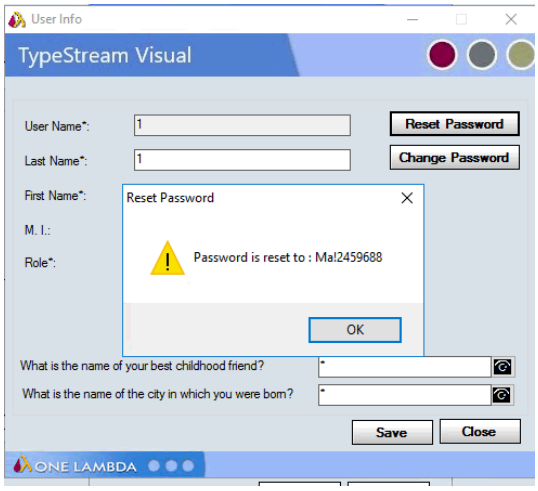


Resetting Passwords

If a user loses or forgets their password, TypeStream Visual can reset the password. 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.

The system displays a random password. Clicking on OK will copy the newly generated password to clipboard.



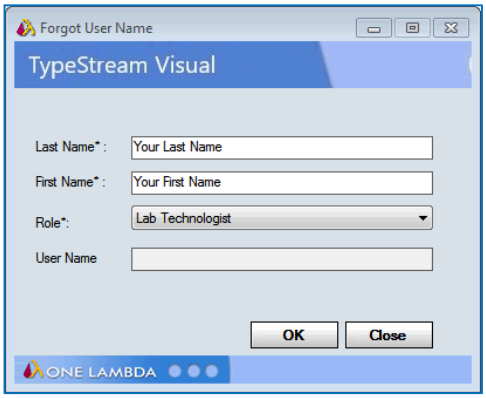
Changing User Privileges

Only Supervisors can modify a user's privilege level.

1. From the main menu, select Profile> List User
2. Double-click to the left of a user to open their profile.
3. 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 TypeStream application.
4. Click **Close** to return to the Main Menu.

Retrieving a Forgotten Username or Password

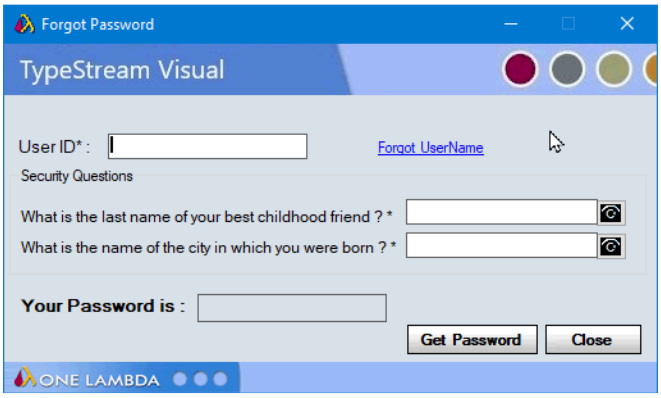
If you forget your Username, click the Forgot Username link, enter your first and last name, and select your lab role, (supervisor or technician). The system displays the username matching the data you provide.



If you forget your password, click the Forgot Password link and answer the two security questions you were asked when you set up your user profile..

New in v3.0

When retrieving your password, as before in the Change Password section, the answers to sensitive security questions are hidden and the **eye control** can be used to view them temporarily when the button is held down with the mouse:



When correct answers are supplied, click the Get Password button.

The password is then displayed in the box "Your Password is" when the questions are answered correctly.

The answers to the security questions are encrypted in the database.

Deactivating Users

Supervisors can deactivate users who are no longer using TypeStream Visual. 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.

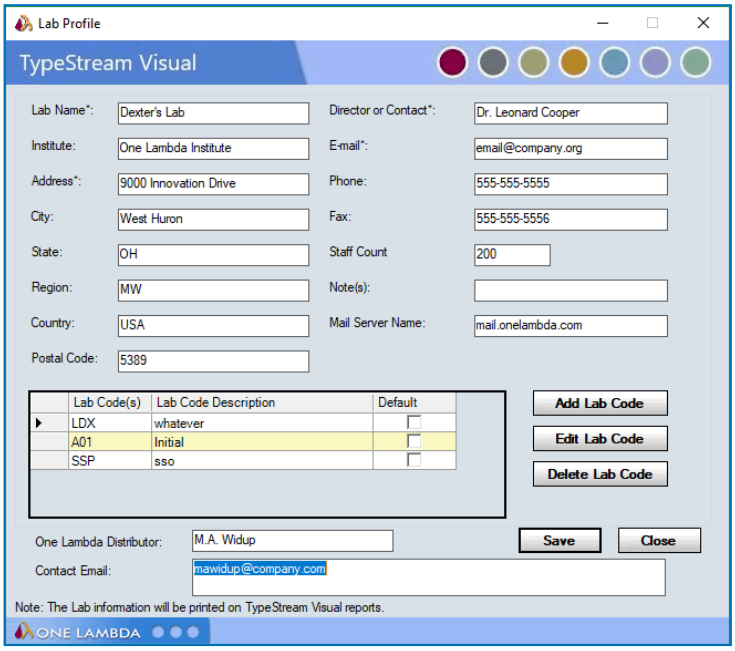
NOTE: If a User ID is still associated with analysis records, the User ID cannot be deleted.

Lab Profile

The Lab Profile menu displays the contact information for your lab, network information used by TypeStream Visual, 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 TypeStream Visual. 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. Add, edit or delete Lab codes:
    a. Click Add Lab Code to add a new lab code. Enter information into the new row.
    b. Highlight a lab code to be edited. Click Edit Lab Code to edit the lab code.
2. Edit lab code information.
3. Highlight a lab code to be deleted.
4. Click Delete Lab Code to delete the lab code.
5. 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.

New in v3.0

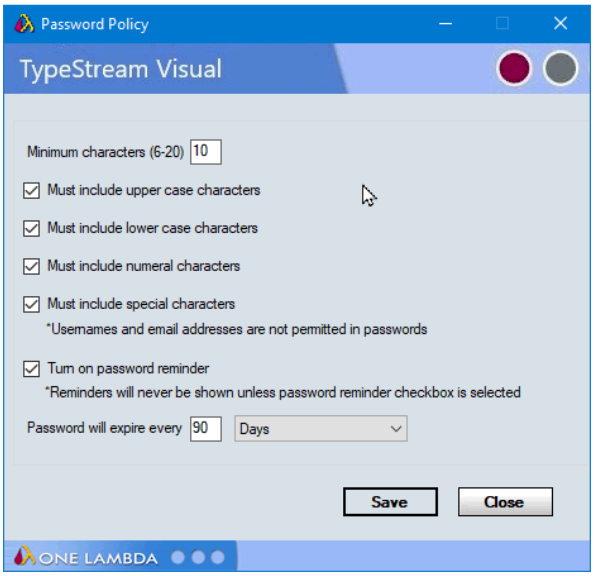
Manage Password Policy

The Manage Password Policy menu is a new feature that enables a strong password policy to be implemented in TSV 3.0, including periodic reminders to change the password. Only lab supervisors have the ability to manage the password policy for a lab.

1. From the main menu, select Profile > Manage Password Policy**.**
2. Edit password complexity rules as desired by choosing options.
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.

The password requirements will be enforced in all areas of the software that allow setting or changing a password. A minimum password length (default is 10 characters), upper case characters, lower case characters, numerals and special characters may be selected as required elements in passwords.

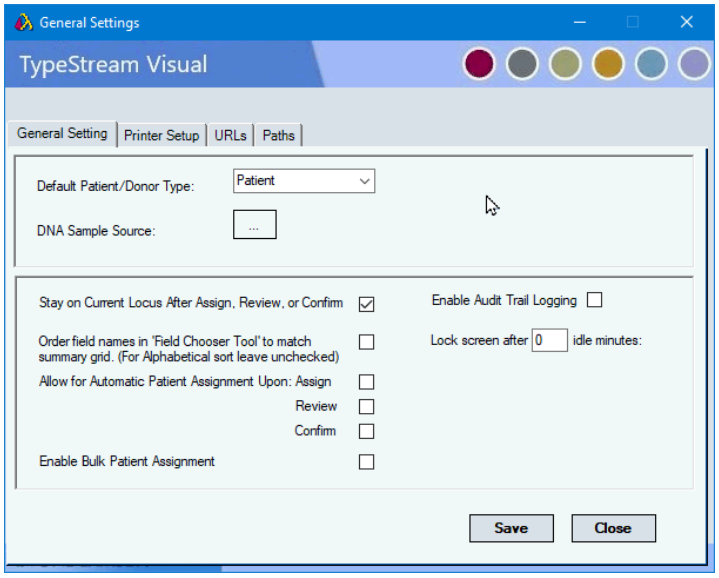
User can also select the password reminder option. If unchecked user will not have a reminder shown to them before password expiry. The user is forced to change the password on the day of expiry to log in back into the application. If the password reminder option is selected, the user is reminded of password expiry upon login starting 11 days before expiry.



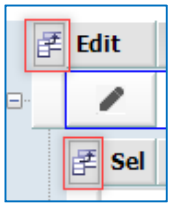
General Settings

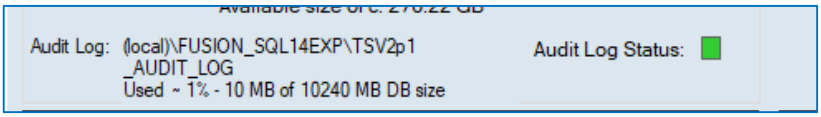
You can set a number of general system settings, including printer defaults and URLs and Paths.

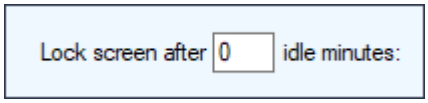
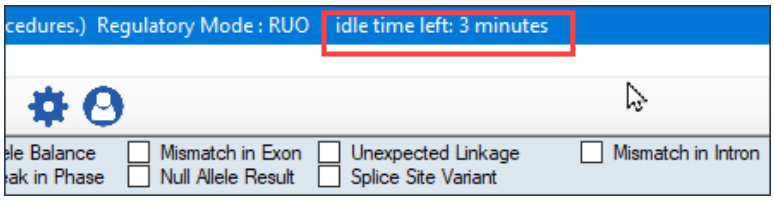
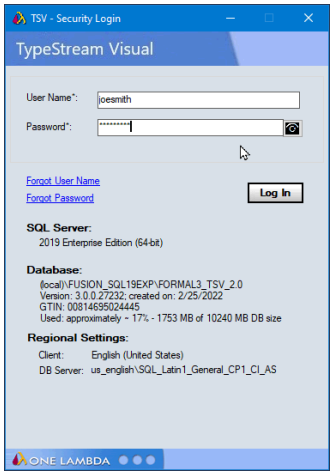
- Select Utilities → General Settings from the TypeStream Visual main menu. The General Settings dialog box is displayed.



- Use the drop-down menus or select check boxes as appropriate to make your selections on this dialog window.
- When you have made all of your selections, click Save.

Item	Definition
Default Patient/Donor Type	The three options are Patient, Donor, or Both. This applies to the creation of new sessions. "Patient/Donor" column on the far right of the sample row will default to the selected option if there is no value already associated with the sample.
DNA Sample Source	The four default options for sample source are Cord Blood, Whole Blood, Filter Paper, and Buccal Swab. User is able to additional sources. The software will not auto-fill source for samples where the source is not given, but a sample source cannot be input on the session import page if it is not on this list.
Stay on Current Locus after Assign, Review or Confirm	When unchecked and the user Assigns (Reviews or Confirms) A locus, for example, the software will automatically move on to the next unassigned or unreviewed or unconfirmed locus. If there is no other locus in the current sample that meet the criteria the software advances to the next sample. When checked, the software will remain on the locus that was just assigned. NOTE: When this option is checked, the designation of "Assigned", "Reviewed" or "Confirmed" will display in the Analysis Panel near Assignment History.
Order field names in 'Field Chooser Tool" to match summary grid. (For Alphabetical sort leave unchecked.)	 On session summary screen, clicking on the icon at the far left on either session or locus header row will bring up the 'Field Chooser' tool, allowing the user to select which fields to display in session summary. When unchecked, the selectable fields will display in alphabetical order. When checked, the fields will display in the order in which they will appear on the sample or locus header. *See session detail section for more information.*

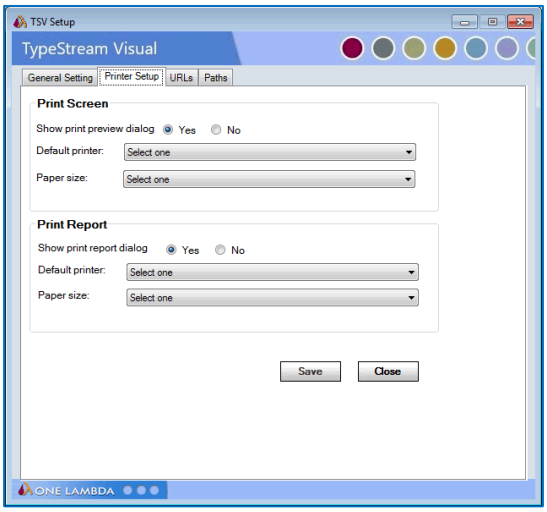
Allow for Automatic Patient Assignment Upon: Assign, Review, Confirm	When checked, the locus assignments will automatically be assigned to the patient file for Assign, Review, and/or Confirm as checked.
Enable Bulk Patient Assignment	When this checked, the user is able to assign, review or confirm patient assignments in bulk.
Enable Audit Trail Logging	When connected to an audit database, will track all changes made by all users. This functionality is available only to Supervisors and Technicians with "Can manage data" privileges. If this is enabled, the audit log status on the Home screen would appear in green color. 

Lock Screen	**New in v3.0** Locks the screen after a user-configurable number of minutes. Sessions that are in the middle of analysis are not disturbed. A visible countdown timer appears at the upper border of the screen that shows the remaining time before the screen is locked. Set to 0 minutes to disable.  When a whole number is entered and the Save button is clicked, the timer is activated. The next time a user fails to move the mouse or keyboard for the set amount of time, the countdown timer begins counting down in increments of minutes. The count appears at the top of the screen. When it gets close to zero, it animates quicker down to 0 in seconds:  If the timer reaches 0 seconds and the mouse or keyboard are not moved, the screen is locked and the Security Login screen appears. If the correct username and password are supplied, the application resumes execution.  Any user can set the timeout value or activate the feature while running the software. The mode are not displayed for the user to select. The user will have to log back in the application in the same mode that was logged in before the timeout.

Printer Defaults

From the Printer Setup tab on the General Settings dialog box, you can select settings such as default printer and paper size, which will be in place when you print reports or do a print screen.

1. Select Utilities > General Settings, and click the Printer Setup tab.+



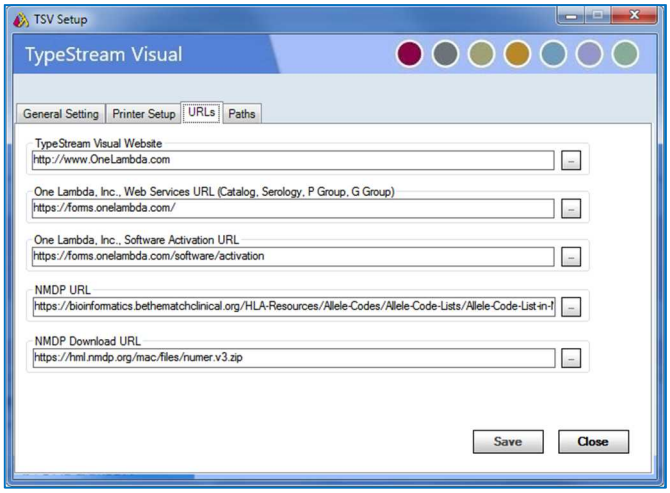
2. Select from the following options for both the Print Screen and Print Report panels of the dialog box:
    a. If you want to see a print preview or print report dialog each time you print, make sure the Yes option is selected. Otherwise, select No.
    b. If you do not want to select a printer each time you print, select the default printer and paper size from the drop-down menus.
    c. This default printer configuration may be overwritten by the specific page properties of certain reports.
3. Click Save [Save].

Setting TypeStream Visual Default URLs and Directory Paths

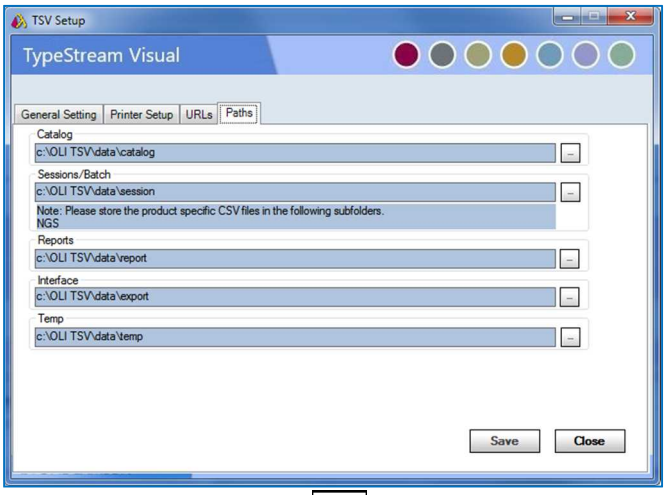
The URLs & Paths option under the General Settings menu allows you to set the default URLs for OLI and NMDP websites to download reference and catalog files, and product updates. This option also allows you to set the directory path where TypeStream Visual, by default, stores catalogs, session/batch 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 TypeStream Visual home page select Utilities > General Settings from the main menu.
2. Select the URLs tab.



3. Enter a URL and verify it works by clicking [...].
4. Click the Paths tab.



5. Use the browse button [...] to locate the directory you want to use for the specified purpose (e.g., where you want to store reports when they are generated).
6. Click Save [Save].

NOTE: In using the Restore Database function (see Chapter on databases), if the user restores a database .bak file from one machine to another, the NGS Session folder must also be copied to the destination machine and the path in General Settings must point to the folder path.

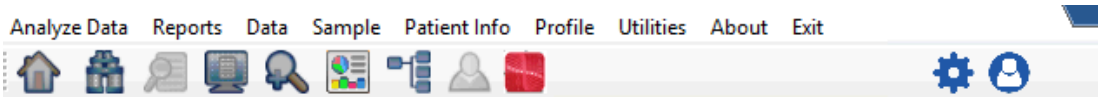
3

Utilities and Support Functions

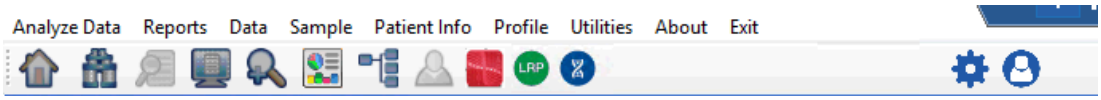
Toolbar Functions

TypeStream Visual provides a toolbar, displayed just below the main menu bar options with access to commonly used functions.

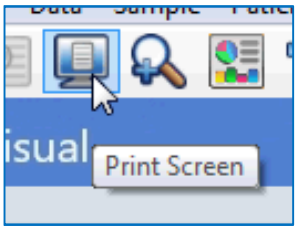
IVD mode



RUO mode



When you hover your mouse over the buttons, a label will pop up with the name of each button.



Home

Clicking this icon from any other page returns the user to the Home screen. This can be

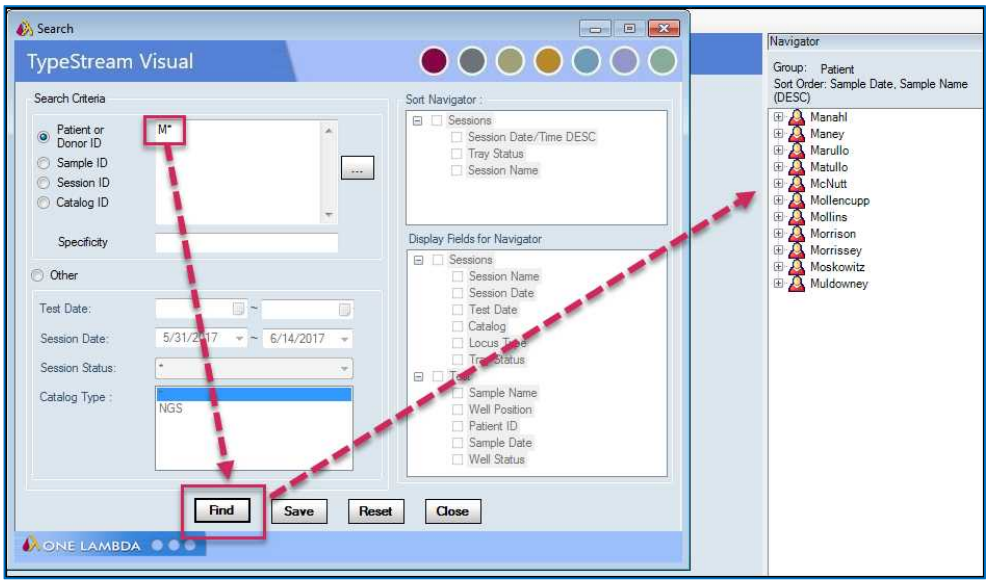
especially useful after submitting sessions for analysis in order to check their progress.

Find: Search

Click the Find ("Bino") button to open the TypeStream Visual Search Window to look for records using various criteria. The Find dialog box also allows you to modify the Navigator Session sort and display criteria.

To use this tool, do the following:

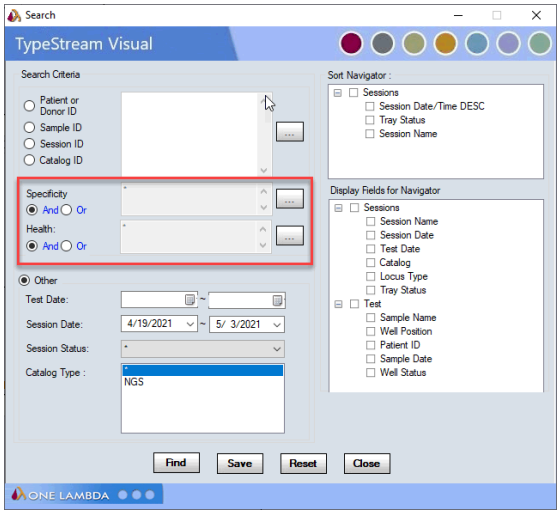
1. Enter a search parameter into the area of interest. In the example below, user wants to find all sessions with a Patient ID beginning with 'M.'
2. Click Find.
3. The Navigator displays all sessions that fit the search parameter with the sort order described above the listing.



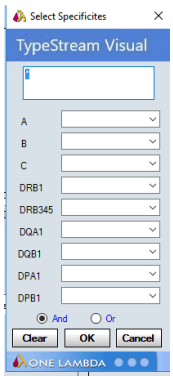
The date range set here, in the Session Date field, is used as the default date range throughout TypeStream Visual, such as in the Navigator and Reports windows. Each time you change it, and click the Find button, the default changes for the rest of the application.

Wildcards such as * (multi-character) and % (single character) can be used to find sessions.

The sessions displayed on the navigator is based on regulatory mode selected.

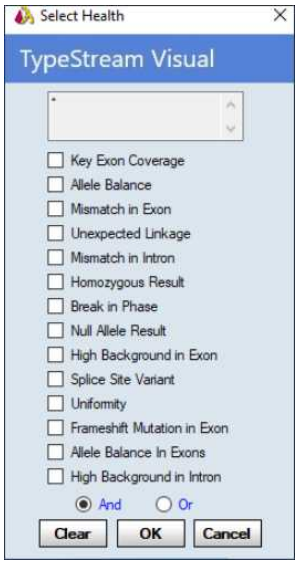


Search by Specificity



Allows users to enter one or more alleles into the search field by separating them by commas. Samples that have the alleles assigned in the computer suggested or in the final assignment are displayed.

Search by Health



Allows users to search samples by the health metrics.

New in v3.0

The High Background in Intron filter has been added (shown).

Quick Reports (Print Preview)

This button allows the user to quickly create any of the following reports for the selected session without having to go to the reports page. When a session is selected which originated from LRS, Illumina or Ion Gene Studio S5, the following options will display:

A. XML Report
B. Genotype Summary (.pdf)
C. Genotype Summary Table (.csv)
D. Genotype Summary Health (.csv)

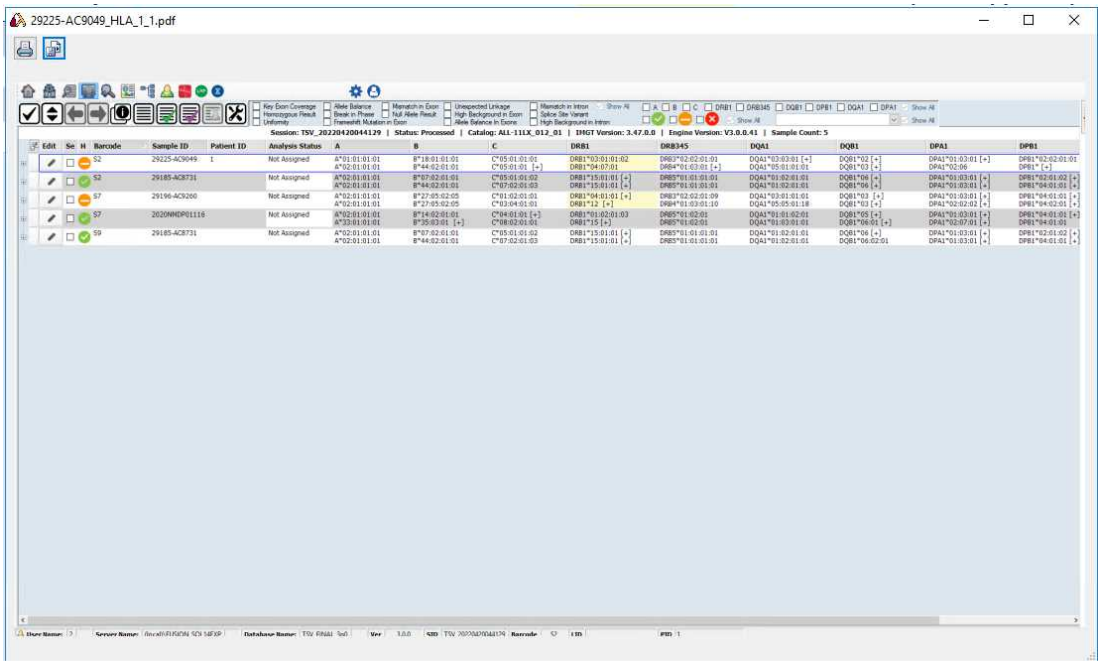
When a Long Read Processing (LRP) session is selected, only the following option will display:

E. LRP Genotype Summary (.pdf)

Reports created will adhere to default settings.

Print Screen

From any Analysis Screen, click the Print Screen button to open a new window containing a screen shot of the current analysis window. Click the Print button, (top, left corner) to send the screen shot to the printer. The software will use the configuration selected for "Print Report" on the settings configuration page. The sample name will display on the top left corner in the format "[Samplename]_HLA_[patient first name_patient last name]."



To close this window, click the Exit button or the Close button.

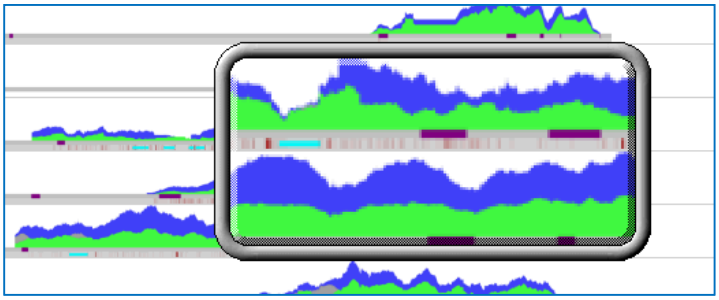
If more than one sample is selected in the summary, then the screenshot is labelled with the last sample that is selected.

Magnify

From any Analysis Window, click the Magnify button to activate the magnifying glass and enlarge any section of the window. Use your mouse to move the magnifier and use the arrow keys on your computer keyboard to increase or decrease the height and width of the magnified area.

Use the right and left arrow keys on the keyboard to increase and decrease the size of the magnified area.

Click anywhere on the screen to deactivate the magnifying glass.



Show Navigator

If the TypeStream Navigator, (normally displayed on the right side of the application window) is not visible, click the Show Navigator button on the toolbar. Once the Navigator tab is displayed, move your cursor over it to slide the Navigator panel open.

Patient/Donor Information

From any Analysis Screen, click the Patient button to display the Patient/Donor Information Screen where you can enter or edit information related to a patient or donor and associate it with the current sample.

You can also open the Patient/Donor Information screen at any time by clicking Patient Info on the TypeStream Menu Bar, followed by Manage Patient.

For detailed information on the operation of this screen and its tabs, please see the section entitled Patient Management.

NGS Session Builder

To create a session to analyze raw data from either Ion S5 sequencers or Illumina MiSeq or MiniSeq sequencers, click the "Analyze S5/Illumina data" icon. This opens the Create Session page in which the user may designate the path to the raw data and then select the analysis parameter set, IMGT library version, and catalog for analysis. This feature is available in both IVD and RUO mode.

Long Read Processing (LRP) Session Builder

To create a session to analyze raw Long Read Processing (LRP) data, click the green "Analyze LRP data" icon. This opens the Create Session page in which the user may designate the path to the raw data and then select the analysis parameter set, IMGT library version, and catalog for long amplicon analysis. This feature is available when RUO mode is selected during login.

New in v3.0

Analyze LRS data

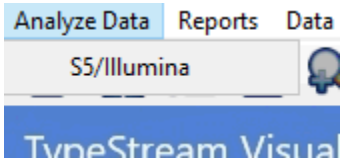
To create a session to analyze raw Long Read Sequencing (LRS) data, click the blue "Analyze LRS data" icon. This opens the Create Session page in which the user may designate the path to the raw data and then select the analysis parameter set, IMGT library version, and catalog for analysis. This feature is available when RUO mode is selected during login.

Main Menu Options

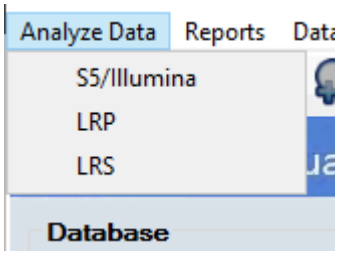
You can access TypeStream Visual functionality at any time from the toolbar's Main Menu, which is displayed at the top of all TypeStream Visual application windows. See the following sections for a list of the options available under each main menu item.

Analyze Data

In IVD mode raw data files can be analyzed coming from Ion S5 and Illumina sequencers using this file option.



In RUO mode raw data files can be analyzed coming LRP and LRS sequencers using this file option.



Reports

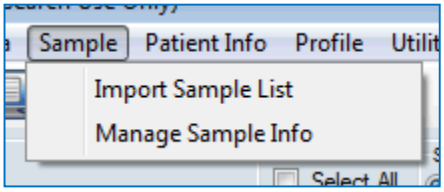
When you select this menu item, the Reports Page is displayed, allowing you to create standard or specialty reports for your analyzed data. *(See Reports Section for detailed information.)*

Data

When you select this menu item, a Data Window displays that allows you to manage, (i.e., search for, delete, archive or activate) sessions and samples. *(See Data and Session Management for detailed information.)*

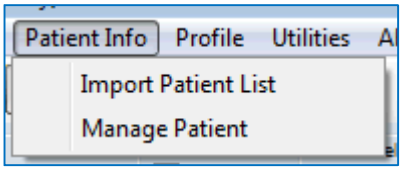
Sample

Options under this menu item pertain to importing, creating and managing sample information. *(See Sample Management)*



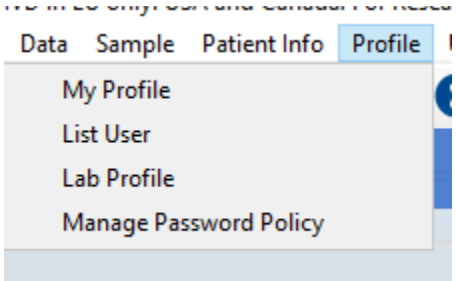
Patient Info

Options under this menu item pertain to importing patient/donor lists and managing individual patient/donor information. *(See Patient Management)*



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 and navigation preference. *(See profile management for more information.)*



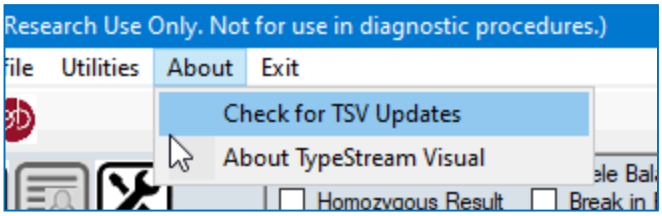
Manage Password Policy menu item is disabled when a Lab technician is using the application.

Utilities

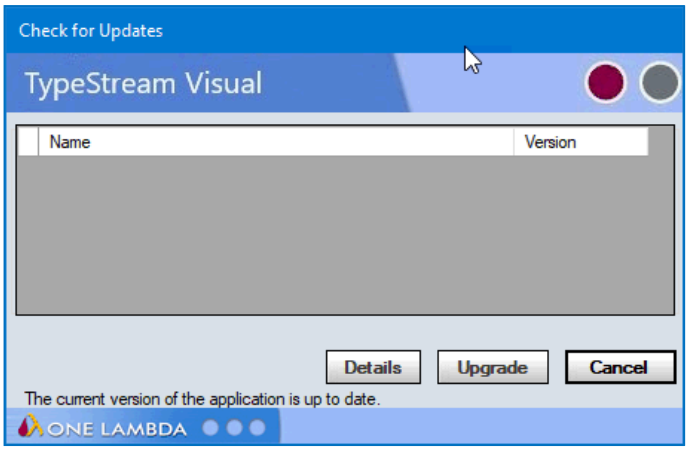
See next section.

About

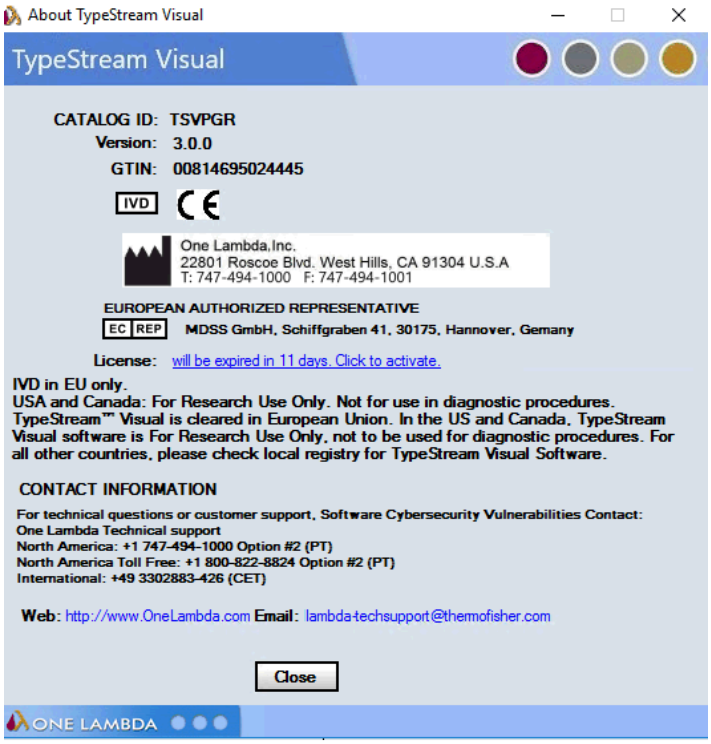
This menu item gives the user two options – to check for TSV updates, or to view application information.



"Check for TSV Updates" brings up the following screen. Progress bar displays while it searches to find possible updates to the software. Any available upgrade will display in the grid. User may then select an upgrade to either view the details or perform the upgrade. The process may be cancelled if user decides not to upgrade at this time.

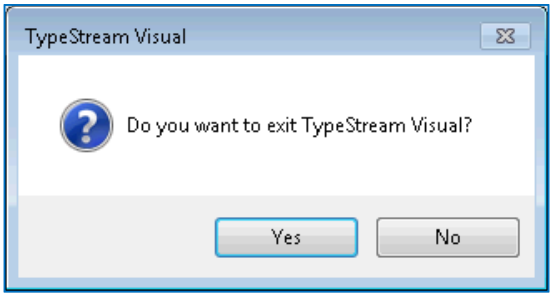


"About TypeStream Visual" allows you to access the following TypeStream Visual Software information:

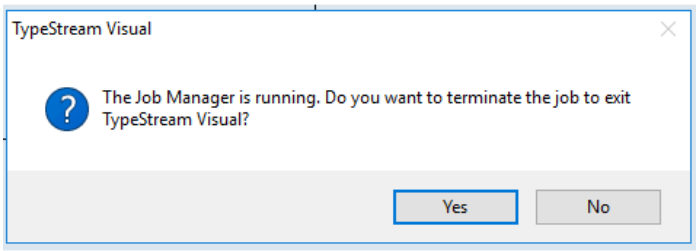


Exit

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



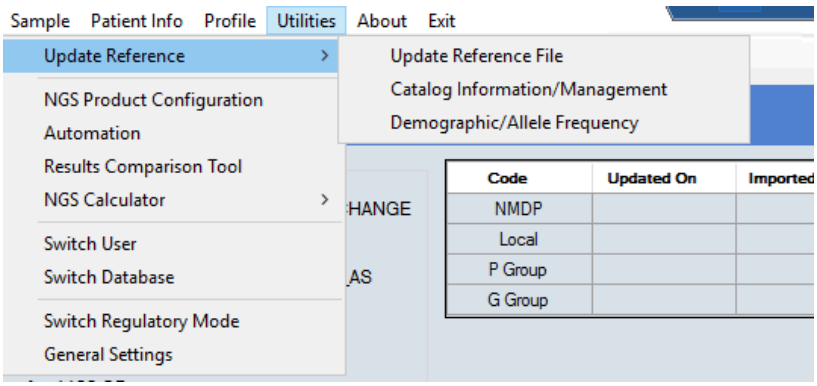
User is prompted with the below message when the Job Manager is running, and the user clicks the Exit menu item.



Utilities

All the controls governing how your files are processed, from catalog and library import to serology settings or metrics to be flagged after analysis are all conveniently located under "Utilities."

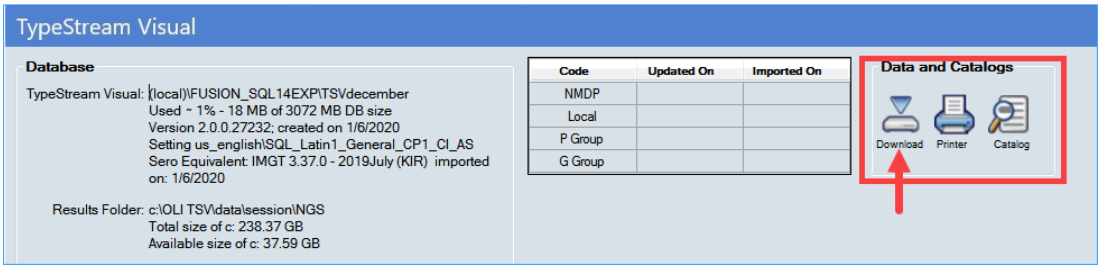
The options under this menu item pertain to importing catalog, code, and serology files, configuring the molecular products, and setting up your TypeStream Visual system. It also allows you to switch users, switch databases, and set up automatic analysis.



Update Reference Files

TypeStream Visual uses a variety of reference files 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.

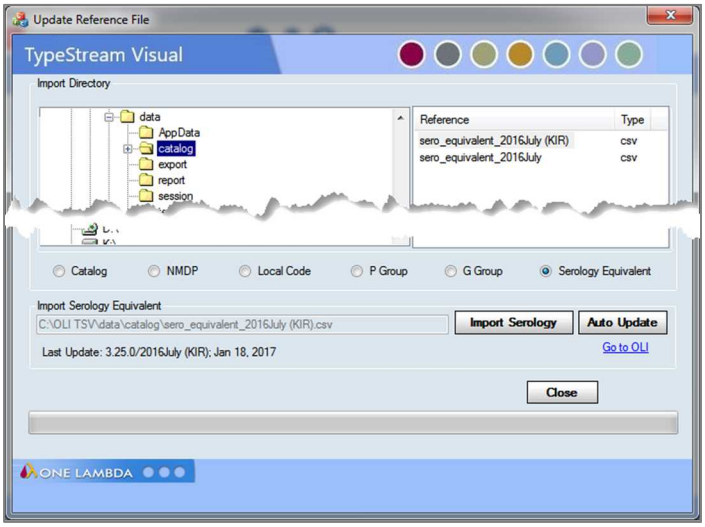
There are two way to access the screen for reference file selection. The first is to click the Download button under Data and Catalogs.



The second way is to navigate to Utilities → Update Reference → Update Reference File. Either method will open the Update Reference File window.

Prior to first analysis, a number of configuration steps will need to be taken. Follow the steps below.

1. Set Serology Reference File
   a. Navigate to Utilities → Update Reference → Update Reference File.
   b. Click 'Serology Equivalent' radio button and click on Auto Update button
   c. Select sero_equivalent reference files from list, click 'Import Serology':



New in v3.0

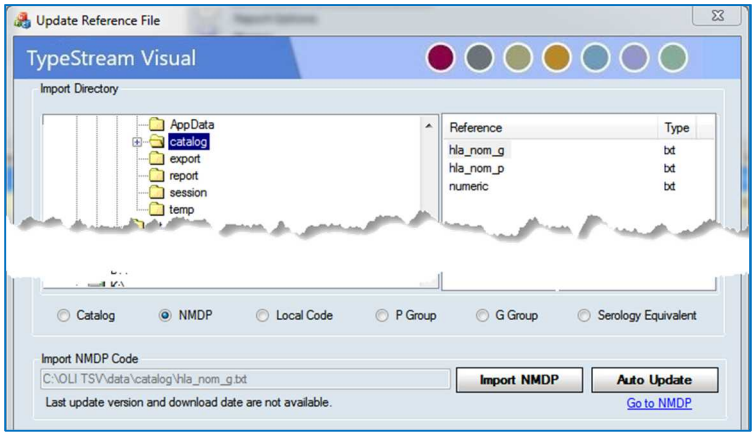
Note: Upon successful import of a Serology file, a new demographic filter is created in the database with the name CWD_TDX_#NOM#.

The CIWD_TDX_#NOM# filter is created based on the serology file format. If the serological equivalent file has a CIWD column, the CIWD filter is automatically created during import.

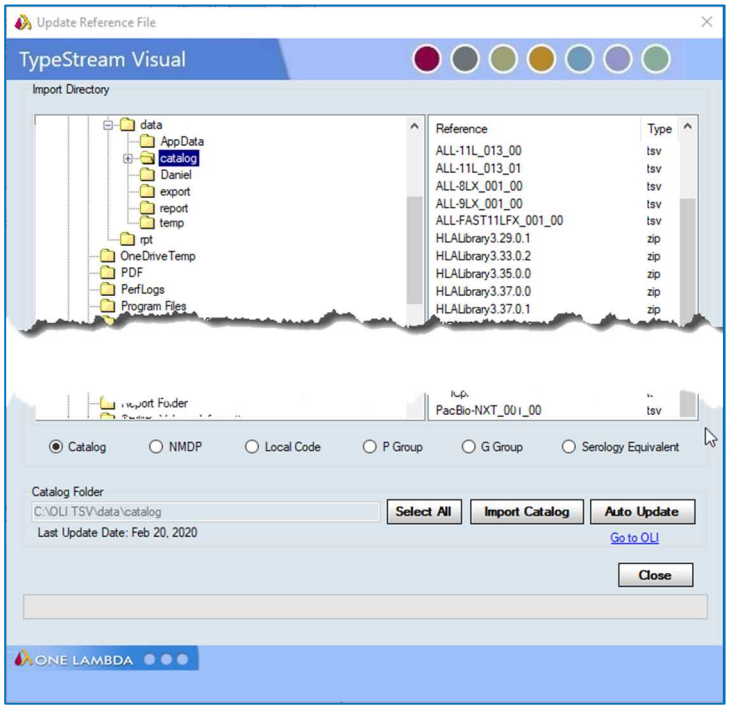
CIWD alleles are represented as follows in analysis screens when a Demographic Filter is applied:

Common	– represented as (c)
Well documented	– represented as (wd)
Intermediate	– represented as (i)
Rare	– represented as (r)
Ambiguous	– no CIWD designation, represented as (+)

2. NMDP, P and G codes
   a. Navigate to Utilities → Update Reference → Update Reference File.
   b. Click the NMDP, P Group or G Group radio button and click on Auto Update button to update the database with the NMDP/P group / G group codes.



3. Select Catalog and library.
    a. Navigate to the folder containing the catalog and library files you wish to download.
        i. Catalog is based on Alltype lot #, e.g. All-11LX_013
        ii. LRP catalogs are based on LRP lot #, e.g. PACBIO-NXT_001_00.
        iii. FastPlex catalogs based on AllFAST lot #, e.g. ALL-FAST11LFX_001_00.
        iv. IMGT catalogs are in zipped files labeled with "HLALibrary" and the particular library release, e.g. "HLALibrary3.37.0.1."
    b. Click on Import catalog.
    c. Users can alternately click on the "Auto Update" button to download the catalogs and HLALibrary.zip files directly from the One Lambda website.
    d. In IVD mode, only catalogs that do not have an X_ in the name are available for import.
    e. In RUO mode, only catalogs that have and X_ or -SB- are available for import.



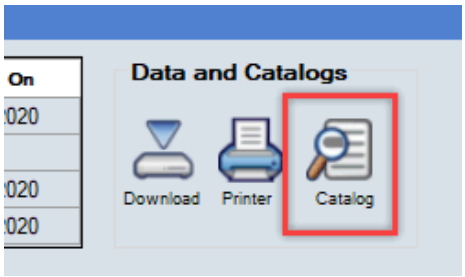
4. Refresh Home Page to display the references just loaded.

> NOTE: When a library file is imported, the application compares the IMGT release to that of the serology file loaded previously. If the two are not of the same release, the software will display a message to that affect and will ask the user whether to proceed with the download.

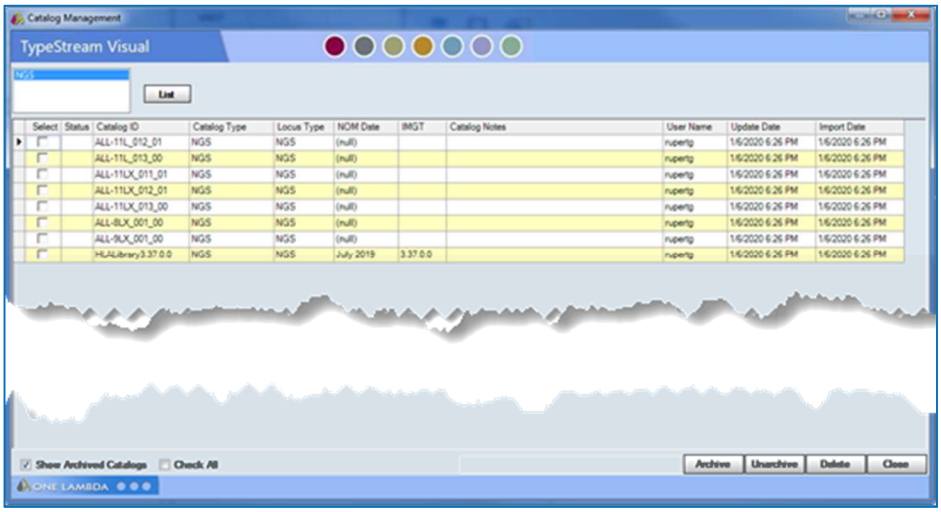
Managing Catalog Reference Files

Catalog reference files contain all of the reaction-specific information needed for analysis. Each new lot or revision of a product needs its own catalog file for analysis results to be accurate.

Catalog Management window may be accessed in one of two ways. The first is by using the 'Catalogs' icon under 'Data and Catalogs."



The second way is to navigate to Utilities → Update Reference → Catalog Information/Management. Both methods open the Catalog Management window where catalogs can be activated, archived, unarchived, or deleted.



A few things to note while working with catalog management:

The list includes both catalogs and IMGT libraries loaded into the current database.
Any catalog that has been used in an analysis cannot be deleted but can be Archived

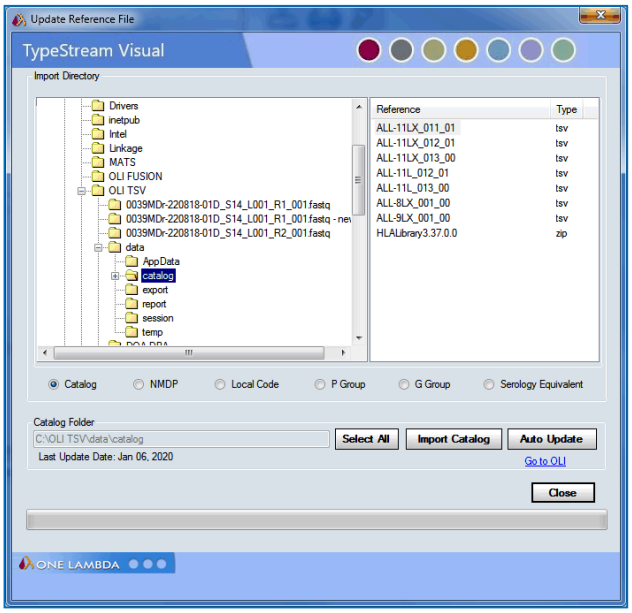
"A" in the 'Status' column indicates that the catalog has been archived.

Updating Catalog Files from a Local or Network Drive

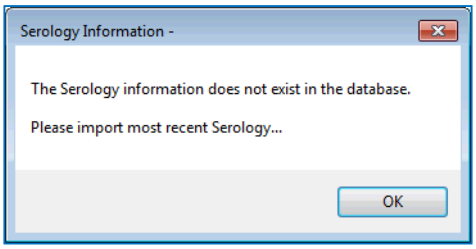
Lab supervisors can input new catalog files for use in analysis when new products, lots, or updates become available. Catalog files are also available on the One Lambda website.

From the main or any of the product home pages, click the download icon, or from the main menu, select Utilities > Update Reference > Update Reference File.

The Update Reference File dialog box displays.



If your serology information is outdated, or you have not yet imported it, the following message will be displayed"



If you see the message, click OK dismiss the message. Select the radio button to import serology first. If you do not see this type of message, go to the next step.

Using the file directory tree on the left, locate catalog files to be imported.

To determine which catalog is the most recent available, TypeStream Visual looks first at the lot number and then the revision number. An 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.

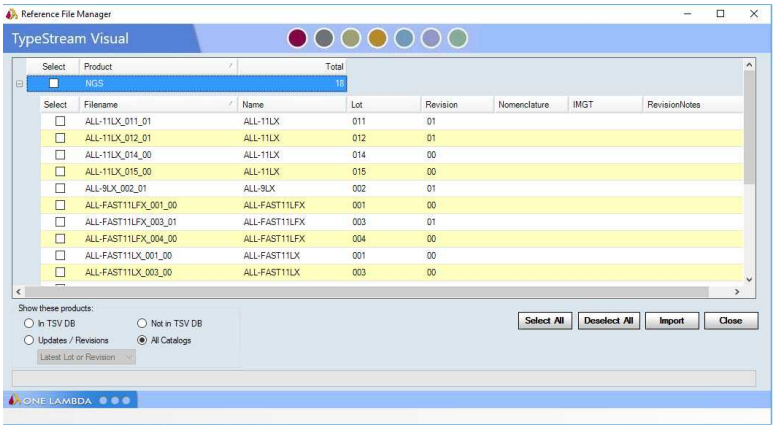
Highlight the files you want to import or click Select All [Select All] to select all files listed.

Updating Catalog Files from the One Lambda Website

Product catalog files are available on the One Lambda website https://www.onelambda.com/en/product/typestream-visual-software.html

From the main or any of the product home pages, click the Download link, or from the main menu, select Utilities > Update Reference > Update Reference File. The Update Reference File dialog box displays.

1. Click Auto Update [Auto Update] to open the One Lambda Catalog Updates Selection window.
   In IVD mode, only catalogs that **do not** have an X_ in the name are available for import.
   In RUO mode, only catalogs that have and X_ or -SB- are available for import.



2. 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.
3. Click Import [Import] to import the selected catalog files.
4. When the confirmation dialog box displays import results, click OK.
5. Click Close [Close] and then Yes to return to the Update Reference menu.
6. Imported catalog files can be used without restarting TypeStream.

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 Web Service URL you set for One Lambda in Utilities > URLs & Paths is correct.

When updating catalogs, user will not get message regarding serology files.

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 download the necessary files:

- NMDP codes
- P-Group and G-Group codes
- Local codes

- 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 TypeStream Visual can access it. The most current NMDP code file is available on the NMDP download site.

- From the main or any of the product home pages, click the Download link, or from the main menu, select Utilities > Update Reference > Update Reference File.
- The Update Reference File dialog box displays.
- Select the NMDP option.
- Navigate to the NMDP file on a local or network drive, using the Import Directory tree.
- Click Import NMDP to import the selected file.
- Click Close to return to the Update Reference menu.

Updating NMDP Files from the NMDP Website

Follow this procedure to import the NMDP list from the NMDP website.

1. From the main or any of the product home pages, click the Download link, or from the main menu, select Utilities > Update Reference > Update Reference File.
2. The Update Reference File dialog box displays.
3. Select the NMDP option.
4. Click Auto Update, which automatically imports the current NMDP file for use with TypeStream Visual. 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 NMDP code template to a local drive.
2. Use a text editor to edit the template and add code definitions.
3. Follow the example format, using a **Tab** to separate each field, and a slash to separate multiple values within a field:
4. letter code <tab> numeric allele extension to which the code applies
5. Save the file as `local_code.txt`

Updating the Local Code File

After a Local Code file has been created, it must be updated in TypeStream Visual.

From the main or any of the product home pages, click the Download link, or from the main menu, select Utilities > Update Reference > Update Reference File.

The Update Reference File dialog box displays.

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

Updating Serology Equivalent File from One Lambda Website

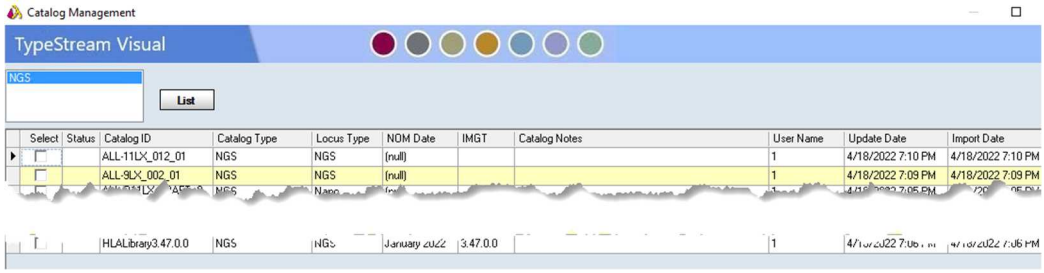
The Serology Equivalent file can be auto updated from the One Lambda website.

1. From the main or any of the product home pages, click the Download link, or from the main menu, select Utilities > Update Reference > Update Reference File.
2. Select the Serology Equivalent option.
3. Click Auto Update [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 Serology to import the selected files. Catalog files are ready for use without restarting TypeStream Visual.
6. A confirmation dialog box displays import results, click OK.
7. Click Close [Close] and then Yes to return to the Update Reference menu.

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

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.



From the Main Menu, select Utilities > Update Reference > Catalog Information/Management.

1. Select the S (select) check box for the catalog files you want to archive and click Archive [Archive].
2. When a pop-up message displays Data Saved, click OK.
3. Click Close to return to the main menu.

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

Un-Archive Catalogs

Archived catalog files display an A in the Status column when you view the catalog list and the check box for Show Archived Catalogs is selected.

From the Archive Catalog window, select the check boxes next to the catalogs you want to unarchive, and click Unarchive.

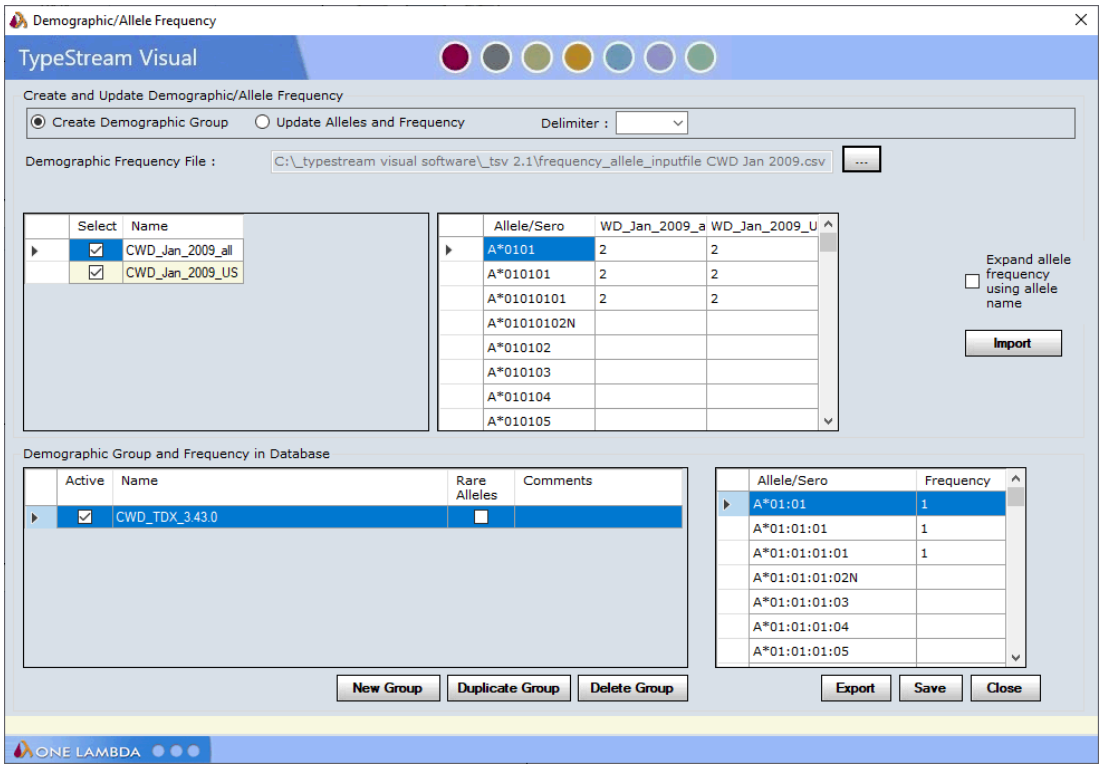
Deleting Catalog File Information

You can delete a catalog file from the Catalog Management menu. Catalog files displayed with an 'A' in their Status column have been archived.

1. From the Main Menu, select Utilities → Update Reference → Catalog Information/Management.
2. Select the check box next to any catalog you want to delete.
3. Click Delete to remove the catalog information.

Users cannot delete catalog files that have been used in a session analysis.

Demographic/Allele Frequency



Importing Allele Frequency Files (Demographic Frequency)

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

1. From the Main Menu, select Utilities > Update Reference ->Demographic/Allele Frequency.

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.

   Template for the Demographic/allele frequency file can be found in C:\Program Files (x86) \One Lambda\TSV 3.0\Demographic frequency Jan 2010 v3

Updating Allele Frequency

Frequency information for each of the alleles in the Allele/Frequency grid in the bottom right can be updated to represent common (1), well documented (2) , intermediate (3) or rare (blank) designation. User can then save the information in the database or have the ability to export the frequency filter file.

Users have the ability to create a new group by selecting one of the existing groups in the database. The frequency for the new created group is blank.

Users can duplicate or create a copy of an existing group by using the "Duplicate Group" feature.

Delete Group allows users to delete an existing group in the database only if the group has not been used in analysis. You cannot attempt to delete a demographic/allele frequency filter with the prefix "CWD_TDX and CIWD_TDX" This prefix is reserved by the system. Please choose another name when creating demographic groups.

All demographic groups that are in the database appear in the Demographic dropdown in NGS Product Configuration Assignment Settings tab.

NGS Product Configuration

All aspects of NGS Product Configuration are located all under the same window option. User will notice a number of elements that have been rearranged from previous versions of TypeStream Visual. Here you will now find the following:

Assignment Configuration to choose codes and/or fields in which assignments display; enable KIR, Bw4/Bw6 and serology settings; select position notation style, and more.
Analysis Parameters
Health Metric
Exclude Region

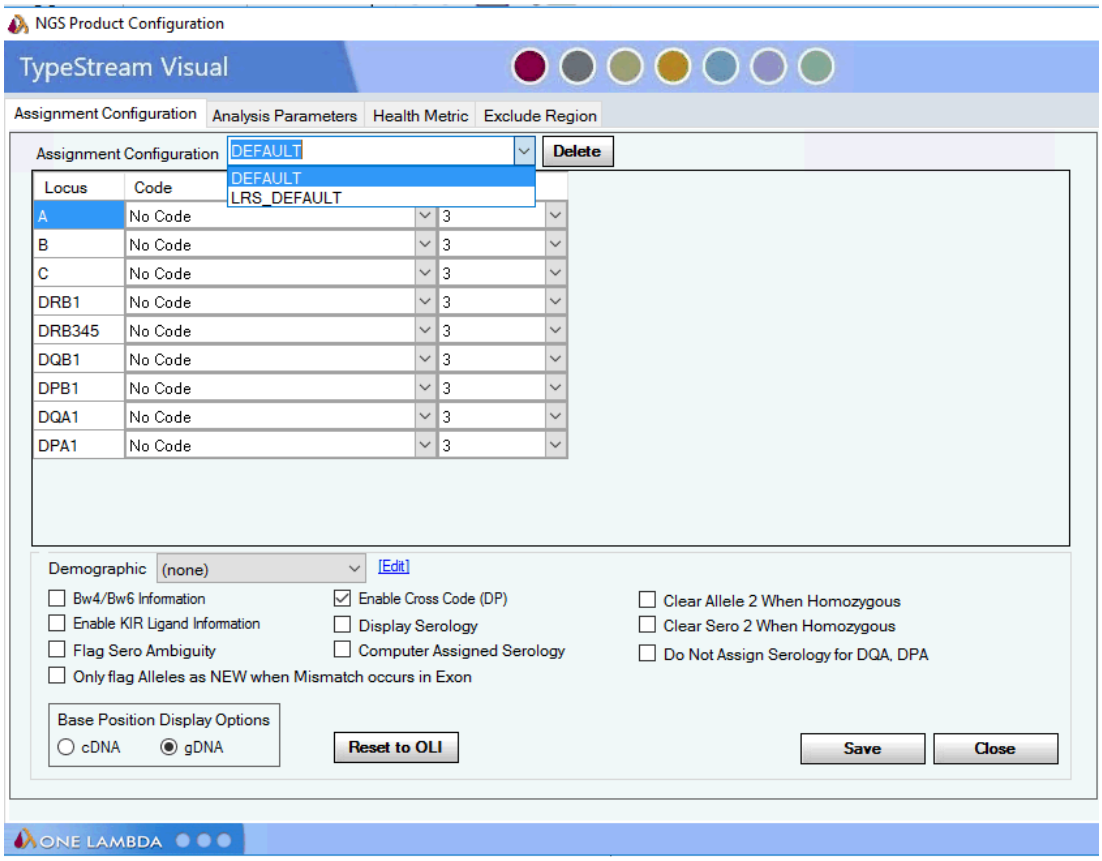
Setting Configuration

Setting overall configuration options in this screen applies to all session and samples analyzed. Many can be overridden on a per-sample basis as described in the chapter on creating sessions.

Analysis Parameters must be selected for each session created; therefore, a session in queue will not change if a new parameter set is created.

New in v3.0

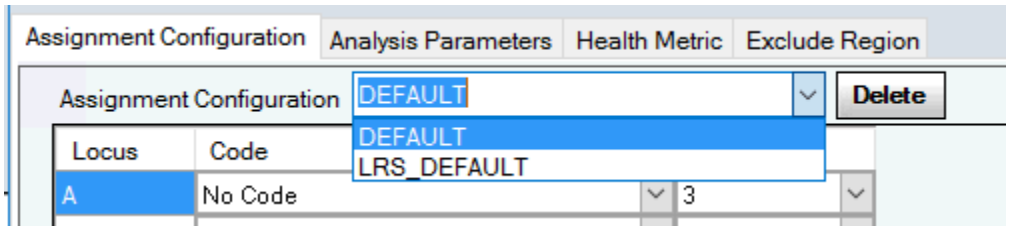
Assignment Settings



Note: Current assignment settings are applied when the session starts the processing of samples.

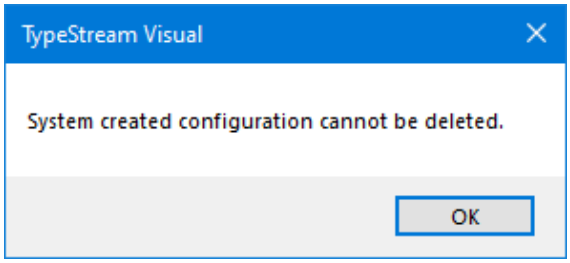
LRS_DEFAULT assignment setting is the default setting when analyzing LRS data. This option is available only in the RUO mode of the software.

The **Assignment Configuration dropdown box** (circled above) allows you to select the default or any user-defined configuration.

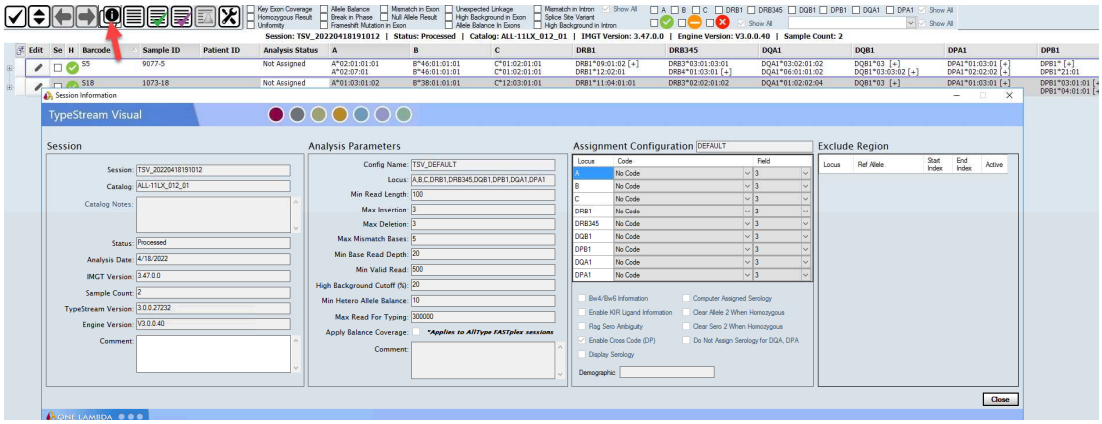


You can also create a new configuration here by typing a name and configuring assignment settings, and clicking Save.

You can delete the currently selected configuration by selecting the configuration and clicking on the Delete button. If you try to delete a system-defined configuration or a configuration that is used in a session analysis, the software will issue a warning.



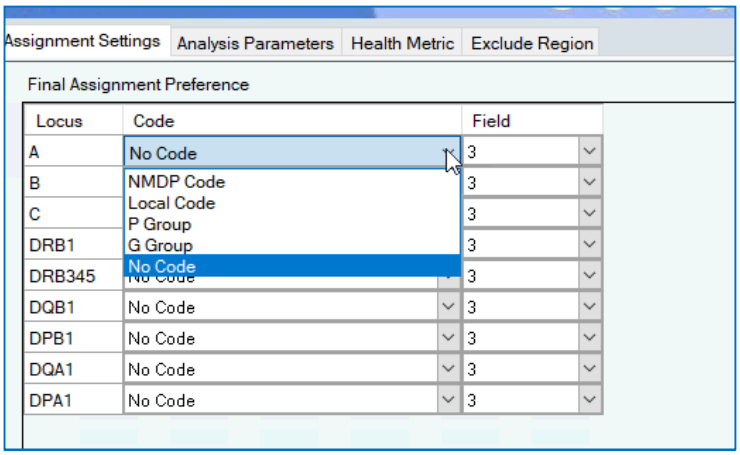
The information saved in the Assignment Configuration window will also be displayed in the Session Summary when the "Show Session Information" button is clicked:



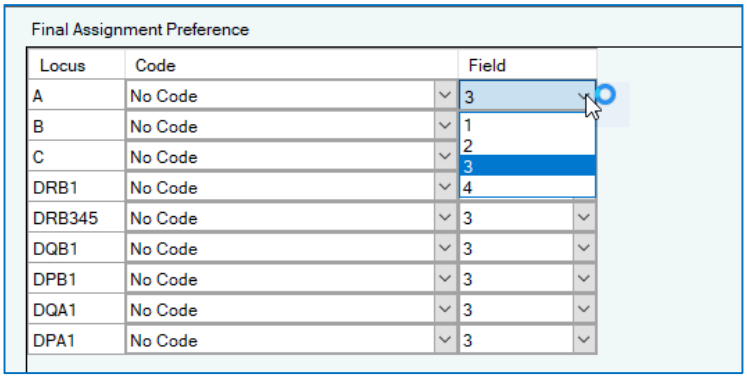
Upgraded database would show the DEFAULT configuration. The samples results would be displayed in the configuration in which it was saved.

Final Assignment Preference

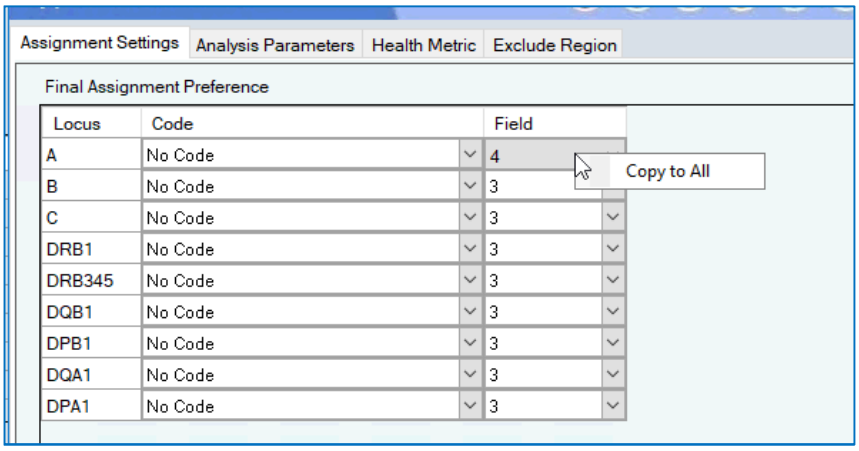
This section governs how final genotype is displayed, e.g. 3-field, P code, NMDP code, etc. For each locus user may select any of five settings: NMDP Code, Local Code, P Group, G Group, or No Code.



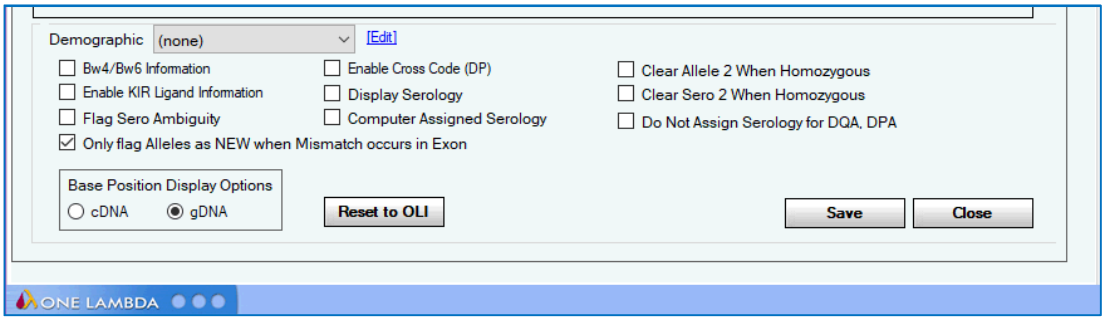
If No Code is selected, user may select the number of fields from 1 to 4.



For both code and field columns, the software enables user to right-click on the selected option and apply it to all the following loci. Note, however, that each locus can be configured with a different code setting if desired.

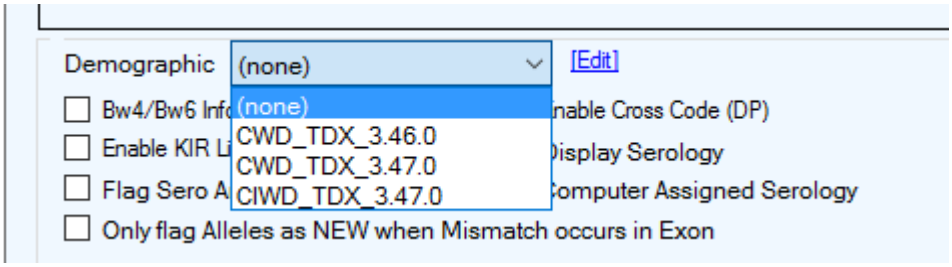


General Options for Configuration



Setting any one of these checkbox options has the following effect:

1. Demographic Group Selection: This option allows you to organize alleles according to their frequency. Select a predefined Demographic Group using the drop-down control. Clicking on Edit link next to the dropdown will navigate the user to Create/Update Demographic /Allele Frequency window.



2. Bw4/Bw6 Information: Includes Bw4/Bw6 information in serology results. These are serological epitopes that differ only at a specific region.

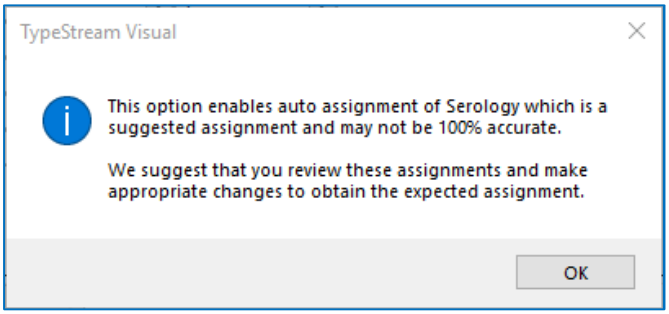
3. Enable Kir Ligand: Includes KIR Ligand information for the C locus in analysis results. The user should import the serological_equivalent file containing the KIR ligand information.

4. Flag Sero Ambiguity: When there is a Serological Ambiguity, it is identified in the System Comments.

5. Enable Cross Code (DP): Enables the utilization of NMDP codes that combine alleles with differing first-fields, using G Code definitions.

6. Display Assigned Serology: Allows the user the option of having the assigned serology display on the analysis panel or not, as preferred.

7. Computer Assigned Serology: Automatically populates serology assignment fields while also storing results in the database. When this option is selected, TypeStream Visual will display the following warning message:



8. Clear Allele 2 When Homozygous: When checked, Allele 2 of a homozygous pair will not display in the Final Allele Assignment panel.

9. Clear Sero 2 When Homozygous: When checked, Sero 2 of a homozygous pair will not display in the Final Sero Assignment panel.

10. Do Not Assign Serology for DQA, DPA: When checked, the software will not assign serology for DQA and DPA loci.

11. Only flag Alleles as NEW when Mismatch occurs in Exon: When checked, will not flag alleles as new if mismatch positions are in introns only.

12. Base Position Display Options: User may select between display cDNA and gDNA base positions on the nucleotide viewer.

    cDNA – Complementary DNA - mirrors IMGT, in which all introns begin with position 1 and each exon continues from the previous exon

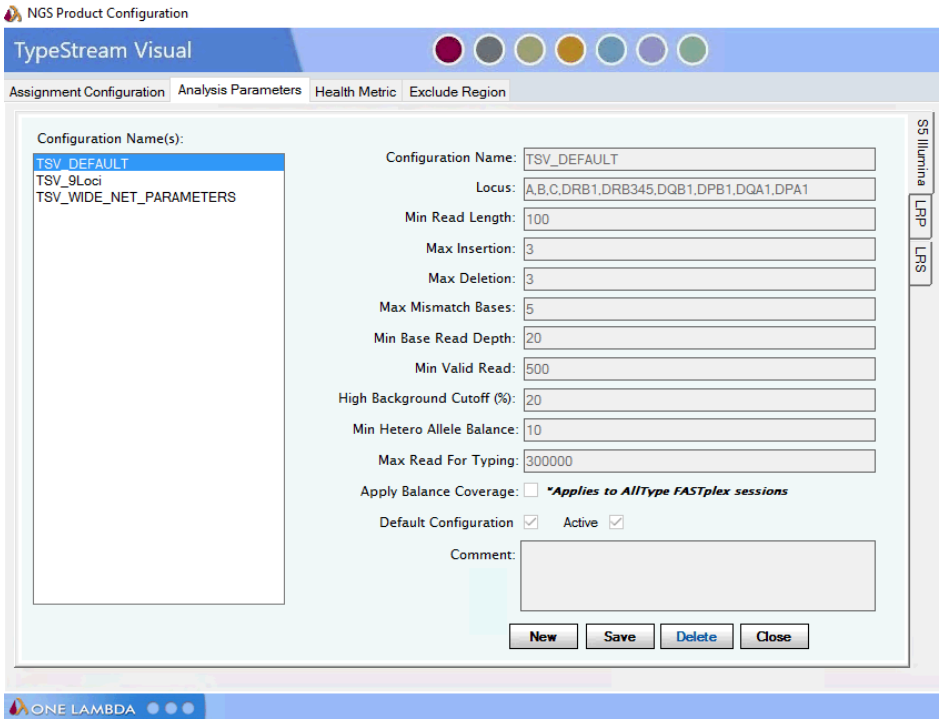
gDNA - position count is continuous, starting with exon 1 (E1) through the remainder of the gene, including 3'UTR. The 5'UTR starts with -1, then continues with negative numbering upstream.

13. Reset to OLI: This button will reset all of the settings on this tab to the defaults established by One Lambda, Inc.

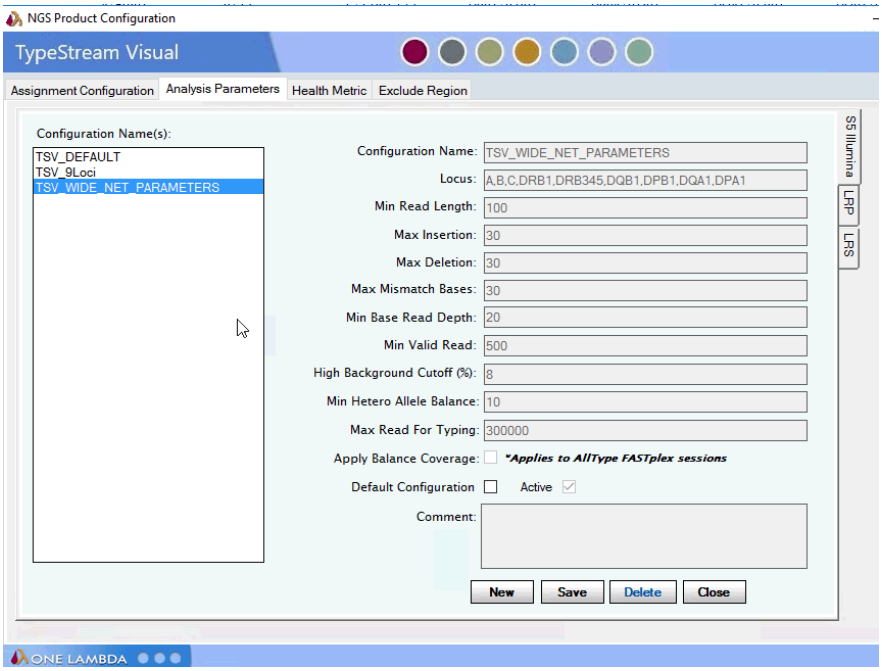
When you are done setting options, click Save to save changes.

Analysis Parameters / S5 and Illumina

The Analysis Parameter tab has a second set of tabs at the right side to select either S5/Illumina or LRP. Analysis Parameters are applied at the session level – the user selects one of the default settings, or creates more to fit his own specifications.



Parameter	Definition

Configuration Name	The name of the configuration. There are two supplied by the software. "TSV_DEFAULT" analyzes 11 loci; "TSV_9Loci" analyzes 9 loci (no DQA1 or DPA1). When creating a new parameter set, user supplies the set name here. "TSV_DEFAULT" is not modifiable by the customer. New in v3.0 TSV_WIDE_NET_PARAMETERS is new in Version 3.0. It is also not modifiable by the user and only applies to the S5 Illumina tab (ION Torrent or Illumina sessions). This configuration may be used for the investigation of samples with failed health metrics such as linkage warning and/or high background. 
Locus	User may enter text that represents a single or multiple loci in a comma-separated list. The engine will only analyze loci present in the library.
Min. Read Length	User may enter the minimum length for valid reads. Reads less than this length will be filtered and not used for analysis.
Max Insertion	User may enter the maximum number of insertions for a valid read. If a read has more insertions than the parameter when compared to the reference allele, it will be filtered and not used for consensus generation.
Max Deletion	User may enter the maximum number of deletions for a valid read. If a read has more deletions than the parameter when compared to the reference allele it will be filtered and not used for consensus generation.
Max Mismatch Bases	User may enter the maximum number of base mismatches for a valid read. If a read has more mismatches than the parameter when compared to the reference allele, it will be filtered and not used for consensus generation.

Min Base Read Depth	User may enter the minimum number of valid reads for any base position for an allele. If the base depth is below the parameter, no consensus base will be added at that position and it will be treated as a wild card when comparing to database to find closest matching allele.
Min Valid Read	User may enter the minimum number of valid reads for the software to make a typing call. If the number of reads found for a locus is less than the parameter, no typing call will be attempted for the locus.
Cutoff Value (%)	User may enter the minimum percentage of alternate bases at a position before the software will mark it with a high background flag.
Min Hetero Allele Balance	User may enter the minimum allele balance percentage used for the software to identify a position as variant (heterozygous). (This should not be confused with the Allele Balance value found in Health Metrics, which is the average allele balance with a value of '20.')
Max Reads for Typing	User may enter the maximum number of reads used for the genotype call. If input file contains more than the specified number of reads, software will randomly select that many reads for analysis.
Apply Balance Coverage	This analysis parameter applies to AllType FASTplex sessions. When checked When checked, the software balances the read coverage across all regions of the genes for only AllType FASTplex sessions. A system comment is applied at the barcode/test level as "*Coverage Balance option is applied*."

Additionally, user may designate any of the analysis parameter sets as the default configuration and may make any of the Active or Inactive.

Analysis parameter sets may only be deleted if they have not been used in a session. If such parameter sets are no longer needed, they may be made inactive and will not appear as an option for selection.

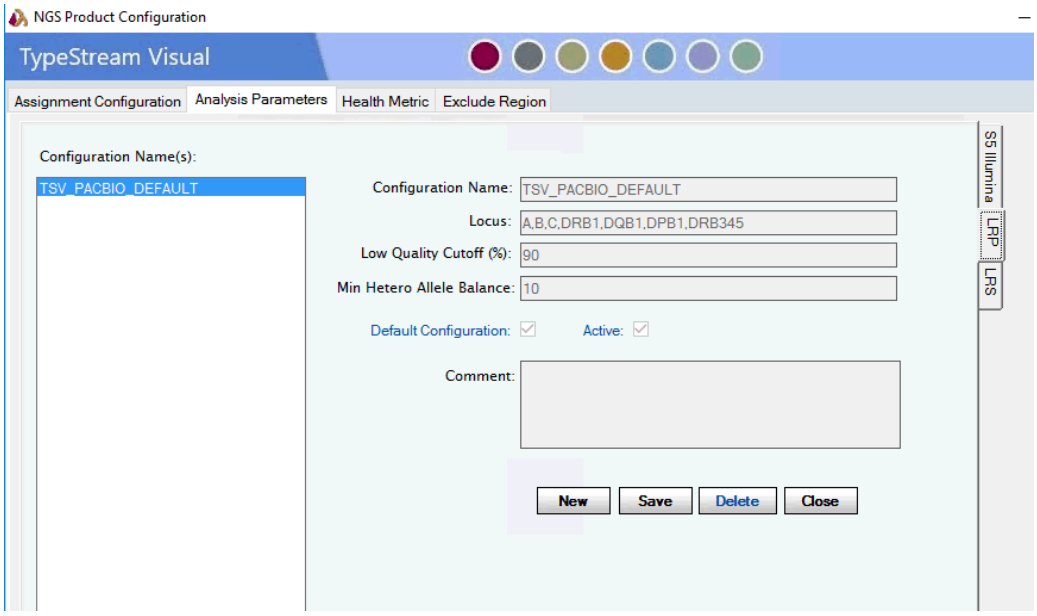
Comments may be optionally added to new parameter sets. These comments will not appear on the analysis, but only on this configuration window.

NOTE: If an expected locus is reported as a "NO CALL" and the "Total Read Count" value for the barcode is the same as the "Max Read for Typing" analysis parameter (or exactly double for paired end samples), it is recommended that the user rerun with an increased value for the "Max Read for Typing" parameter. This will allow the software to analyze more reads from the raw data and may detect enough for the locus to provide a typing.

Analysis Parameters – LRP

Long Read Processing data has different default parameters.

This tab is available only when logged into the application in RUO mode.



Parameter	Definition
Configuration Name	The name of the configuration. There is one supplied by the software. "TSV_PACBIO_Default" analyzes 9 loci. When creating a new parameter set, user supplies the set name here.
Locus:	User may enter text that represents a single or multiple locus in a comma-separated list. The engine will only analyze loci present in the library.
Low Quality Cutoff (%)	Default is 90%. QV score is taken from the LRP package file on import.
Min. Hetero Allele Balance	User may enter the minimum allele balance percentage used for the software to identify a position as variant (heterozygous).

As with the S5/Illumina parameters, user may designate any of the analysis parameter sets as the default configuration and may make any of the Active or Inactive.

Analysis parameter sets may only be deleted if they have not been used in a session. If such parameter sets are no longer needed, they may be made inactive and will not appear as an option for selection.

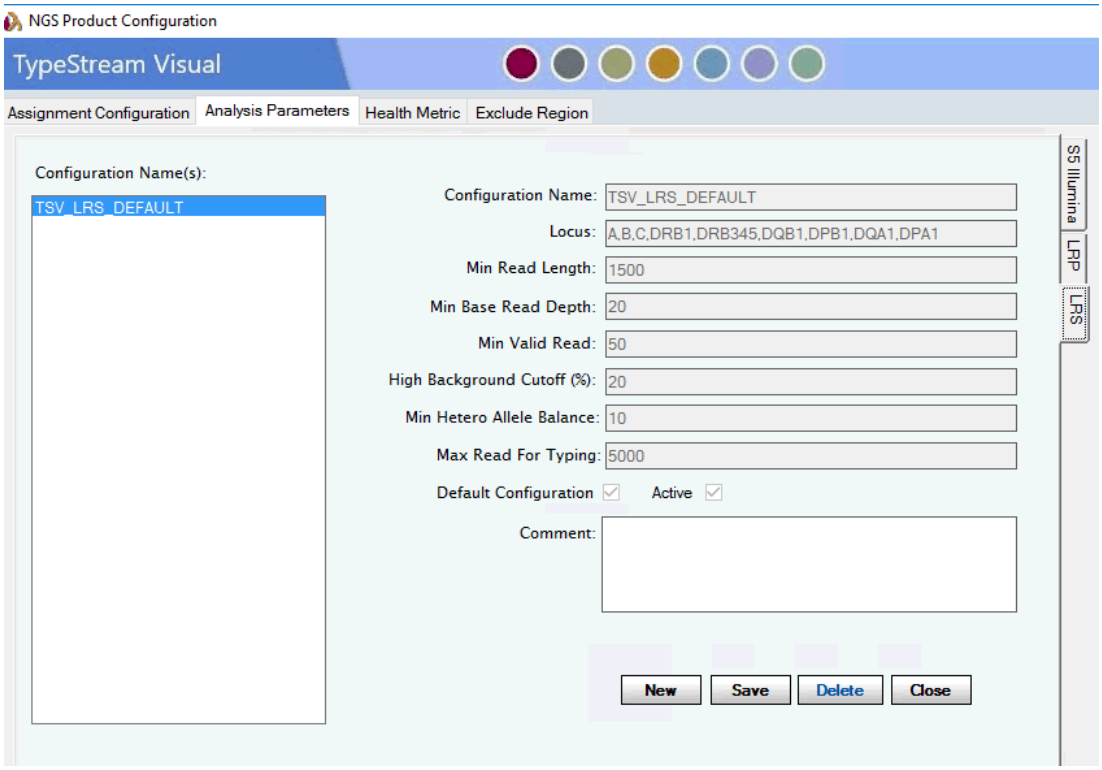
Comments may be optionally added to new parameter sets. These comments will not appear on the analysis, but only on this configuration window.

New in v3.0

Analysis Parameters – LRS

The Analysis Parameter tab has a third tab at the right side to select the LRS configuration.

This tab is available only when logged into the application in RUO mode.



Parameter	Definition
LRS	The name of the configuration. There is one supplied by the software. "TSV_LRS_DEFAULT" is default. When creating a new parameter set, user supplies the set name here.
Config Name	Displays all currently saved parameter sets. If a parameter set is selected from this list, the corresponding parameter values display on the right. User may enter a name for a new parameter set here. The name has to be unique in the system. If user tries to save a new configuration with an existing name or no name, a warning will be displayed
Locus	User may enter text that represents a single or multiple locus in a comma separated list, the engine will only analyze loci present in library.
Min Read Length	User may enter the minimum length for valid reads. Default 1500, allowed characters [0-9.]
Min Base Read Depth	User may enter the minimum number of valid reads for any base position. Default 20, allowed characters [0-9.]
Min Valid Reads	User may enter the minimum number of valid reads for the software to make a typing call. Default 50, allowed characters [0-9.]
High Background Cutoff (%)	User may enter the maximum percentage of alternate bases before the software will make as high background. Default 20, allowed characters [0-9.]

Min Hetero Allele Balance	User may enter the minimum allele balance ratio required between allele 1 and allele 2 used to determine a heterozygous, variant, position. Default 10, allowed characters [0-9.]
Max Reads for Typing	User may enter the maximum number of reads used for the genotype call. If input contains more than the specified number, software will randomly select that many reads for analysis. Default is 5000, allowed characters [0-9.]

As with the S5/Illumina parameters, user may designate any of the analysis parameter sets as the default configuration and may make any of the Active or Inactive.

Analysis parameter sets may only be deleted if they have not been used in a session. If such parameter sets are no longer needed, they may be made inactive and will not appear as an option for selection.

Comments may be optionally added to new parameter sets. These comments will not appear on the analysis, but only on this configuration window.

Health Metric

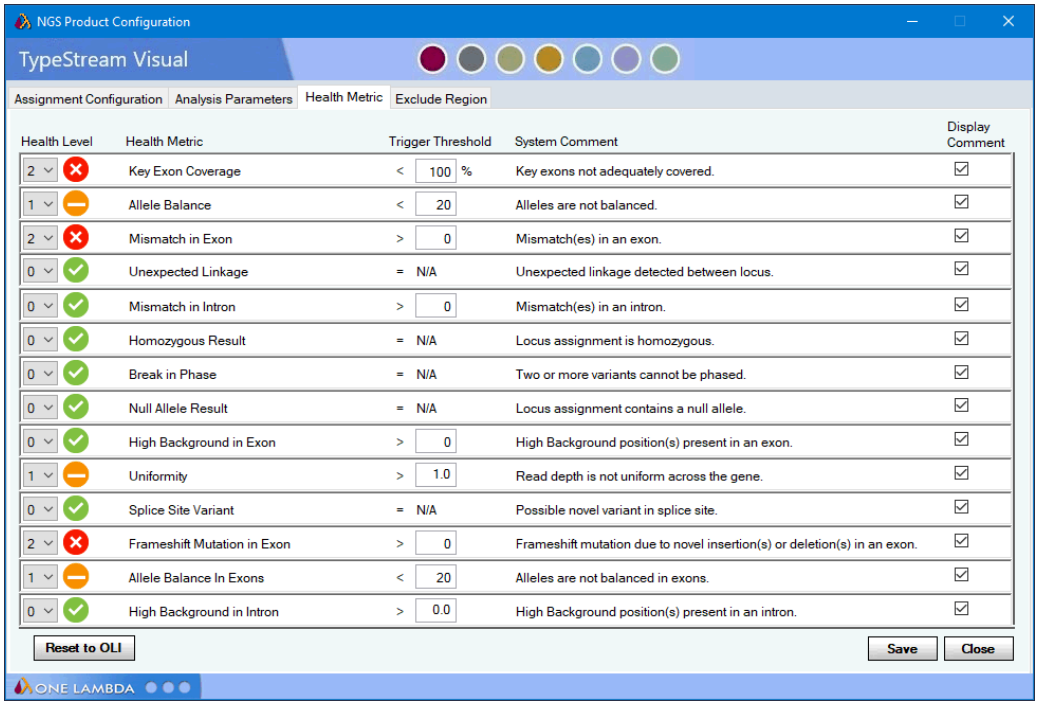
Users may configure the health metrics with respect to the following:

1. Health Level: For each of the health warning flags, the user may give it the weight appropriate to the task. Use the dropdown on the far left to select a numerical level, which is paired with an appropriate icon.

Level	Icon	Meaning
0		Least level of severity. If this level is chosen, the icon will display green even if the metric fails. The green icon also displays when no metrics for the locus fail.
1		Failure of this metric is of medium concern.
2		Level two failures are considered unacceptable. Further investigation is required.

2. Trigger Threshold: The value at which the flag will be triggered. User can set the default threshold for each health metric, with the exception of Unexpected Linkage, Homozygous Result, Break in Phase, Null Allele Result and Splice Site Variant.
3. System Comment: the wording that will display in the system comments for the locus if metric is triggered.
4. Display comment: The user may decide for each metric whether it is necessary to display the comment in the locus system comments.

The current health metrics are used in the analysis when a session starts processing. However, the user may reset the health level and display choice at the locus level from the analysis panel. More will be given on this in chapter on creating sessions.



Health Level	Health Metric	Trigger Threshold	System Comment	Display Comment
2	Key Exon Coverage	< 100 %	Key exons not adequately covered.	☑
1	Allele Balance	< 20	Alleles are not balanced.	☑
2	Mismatch in Exon	> 0	Mismatch(es) in an exon.	☑
0	Unexpected Linkage	= N/A	Unexpected linkage detected between locus.	☑
0	Mismatch in Intron	> 0	Mismatch(es) in an intron.	☑
0	Homozygous Result	= N/A	Locus assignment is homozygous.	☑
0	Break in Phase	= N/A	Two or more variants cannot be phased.	☑
0	Null Allele Result	= N/A	Locus assignment contains a null allele.	☑
0	High Background in Exon	> 0	High Background position(s) present in an exon.	☑
1	Uniformity	> 1.0	Read depth is not uniform across the gene.	☑
0	Splice Site Variant	= N/A	Possible novel variant in splice site.	☑
2	Frameshift Mutation in Exon	> 0	Frameshift mutation due to novel insertion(s) or deletion(s) in an exon.	☑
1	Allele Balance In Exons	< 20	Alleles are not balanced in exons.	☑
0	High Background in Intron	> 0.0	High Background position(s) present in an intron.	☑

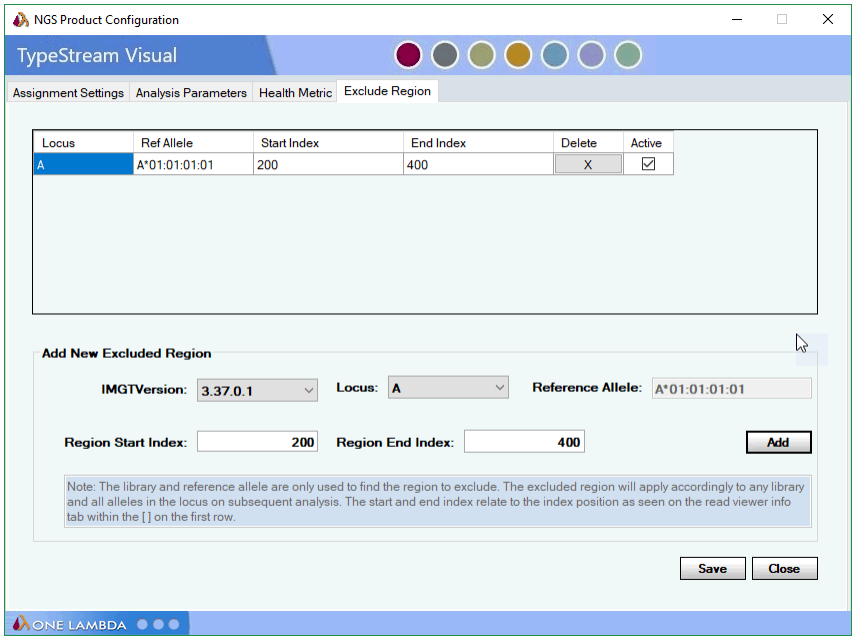
New in v3.0

The **High Background in Intron**/non-coding region metric has been added. This flag is raised when a sample has a high background position in the intron. The default health level for this health metric is a 0 and displays a system comment "High Background position(s) present in an intron" if the option to display the comment is checked.

Results can be reset to the OLI factory settings. Be certain to save after changing. *(See "Filters" section in View Analysis chapter for definitions of each of the metrics.)*

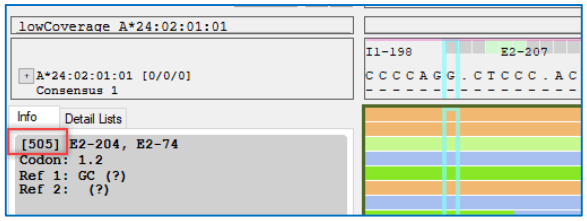
Exclude Region

The Exclude Region Tool allows a user to exclude any region – intron or exon – from analysis.



The Exclude Region window allows the user to select the locus and specify as many regions for exclusion as necessary. To use the tool, do the following:

1. Select IMGT Version. You may select any of the libraries in your active database.
2. Select Locus.
3. When locus is selected, the Reference Allele will populate in the Reference Allele text field.
4. Enter Region Start Index. This is the raw position number, irrespective of its cDNA or gDNA designation. Position number can be found by going to reads viewer. In this example you want to begin the exclusion at the beginning of Exon 2, E2-74 in cDNA. When that position is selected on the reads viewer, the info panel shows you that it is position '505'. So '505' is the Region start index. Determine Region End Index in the same manner.



5. Click Add.
6. Your region for exclusion displays in the grid.
7. You may add as many regions for exclusion as necessary. If any of them overlap, you will get a message to that effect and the software will not accept it.
8. When finished, click Save and Close.

Other things to note about the Exclude Region tool:

1. The current exclude region metrics are used in the analysis when a session starts processing. Any region exclusion can be deleted or de-activated. Note that those changes will not apply to sessions already analyzed.
2. An exclusion that has been made inactive still displays on the exclusion grid but will not be used in the analysis.
3. If the user wants to load a different library but keep the excluded regions, the

application will automatically adjust and exclude the correlated region using the new library.

4. Reference alleles were selected for the greatest homology for all locus alleles.

Default Reference Alleles		
A*01:01:01:01	B*07:02:01	C*01:02:01:01
DRB1*01:02:01	DRB3*02:02:01:02	DQB1*02:01:01
DPB1*01:01:01:01	DQA1*01:01:01:01	DPA1*01:03:01:01

Automation

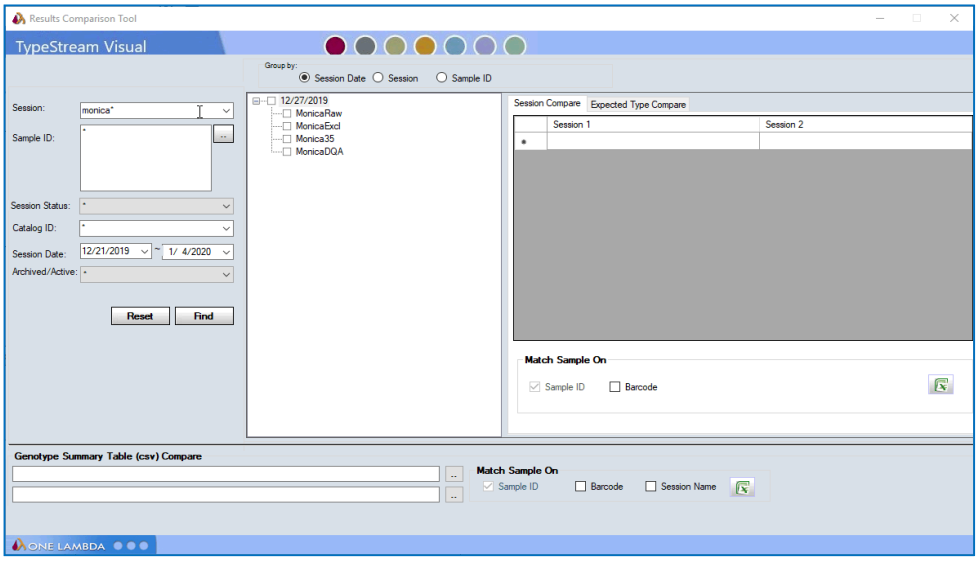
Please see next chapter for instructions on automatically analyzing sessions from Ion S5 or Illumina sequencers.

Results Comparison Tool

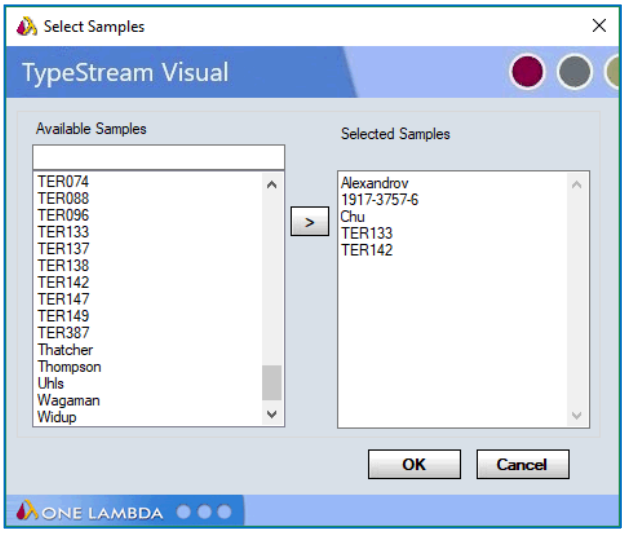
Users may employ this tool to make comparisons from session to session for samples of the same name for the purpose of establishing concordance or detecting discrepancies.

On the left side of the tool window is a search panel. Search can be conducted by Session name, Sample ID, Session status, Catalog ID, Session Data, or Archived/Active status. When the search criteria is ready, click 'Find' and display results in the center panel, grouped according to the method selected via radio buttons above.

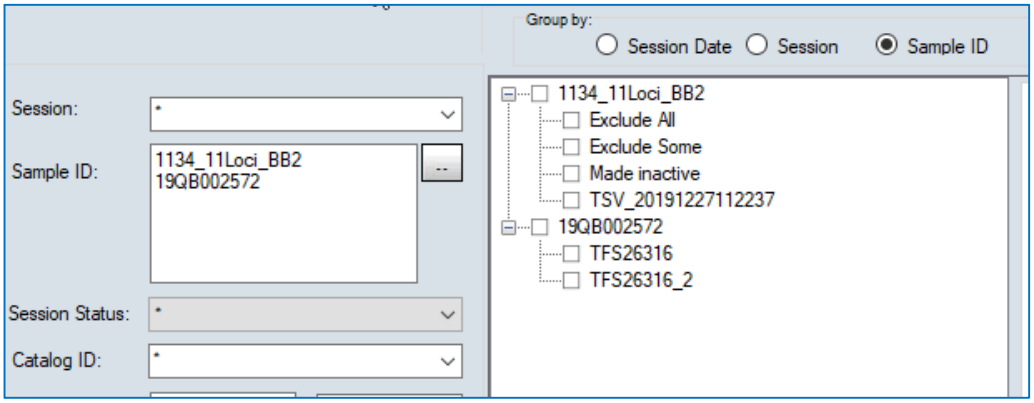
In the example below, several sessions had been named beginning with 'Monica'. All sessions fitting the search criteria display under the date they were analyzed.



If sample names are unknown, clicking the search box will display a list of available samples from the sessions in the currently active database. Select the desired session names and use the right arrow to move them to the Selected Samples panel. When you have completed sample selection, click OK.

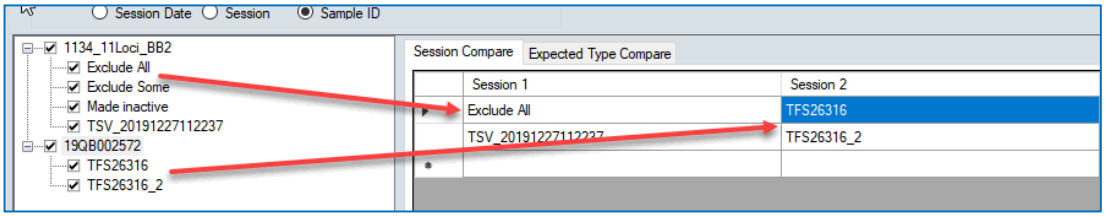


The selected sample names display in the sample ID panel on the tool window. Clicking 'find' will then show, with "Sample ID" radio button selected, which sessions contain those samples.



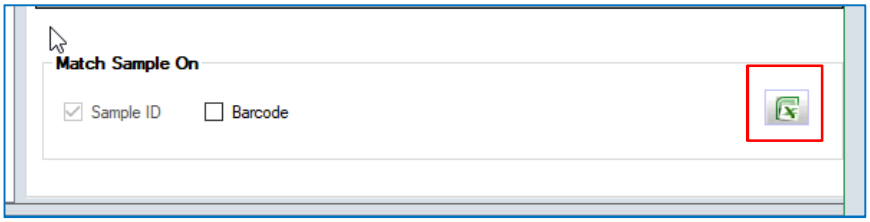
At this point, drag-and-drop the desired session names into the Session Compare window.

Known anomaly: when a session is checked, it has no affect on inclusion in the tool. The user must drag and drop sessions into their correct position.



Make comparison type selection at the bottom of the session compare window.

- Compare by Sample compares the results of the two session by sample.
- Compare by Sample and Barcode compares the results of the two session by Sample and barcode.
- If there are more than one row of session pairs, the summary excel will output one session comparison followed by the next.
- The comparison of the results are exact string matches. Any differences will be highlighted in yellow in the IsSameAllele(s) and IsSameKNI column.



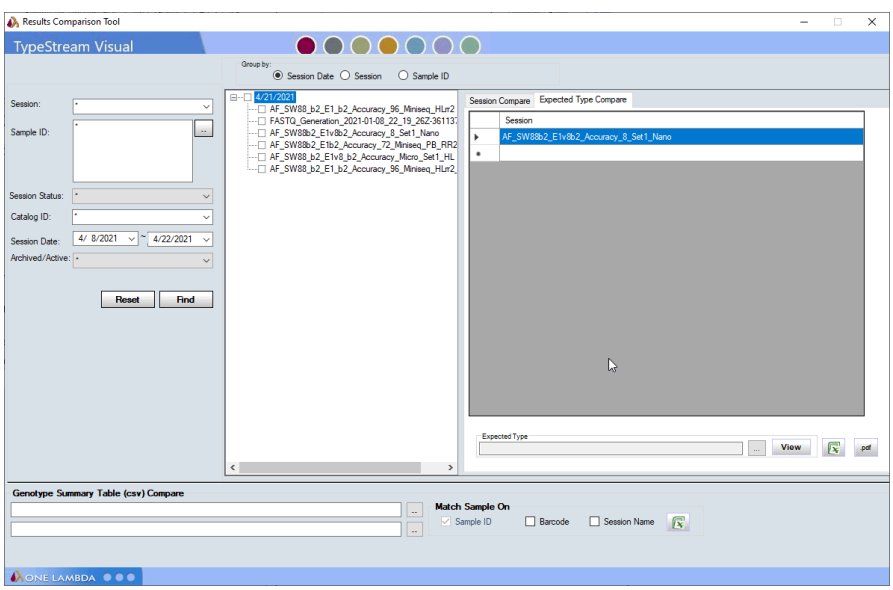
Click the Excel icon, and the software provides a spread sheet which compares each of the sessions for allele and K/N/I values, returning "True" if the values match.

Session 1	Catalog	Imgt Version	Engine Version	Sample	Barcode	Locus	Allele1	K/N/I	Allele2	K/N/I	Is Same Allele(s)	Is Same KNI
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	A	A*02:01:01:01/A*02:01:01:5	[0/0/0]	A*68:01:02:02	[0/0/0]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	B	B*40:01:02:01/B*40:01:02:04	[0/0/0]	B*40:02:01:01=B*40:420	[0/0/0]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	C	C*03:04:01:02/C*03:04:01:12	[0/0/0]	C*03:04:01:02	[0/0/6]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	DPA1	DPA1*01:03:01:04	[0/0/0]	DPA1*02:02:02:01/DPA1*02:	[0/0/0]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	DPB1	DPB1*04:01:41=DPB1*350:0:	[0/2/0*]	DPB1*05:01:01:01/DPB1*05:	[0/0/1]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	DQA1	DQA1*01:02:02:01/DQA1*01	[0/0/2]	DQA1*04:01:01:02/DQA1*04	[0/0/0]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	DQB1	DQB1*04:02:01:04/DQB1*04	[0/0/0]	DQB1*05:02:01:01/DQB1*05	[0/0/1]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	DRB1	DRB1*08:02:01:01/DRB1*08:	[0/0/0]	DRB1*16:09:01	[0/0*/0*]	True	True
Exclude All	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	063	DRB345	DRB5*02:02:01	[0/0/0]	DRB5*02:02:01	[0/1/0]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	A	A*02:01:01:01/A*02:01:136	[0/0/0]	A*68:01:02:02	[0/0/0]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	B	B*40:01:02:01/B*40:01:02:04	[0/0/0]	B*40:02:01:01=B*40:420	[0/0/1]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	C	C*03:04:01:02/C*03:04:01:12	[0/0/0]	C*03:04:01:02	[0/0/1]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	DPA1	DPA1*01:03:01:04	[0/0/0]	DPA1*02:02:02:01/DPA1*02:	[0/0/0]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	DPB1	DPB1*04:01:01:02=DPB1*35(	[0/0/0]	DPB1*05:01:01:01/DPB1*05:	[0/0/0]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	DQA1	DQA1*01:02:02:01/DQA1*01	[0/0/1*]	DQA1*04:01:01:01/DQA1*04	[0/0/1*]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	DQB1	DQB1*04:02:01:01/DQB1*04	[0/0/1]	DQB1*05:02:01:01/DQB1*05	[0/0/2]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	DRB1	DRB1*08:02:01:01/DRB1*08:	[0/0/0]	DRB1*16:09:01	[0/0*/0*]	True	True
TSV_20191227112237	ALL-11LX_007_01	3.37.0.1	V2.0.0.51	1134_11Loci_BB2	062	DRB345	DRB5*02:02:01	[0/0/0]	DRB5*02:02:01	[0/1/0]	True	True

Expected Type Compare

Expected type comparing allows the user to compare a selected session against an expected type file.

- Template "example_expected_types" for the expected type file is located in the Application install folder.
- View (Button) allows the user to view the contents of the expected type file. Note: If no expected type file is provided, the View button displays the template of the expected type file.
- Output file is in Excel format and displays the concordance at 3 field , 4 field and 2 field level.
- When the sample is discordant at 2 field level the typing is highlighted in pink.
- When the sample is discordance at 3 field level the typing is highlighted red.
- When the sample is discordant at 4 field level, the typing is highlighted yellow.
- If there is no expected typing at the 2nd, 3rd or 4th field level, it will be indicated by "No Ref."



.pdf Report

Allows the user to create a results comparison report in a .pdf format. The exported file is saved by default under C:\OLI TSV\data\export\ExpectedTypePdf folder. If multiple sessions are selected multiple .pdfs are generated with the session name as the file name.

Results Comparison Report

Session ID: AF SW88b2 E1v8b2 Accuracy 8 Set1 Nano
TSV Application Version: 2.1.0.27232 **Catalog ID:** ALL-FAST11LF_002_00 **Lot #:**
TSV Engine Version: V2.1.0.40 **HLA Library Version:** 3.43.0.0 **Sample #:** 8
Expect Type File: C:_typestream visual software_naa phase out - pcr\file formats\Nexus CS Reference File v1.6_Proposedformat.xlsx **Version:** 1.6

Concordance (3-Fields)

	A	B	C	DRB1	DRB345	DQA1	DQB1	DPA1	DPB1	Total
Concordant	14	14	14	14	13	14	14	14	14	125
Discordant	0	0	0	0	1	0	0	0	0	1
No Calls	0	0	0	0	0	0	0	0	0	0
No Locus Ref	2	2	2	2	2	2	2	2	2	18
Concordance %										86.81 %

Exon 2 Average Depth

A	B	C	DRB1	DRB345	DQA1	DQB1	DPA1	DPB1	% CV
694	785	637	731	734	650	1,126	721	707	19.43

Exon 2 Average Depth

A	B	C	DRB1	DRB345	DQA1	DQB1	DPA1	DPB1	% CV
694	785	637	731	734	650	1,126	721	707	19.43

Barcode	Locus	Sample	Expected Type Allele 1	Expected Type Allele 2	Allele 1	Allele 2	Field Concordant 3	Field Concordant 4
S1	A	9255	A*02:03:01	A*29:01:01:01	A*02:03:01	A*29:01:01:01	True	True
Exon 2 Average Depth:		813	Exon 2 Min Depth:	437	Average Allele Balance:	0.929		
S1	B	9255	B*07:05:01:01/07:05:01:03	B*15:19	B*07:05:01:01/B*07:05:01:03	B*15:19	True	True
Exon 2 Average Depth:		909	Exon 2 Min Depth:	433	Average Allele Balance:	0.897		
S1	C	9255	C*04:03:01	C*15:05:02	C*04:03:01:01	C*15:05:02:01	True	True
Exon 2 Average Depth:		760	Exon 2 Min Depth:	424	Average Allele Balance:	0.910		
S1	DRB1	9255	DRB1*10:01:01:03	DRB1*15:02:01/15:140/15:149	DRB1*10:01:01:03	DRB1*15:02:01:01	True	True
Exon 2 Average Depth:		881	Exon 2 Min Depth:	598	Average Allele Balance:	0.668		
Exon 1 Average Depth:		212	Exon 1 Min Depth:	180	Ratio:	4.16		
S1	DRB345	9255	DRB345*X	DRB5*01:03	DRB5*01:03	DRB5*01:03	False	False
Exon 2 Average Depth:		523	Exon 2 Min Depth:	384	Average Allele Balance:	NA		
S1	DQA1	9255	DQA1*01:01:01	DQA1*01:05:01	DQA1*01:01:01:07	DQA1*01:05:01:01	True	True
Exon 2 Average Depth:		548	Exon 2 Min Depth:	426	Average Allele Balance:	0.925		
S1	DQB1	9255	DQB1*05:01:01:02	DQB1*05:02:01:01	DQB1*05:01:01:02	DQB1*05:02:01:01	True	True
Exon 2 Average Depth:		817	Exon 2 Min Depth:	311	Average Allele Balance:	0.970		
Exon 1 Average Depth:		430	Exon 1 Min Depth:	382	Ratio:	1.9		
S1	DPA1	9255	DPA1*01:03:01	DPA1*01:03:01	DPA1*01:03:01:01/DPA1*01:03:01:11/DPA1*01:03:01:31/DPA1*01:03:01:33/DPA1*01:03:01:35/DPA1*01:03:01:36/DPA1*01:03:01:37	DPA1*01:03:01:12	True	True
Exon 2 Average Depth:		303	Exon 2 Min Depth:	267	Average Allele Balance:	0.675		
S1	DPB1	9255	DPB1*02:01:02	DPB1*104:01:01:03	DPB1*02:01:02:11	DPB1*104:01:01:03	True	True
Exon 2 Average Depth:		444	Exon 2 Min Depth:	310	Average Allele Balance:	0.874		
Exon 1 Average Depth:		67	Exon 1 Min Depth:	59	Ratio:	6.63		

Report consists of the following information

- Session Information – Includes the session name, TSV application version, catalog id, Lot # (blank field for manual entry), TSV engine version, HLA Library file version,

number of samples, the path of the expected type file selected as input and the version of the file (derived from the file content)

- Concordance Table at 3 field resolution for Allele 1 and Allele 1 per sample.
- No Locus Ref references samples that do not have an expected type in the input file
- An expected No call is considered concordant if there are no call for the sample.
- %CV based on Exon 2 average Depth at the locus level across all samples.
- The Exon 2 min depth is highlighted pink, if %CV > 38%, exon 2 min depth < 100.
- The Exon 2 average allele balance is highlighted if it is <=0.2.
- The Exon 1 min depth is highlighted as pink, if it is < 25.
- Each locus for a barcode has the Sample name, expected type for Allele1, expected type for allele 2, allele 1 ,allele 2, concordance at 3 field , concordance result at 4 field resolution, exon 2 average depth, exon 2 minimum depth and average allele balance
- For samples that were run with Exon 1 DRB1, DQB1 and DPB1 Exon 1 average Depth, Exon 1 Minimum depth and Ratio information is displayed for each barcode.
- Rows with a blue highlight indicate the lack of reference type in the expected fie
- Yellow highlights indicate that the allele is discordant at the 3rd field resolution.
- Red highlights indicate that the allele is discordant at the 4th field resolution.
- Section to include comments, signature and the date.

Expected Type file Format (Excel format)

A	B	C	D	E	F	G	H	I	J	K	L	M	N
Version	1.6												
SAMPLE ID	Code Name	A	A	B	B	C	C	DRB1	DRB1	DRB345	DRB345	DQA	DQA

The format of the file should be .xls

- Cell 1B contains version information (lab can maintain versioning of their internal expected file)
- Header Text for columns A -T on row 2 are in the order of Sample ID, Code Name, A , A, B , B, C, C , DRB1, DRB1, DRB345, DRB345, DQA1, DQA1,DQB1, DQB1,DPA1, DPA1,DPB1, DPB1.
- Homozygous typing should be repeated in both allele cells.
- If a locus is expected to be a No call, it should be marked as an X
- If there is no sequencing information for a particular sample/locus it should be marked as hyphen(-)
- When generating the .pdf report, the software first scans the Sample ID column to match with the sample name in the test sample and then does a secondary scan against the code name column for a match for sample name.

New in v3.0

The results comparison tool displays 2-field Concordance and a summary section when the expected type report is used.
When the reference type for a given sample is missing in the expected type file, the 3, 4 and 2 field concordance is marked as 'No Ref'

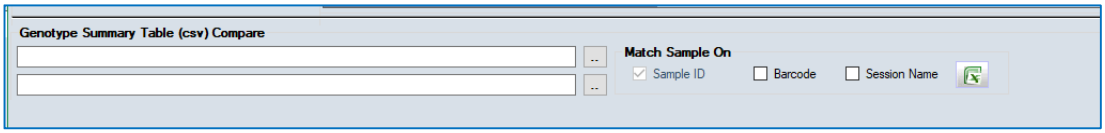
IMGT Version	TSV Engine Version	Barcode	Locus	Expected Type Sample	Expected Type Allele1	Expected Type Allele2	Sample	Allele1	K/N/I	Allele2	K/N/I	3 Field Concordant	4 Field Concordant	2 Field Concordant
3.47.0.0	V3.0.0.40	S18	A	1073	A*01:03	A*26:01:01	1073-18	A*01:03:01:02	[0/0/0]	A*26:01:01:01	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S18	B	1073	B*38:01:01	B*73:01	1073-18	B*38:01:01:01	[0/0/0]	B*73:01:01:01	[0/0/0*]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S18	C	1073	C*12:03:01:01	C*15:05:01	1073-18	C*12:03:01:01	[0/0/0]	C*15:05:01:01	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S18	DRB1	1073	DRB1*11:04:01	DRB1*15:01:01:01	1073-18	DRB1*11:04:01:01	[0/0/0]	DRB1*15:01:01:03/DRB1*15	[0/0/0]	TRUE	FALSE	TRUE
3.47.0.0	V3.0.0.40	S18	DRB345	1073	DRB3*02:02/02:27/02:28	DRB5*01:01	1073-18	DRB3*02:02:01:02	[0/0/0]	DRB5*01:01:01:01	[0/0/16]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S18	DQA1	1073	DQA1*01:02:02	DQA1*05:05:01:01	1073-18	DQA1*01:02:02:04	[0/0/0*]	DQA1*05:05:01:02	[0/0/0]	TRUE	FALSE	TRUE
3.47.0.0	V3.0.0.40	S18	DQB1	1073	DQB1*03:01:01:01	DQB1*05:02:01	1073-18	DQB1*03:01:01:02/DQB1*03	[0/0/0]	DQB1*05:02:01:01/DQB1*05	[0/0/0]	TRUE	FALSE	TRUE
3.47.0.0	V3.0.0.40	S18	DPA1	1073	DPA1*01:03:01:01		1073-18	DPA1*01:03:01:03/DPA1*01	[0/0/0]	DPA1*01:03:01:04/DPA1*01	[0/0/0]	TRUE	FALSE	TRUE
3.47.0.0	V3.0.0.40	S18	DPB1	1073	DPB1*03:01:01	DPB1*04:01:01:01	1073-18	DPB1*03:01:01:01/DPB1*03:	[0/0/0]	DPB1*04:01:01:01/DPB1*04:	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	A	9077	A*02:01:01	A*02:07	9077-5	A*02:01:01:01	[0/0/0]	A*02:07:01:01	[0/0/1]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	B	9077	B*46:01		9077-5	B*46:01:01:01	[0/0/0]	B*46:01:01:01	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	C	9077	C*01:02		9077-5	C*01:02:01:01	[0/0/0]	C*01:02:01:01	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	DRB1	9077	DRB1*09:01:02	DRB1*12:02:01	9077-5	DRB1*09:01:02:01/DRB1*09:	[0/0/0]	DRB1*12:02:01:06	[0/0/1]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	DRB345	9077	DRB3*03:01:03	DRB4*01:03:01	9077-5	DRB3*03:01:03:01	[0/0/0]	DRB4*01:03:01:05/DRB4*01:	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	DQA1	9077	DQA1*03:02	DQA1*06:01	9077-5	DQA1*03:02:01:02	[0/0/0]	DQA1*06:01:01:02	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	DQB1	9077	DQB1*03:01	DQB1*03:03	9077-5	DQB1*03:01:01:07/DQB1*03	[0/0/0]	DQB1*03:03:02:02/DQB1*03	[0/0/0]	TRUE	TRUE	TRUE
3.47.0.0	V3.0.0.40	S5	DPA1	9077			9077-5	DPA1*01:03:01:03/DPA1*01:	[0/0/0]	DPA1*02:02:02:01/DPA1*02:	[0/0/0]	No Ref	No Ref	No Ref
3.47.0.0	V3.0.0.40	S5	DPB1	9077	DPB1*05:01	DPB1*21:01	9077-5	DPB1*05:01:01:01/DPB1*05:	[0/0/0]	DPB1*21:01	[0/0/0]	TRUE	TRUE	TRUE
										Total Concordance Count		17	13	17
										No ref rows		1	1	1
										Total number of rows - "No Ref" rows		17	17	17
										%concordant		100	76.47058824	100

The report includes a total concordance percent for 3 Field, 4 field and 2 field concordance. The concordance calculation does not take the No ref rows in account.

Total Concordance Count	17	13	17
No ref rows	1	1	1
Total number of rows - "No Ref" rows	17	17	17
%concordant	100	76.47058824	100

Comparing Genotype Table reports

Compares the results from the **export** of two genotype summary report. Comparison of the two reports can be a combination of Sample, Barcode and/or Session.



Use the ellipsis search buttons to navigate to and select two existing Genotype Summary Table (csv). Click the Excel icon and receive a comparison of the files. Results are exact string matches.

Any difference in Allele calls or K/N/I will be flagged with a yellow highlight. The comparison tool does comparison of the alleles in the two selected sessions.

The columns are in the following order.

- Session1, Barcode, Sample, Locus, Allele1, K/N/I, Allele2, K/N/I
- Session2, Barcode, Sample, Locus, Allele1, K/N/I, Allele2, K/N/I
- Is Same Allele(s), Is Same KNI, Is Same 3 Field**, Is Same 2 Field**

New in v3.0

The genotype session comparison export reports results now include two additional columns, as denoted above with **

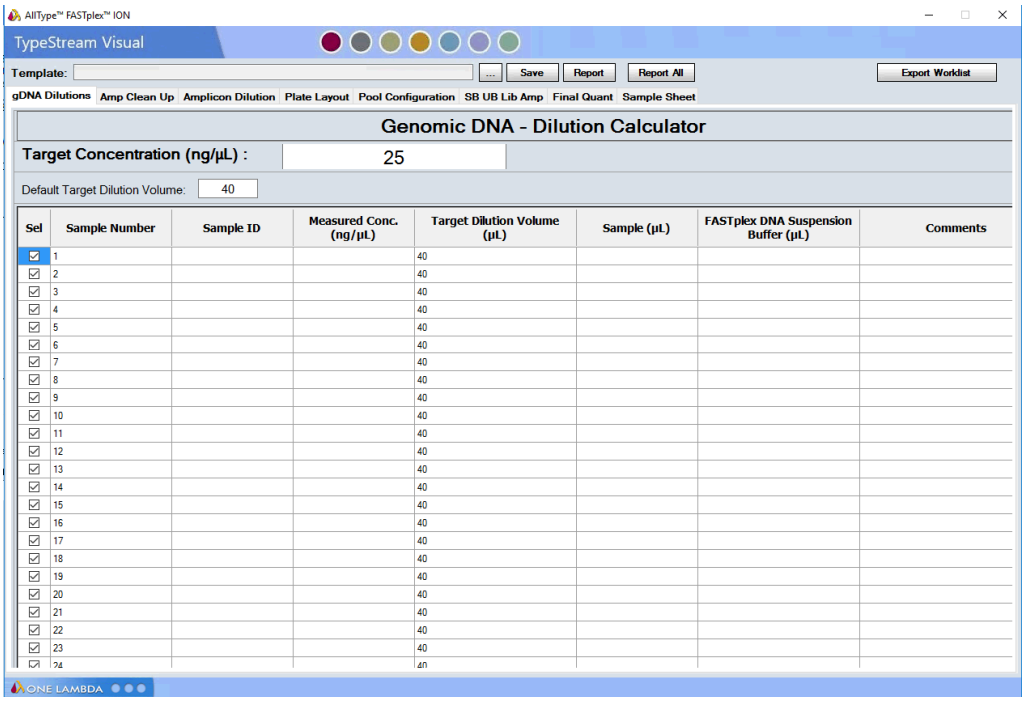
- Is Same 3 Field
- Is Same 2 Field

NGS Calculator

TypeStream Visual provides a calculation tool for AllType FASTplex ION and AllType FASTplex Illumina

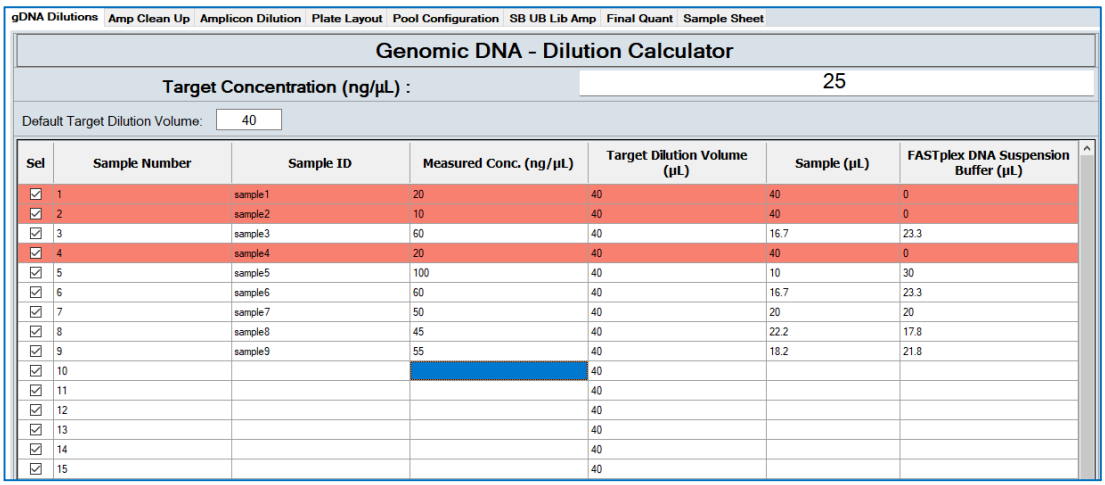
From the TypeStream Main Menu, select Utilities → NGS Calculator

AllType FASTplex ION



NGS Calculator tool is provided within TSV for ION and Illumina for AllType FASTplex Lot 2 and above in place of the "AllType Calculation Tool" supplementary Excel tool. Excel tool will still be required for AllType NGS and AllType FASTplex lot 01.

gDNA Dilutions



Provides calculations for normalizing genomic DNA to 25ng/uL in preparation for Primary PCR amplification. Default dilution volume is 40uL, but this could be adjusted by the user. Users can paste data copied from Excel into the Sample ID and measured conc. Column.

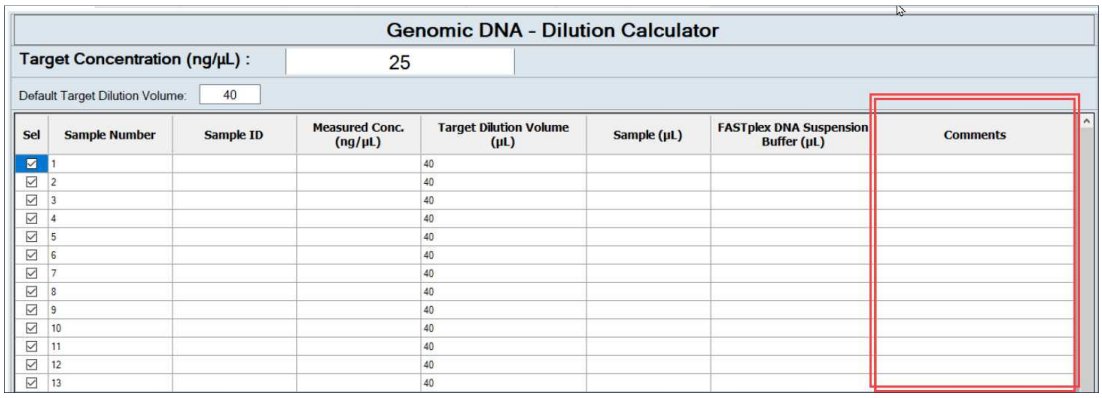
Rows are highlighted in red when the Measured Conc. (ng/µL) value is less than Target Concentration (ng/µL) value.

Users can choose the samples that should be amplified by checking the boxes in the Sel

column.

New in v3.0

The Genomic DNA Dilution Calculator includes a Comments column, which can be used for any purpose desired, such as entering comments for each sample:



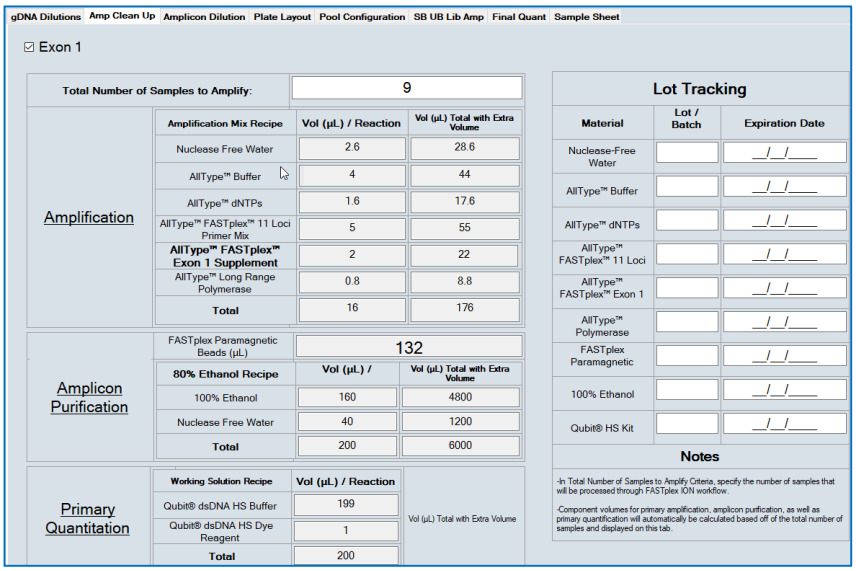
Genomic DNA - Dilution Calculator

Target Concentration (ng/µL) : 25

Default Target Dilution Volume: 40

Sel	Sample Number	Sample ID	Measured Conc. (ng/µL)	Target Dilution Volume (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Comments
☑	1			40			
☑	2			40			
☑	3			40			
☑	4			40			
☑	5			40			
☑	6			40			
☑	7			40			
☑	8			40			
☑	9			40			
☑	10			40			
☑	11			40			
☑	12			40			
☑	13			40			

Amp Clean Up



gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

☑ Exon 1

Total Number of Samples to Amplify: 9

Amplification

Amplification Mix Recipe	Vol (µL) / Reaction	Vol (µL) Total with Extra Volume
Nuclease Free Water	2.6	28.6
AllType™ Buffer	4	44
AllType™ dNTPs	1.6	17.6
AllType™ FASTplex™ 11 Loci Primer Mix	5	55
AllType™ FASTplex™ Exon 1 Supplement	2	22
AllType™ Long Range Polymerase	0.8	8.8
Total	16	176

Amplicon Purification

FASTplex Paramagnetic Beads (µL): 132

80% Ethanol Recipe	Vol (µL) /	Vol (µL) Total with Extra Volume
100% Ethanol	160	4800
Nuclease Free Water	40	1200
Total	200	6000

Primary Quantitation

Working Solution Recipe	Vol (µL) / Reaction	Vol (µL) Total with Extra Volume
Qubit® dsDNA HS Buffer	199	
Qubit® dsDNA HS Dye Reagent	1	
Total	200	

Lot Tracking

Material	Lot / Batch	Expiration Date
Nuclease-Free Water		__/__/____
AllType™ Buffer		__/__/____
AllType™ dNTPs		__/__/____
AllType™ FASTplex™ 11 Loci		__/__/____
AllType™ FASTplex™ Exon 1		__/__/____
AllType™ Polymerase		__/__/____
FASTplex Paramagnetic		__/__/____
100% Ethanol		__/__/____
Qubit® HS Kit		__/__/____

Notes

-In Total Number of Samples to Amplify Criteria, specify the number of samples that will be processed through FASTplex ION workflow.

-Component volumes for primary amplification, amplicon purification, as well as primary quantification will automatically be calculated based off of the total number of samples and displayed on this tab.

Provides volume calculations for amplification, purification and quantitation reagents. The number of samples to amplify is populated automatically based on the samples that were selected in the gDNA dilutions tab. The control is highlighted in red if the number of samples is less than 8.

Users also have an option to include/exclude Exon 1 supplement in the amplification mix by selecting the Exon 1 checkbox.

Lot Tracking section of the screen allows the user to enter material information and its expiration date.

Amplicon Dilution

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

Sel	Sample Number	Sample ID	Amplicon Conc. (ng/µL)	Range	Approximate Input (ng)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)
☑	1	sample1	4		4.186	2	13.3
☑	2	sample2	4		4.186	2	13.3
☑	3	sample3	4		4.186	2	13.3
☑	4	sample4	4		4.186	2	13.3
☑	5	sample5	5		5.233	2	13.3
☑	6	sample6	55	High	10	2.3	97.7
☑	7	sample7	2	Low	8	10	10
☑	8	sample8	4		4.186	2	13.3
☑	9	sample9	4		4.186	2	13.3
☐	10						
☐	11						
☐	12						
☐	13						
☐	14						
☐	15						
☐	16						
☐	17						
☐	18						
☐	19						
☐	20						

Average Input	9.56
Dilution Factor	7.64

Please add amplicon quant values to Input (ng/µL) column.

Enter Stock Sample Volume (µL)	Amplicon Available (µL)	FastPlex DNA Susp Buff (µL)
2	20	13.3

User will input concentration of each purified amplicon in the Amplicon Conc. column. The default amplicon stock volume for dilution is 2uL (Ion and Illumina) but this volume could be adjusted by user.

The row gets highlighted red when the standard dilution > 0 and less than 3 and the Range is marked as "Low". It gets highlighted orange when the standard dilution > 30 and the Range value is marked as "High". The row is read only when there is no Sample ID passed from the gDNA Dilutions which is represented by light grey background and unchecked check box in the first column.

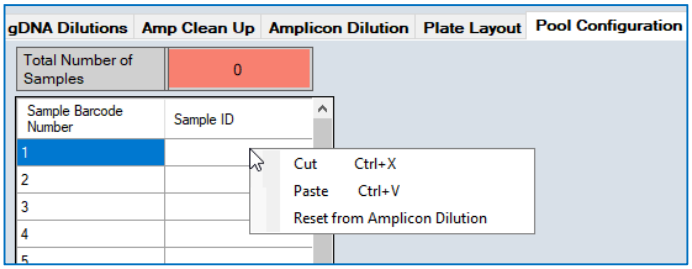
Plate Layout

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

	1		2		3		4		5		6	
A	2	13.3	2	13.3								
B	2	13.3										
C	2	13.3										
D	2	13.3										
E	2	13.3										
F	2.3	97.7										
G	10	10										
H	2	13.3										
	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)
	Samples 1-8		Samples 9-16		Samples 17-24		Samples 25-32		Samples 33-40		Samples 41-48	

Provides a visual aid to assist users identify outliers or samples that need individual concentration adjustment.

Pool Configuration

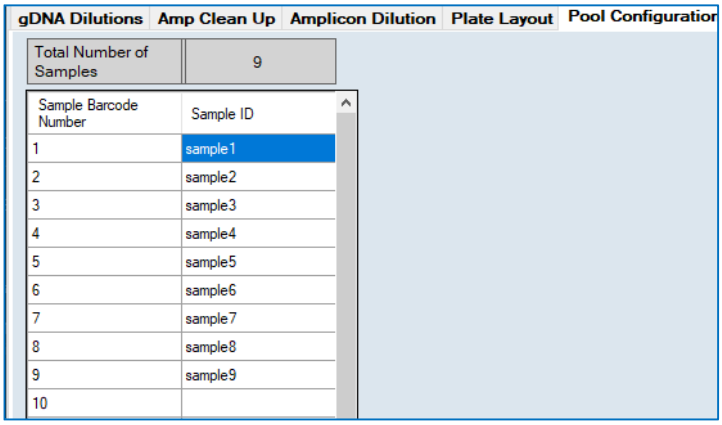


Provides the ability for users to populate the Sample ID column from the amplicon dilution tab. Clicking on "Reset from Amplicon Dilution" will populate the sample ID column with the samples that were selected for final pooling in the amplicon dilution tab. The samples are placed starting on the cell where the user clicked the menu item.

If the user chooses to exclude any samples, they can exclude them in the Amplicon Dilution tab and then redo the pool configuration by selecting the Reset from Amplicon Dilution menu item.

If the user wishes to change the barcode to which the sample will be associated, they can use the Cut and Paste options. Users are warned if the if the count of barcodes to be pasted exceeds the available barcodes in the target location, barcodes might be overwritten.

The sample ID column is read only.



SB UB Lib Amp

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

Sample and Universal Barcoding	9
Sample Barcode Tag	Volume (µL)
Diluted Amplicon	8
FASTplex Sample Barcode Reagent	16
FASTplex Barcoding Buffer	12
Sample Barcode Stop	Volume (µL)
FASTplex Stop Solution	18
Purification of stopped, pooled SB reaction	Volume (µL)
Volume of stopped, pooled SB reaction	162
Volume of Paramagnetic Beads	162
Ethanol Formulation for Each Purification	Volume (µL)
Volume 100% Ethanol	4000
Volume of Nuclease Free Water	1000
Sample Barcode Resuspension	Volume (µL)
FASTplex DNA Suspension Buffer	50
UB reaction set-up	Volume (µL)
Volume of purified SB eluate	48
Volume of UB reagent	1.9
Volume of Barcoding Buffer	25
UB reaction Stop	Volume (µL)
Volume of Stop Solution	37
Purification of stopping UB reaction	Volume (µL)
Volume of stopped UB reaction	112
Volume of Paramagnetic Beads	112
Universal Barcode Resuspension	Volume (µL)
FASTplex DNA Suspension Buffer	13

Library Amplification	
Library Amplification Mix Recipe	Volume (µL)
Volume of Purified Library Pool	10
Volume of FASTplex Library Amp Mix	75
Volume of FASTplex Library Primer Flex Mix	15
Library Purification	Volume (µL)
Volume of Diluted Library	400
Volume of Paramagnetic Bead(1st Add)	240
Volume of Supernatant Transfer	580
Volume of Paramagnetic Bead (2nd Add)	65.5
Library Resuspension	Volume (µL)
FASTplex DNA Suspension Buffer	35

Lot Tracking

Material	Lot / Batch Number	Expiration Date
FASTplex Sample Barcode Reagent		__/__/____
FASTplex Barcoding Buffer		__/__/____
FASTplex Stop Solution		__/__/____
FASTplex Paramagnetic Beads		__/__/____
FASTplex Univ Barcode P1		__/__/____
FASTplex DNA Suspension Buffer		__/__/____
FASTplex Paramagnetic Beads		__/__/____
FASTplex Library Amp Mix		__/__/____
100% Ethanol		__/__/____
Nuclease Free Water		__/__/____

Notes

-Total number of samples and number of sample barcodes will be based off of the number of Sample IDs input in the Pool Configuration tab.

-Component volumes for sample barcoding purification, universal barcoding reaction, universal barcoding stop reaction, universal barcode purification, as well as library amplification will automatically be calculated based off of the number of sample barcodes per pool and displayed on this tab.

Provides calculations for Sample Barcoding, Universal Barcoding, and Library Amplification steps. The reagent volumes will change depending on the number of samples.

The Lot Tracking section allows users to enter the Lot /Batch number for each of the materials that will be saved as part of the Save Template feature.

Final Quant

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

Pool Quantitation

Working Solution Recipe	Vol (µL)/Reaction	Vol (µL)
Qubit® dsDNA HS Buffer	199	1990
Qubit® dsDNA HS Dye Reagent	1	10
Total	200	2000

Recommended: Once made according to the recipe below, read diluted pool to ensure target concentration has been met.

Pool Dilution	Total Number of Pools	1
Readings	-	
Pool Quant Values (ng/µL)	0	
Dilution Concentration and Volume Targets	-	
Desired Target Concentration (ng/µL)	0.045	
Diluted Pool Volume (µL)	100	
Dilution Formulation	-	
Sample Pool Volume for Dilution (µL)	100	
FASTplex DNA Suspension Buffer (µL)	0	
Final Loaded Library Concentration		

Lot Tracking

Material	Lot / Batch Number	Expiration Date
Qubit® HS Kit		__/__/____
FASTplex DNA suspension Buffer		__/__/____

Notes

-Once measured, input readings into the Pool Quant Values (ng/µL) section for each pool measured.

-Ensure the target concentration matches the recommended concentration for the platform being used.

-Adjust diluted pool volume if necessary.

-Formulate pool dilutions as detailed on this tab.

-Confirm target concentration has been met once formulation has been completed.

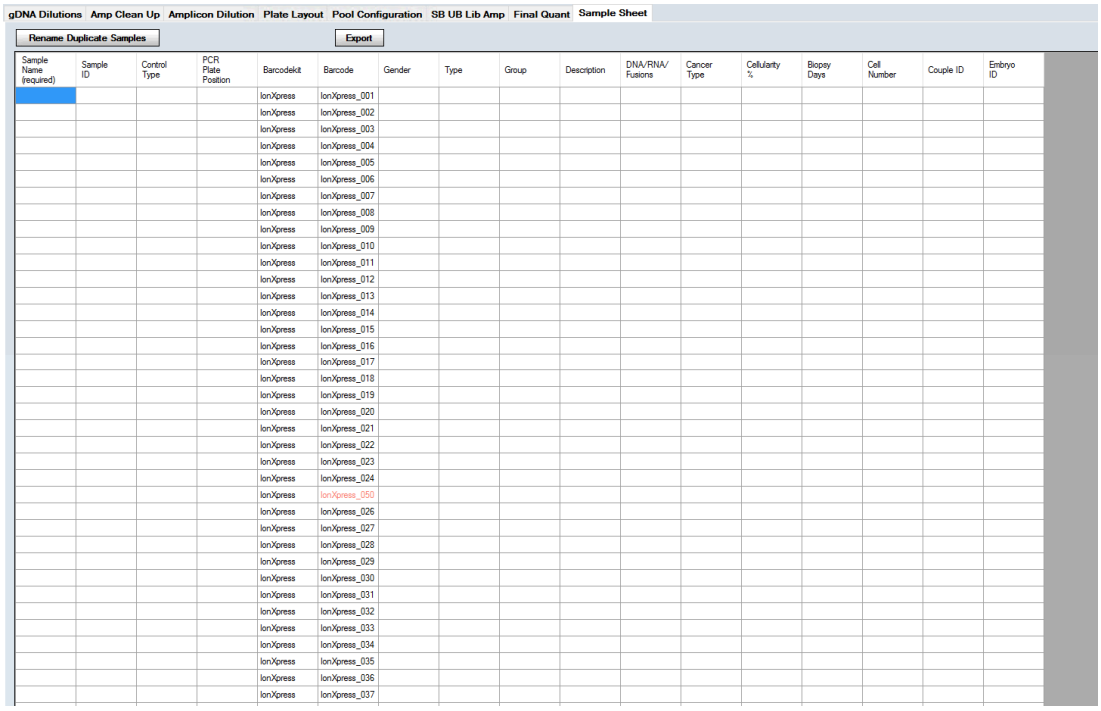
Default Desired Target Concentration (ng/µL): 0.045

User will input library concentration in yellow cell, and concentration will be adjusted for sequencing on the Ion Gene Studio (0.045ng/uL).

The Lot Tracking section allows users to enter the Lot /Batch number for each of the materials

that will be saved as part of the Save Template feature.

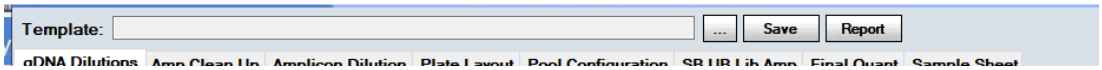
Sample Sheet



Allows users to create a sample sheet that can be used for the sequencing run.

Rename Duplicate Sample ID button renames the duplicate Sample ID's by appending a sequential number to the end of the sample name with a hypen. Both the Sample Name and the Sample ID column values are duplicated in its value.

> **NOTE:** Barcode 24 is replaced by Barcode 50 and barcode 44 replaced by Barcode 49.
>
> Save and Report button from the Sample Sheet perform no action when clicked from the Sample Sheet tab.

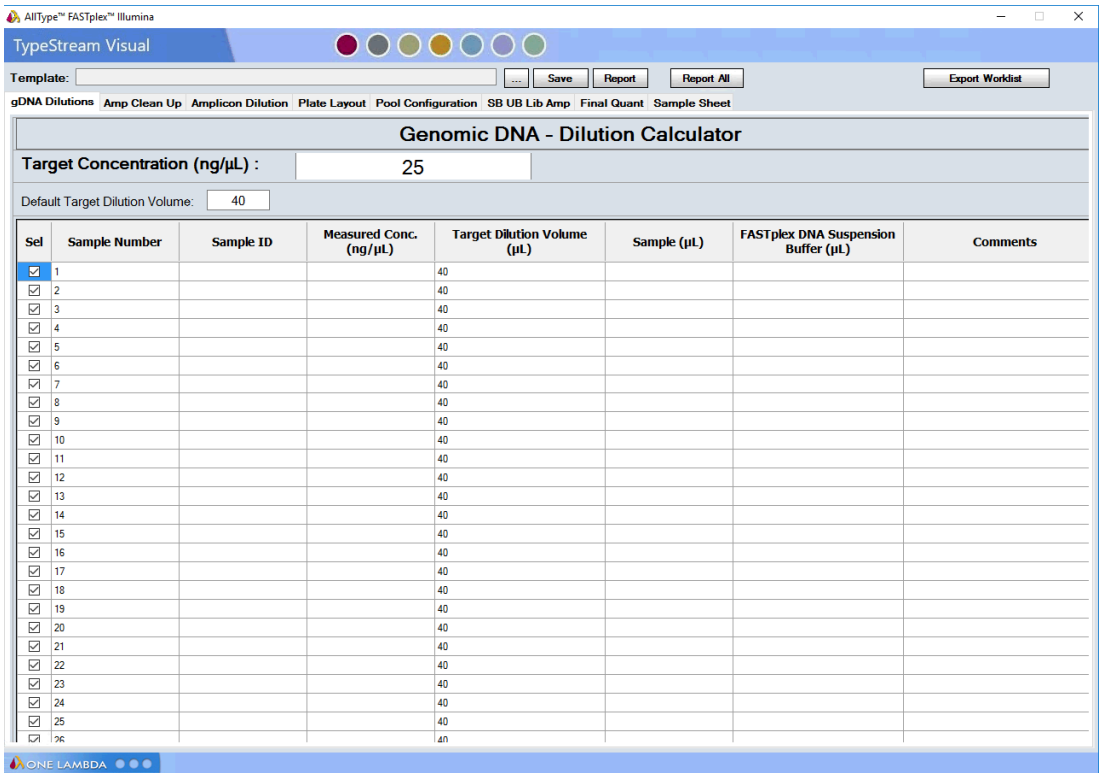


Save button allows the user to save the changes made in each of the tabs below.

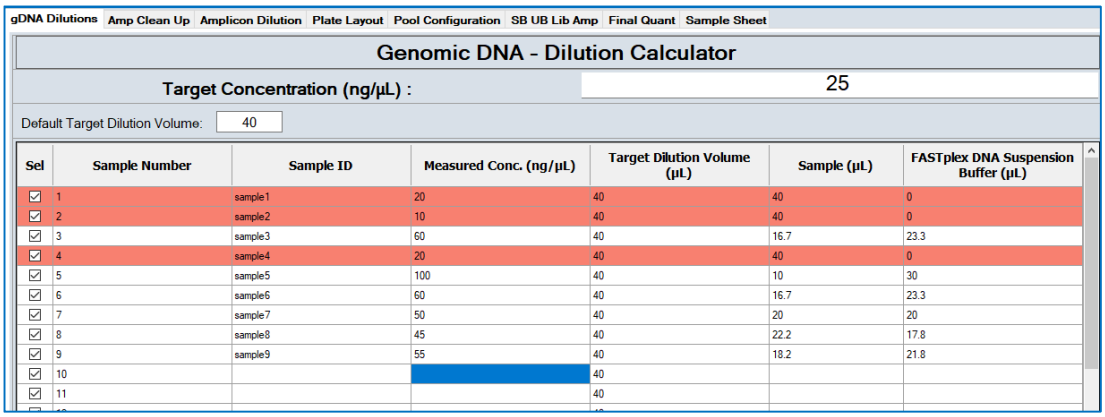
User can retrieve the saved data by clicking the Browse button.

Report button allows the user to generate a report for the current selected tab in the NGS calculator window.

AllType FASTplex Illumina



gDNA Dilutions



Provides calculations for normalizing genomic DNA to 25ng/uL in preparation for Primary PCR amplification. Default dilution volume is 40uL, but this could be adjusted by user. Users can paste data copied from Excel into the Sample ID and measured conc. Column.

Rows are highlighted in red when the Measured Conc. (ng/µL) value is less than Target Concentration (ng/µL) value.

Users can choose the samples that should be amplified by checking the boxes in the Sel column.

New in v3.0

The Genomic DNA Dilution Calculator includes a Comments column, which can be used for any

purpose desired, such as entering comments for each sample:

Genomic DNA - Dilution Calculator

Target Concentration (ng/µL) : 25

Default Target Dilution Volume: 40

Sel	Sample Number	Sample ID	Measured Conc. (ng/µL)	Target Dilution Volume (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Comments
☑	1			40			
☑	2			40			
☑	3			40			
☑	4			40			
☑	5			40			
☑	6			40			
☑	7			40			
☑	8			40			
☑	9			40			
☑	10			40			
☑	11			40			
☑	12			40			
☑	13			40			

Amp Clean Up

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

☑ Exon 1

Total Number of Samples to Amplify: 9

Amplification

Amplification Mix Recipe	Vol (µL) / Reaction	Vol (µL) Total with Extra Volume
Nuclease Free Water	2.6	28.6
AllType™ Buffer	4	44
AllType™ dNTPs	1.6	17.6
AllType™ FASTplex™ 11 Loci Primer Mix	5	55
AllType™ FASTplex™ Exon 1 Supplement	2	22
AllType™ Long Range Polymerase	0.8	8.8
Total	16	176

Amplicon Purification

FASTplex Paramagnetic Beads (µL): 132

80% Ethanol Recipe	Vol (µL) /	Vol (µL) Total with Extra Volume
100% Ethanol	160	4800
Nuclease Free Water	40	1200
Total	200	6000

Primary Quantitation

Working Solution Recipe	Vol (µL) / Reaction
Qubit® dsDNA HS Buffer	199
Qubit® dsDNA HS Dye Reagent	1
Total	200

Vol (µL) Total with Extra Volume

Lot Tracking

Material	Lot / Batch	Expiration Date
Nuclease-Free Water		__/__/____
AllType™ Buffer		__/__/____
AllType™ dNTPs		__/__/____
AllType™ FASTplex™ 11 Loci		__/__/____
AllType™ FASTplex™ Exon 1		__/__/____
AllType™ Polymerase		__/__/____
FASTplex Paramagnetic		__/__/____
100% Ethanol		__/__/____
Qubit® HS Kit		__/__/____

Notes

-In Total Number of Samples to Amplify Criteria, specify the number of samples that will be processed through FASTplex Illumina workflow.

-Component volumes for primary amplification, amplicon purification, as well as primary quantification will automatically be calculated based off of the total number of samples and displayed on this tab.

Provides volume calculations for amplification, purification and quantitation reagents. The number of samples to amplify is populated automatically based on the samples that were selected in the gDNA dilutions tab. The number of samples can be updated as well.

The control is highlighted in red if the number of samples is less than 8.

Users also have an option to include/exclude Exon 1 supplement in the amplification mix by selecting the Exon 1 checkbox.

Lot Tracking section of the screen allows the user to enter material information and it's expiration date.

Amplicon Dilution

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

Sel	Sample Number	Sample ID	Amplicon Conc. (ng/µL)	Range	Approximate Input (ng)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)
☑	1	sample1	4	Low	8	5	15
☑	2	sample2	4	Low	8	5	15
☑	3	sample3	4	Low	8	5	15
☑	4	sample4	4	Low	8	5	15
☑	5	sample5	44	High	20	5.7	94.3
☑	6	sample6	55	High	20	4.5	95.5
☑	7	sample7	5		3.543	2	9.3
☑	8	sample8	3	Low	8	6.7	13.3
☑	9	sample9	4	Low	8	5	15
☐	10						
☐	11						
☐	12						
☐	13						
☐	14						
☐	15						
☐	16						
☐	17						
☐	18						
☐	19						
☐	20						

Average Input	14.11
Dilution Factor	5.64

Please add amplicon quant values to Input (ng/µL) column.

Enter Stock Sample Volume (µL)	Amplicon Available (µL)	FastPlex DNA Susp Buff (µL)
2	20	9.3

User will input concentration of each purified amplicon in the Amplicon Conc. column. The default amplicon stock volume for dilution is 2uL but this volume could be adjusted by user. Average amplicon input is 20ng, and the acceptable range is 3-30ng for both Ion and Illumina. Any sample outside the acceptable range (3-30ng) is flagged and adjusted manually to reach an input of 8ng (Ion) or 4ng (Illumina).

The row gets highlighted red when the standard dilution > 0 and less than 3 and the Range is marked as "Low". It gets highlighted orange when the standard dilution > 30 and the Range value is marked as "High". The row is read only when there is no Sample ID passed from the gDNA Dilutions which is represented by light grey background and unchecked check box in the first column.

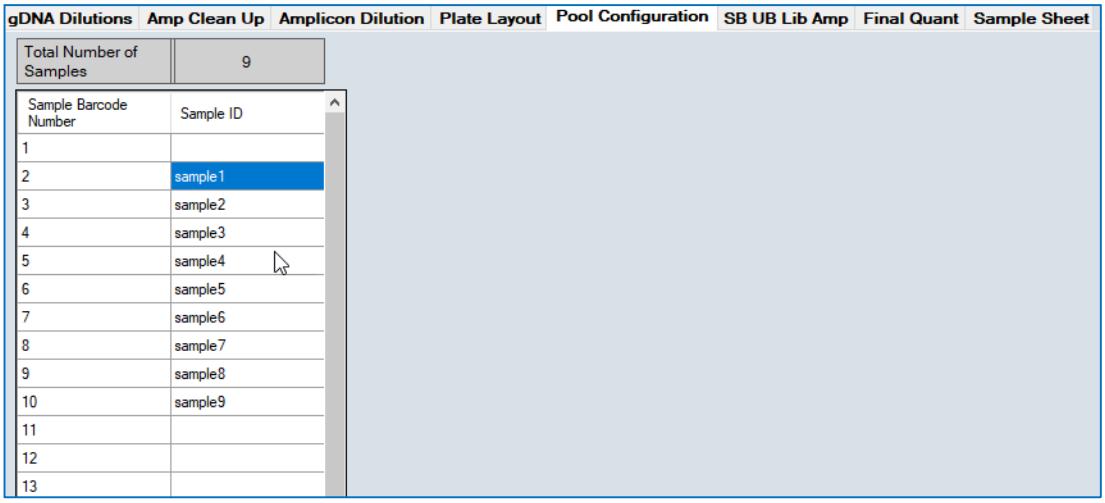
Plate Layout

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

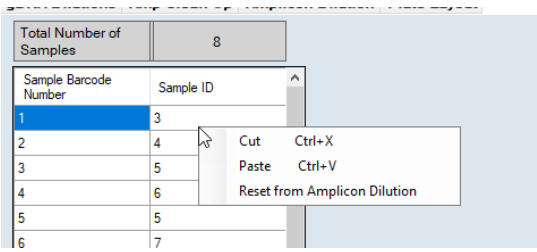
	1		2		3		4		5		6		7		8		9		10		11		12	
A	5	15	5	15																				
B	5	15																						
C	5	15																						
D	5	15																						
E	5.7	94.3																						
F	4.5	95.5																						
G	2	9.3																						
H	6.7	13.3																						
	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)	Sample (µL)	FASTplex DNA Suspension Buffer (µL)
	Samples 1-8		Samples 9-16		Samples 17-24		Samples 25-32		Samples 33-40		Samples 41-48		Samples 49-56		Samples 57-64		Samples 65-72		Samples 73-80		Samples 81-88		Samples 89-96	

Provides a visual aid to assist users identify outliers or samples that need individual concentration adjustment.

Pool Configuration



Right clicking on the Sample ID columns displays a menu item as below.

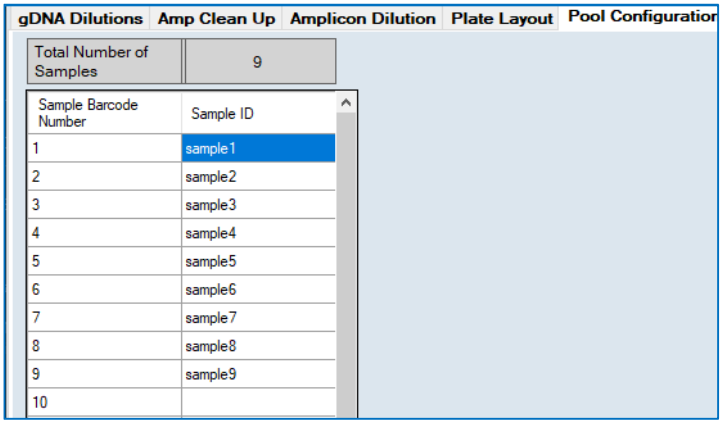


Provides the ability for users to populate the Sample ID column from the amplicon dilution tab. Clicking on "Reset from Amplicon Dilution" will populate the sample ID column with the samples that were selected for final pooling in the amplicon dilution tab. The samples are placed starting on the cell that the user clicked the menu item.

If the user chooses to exclude any samples, they can exclude in the Amplicon Dilution tab and then redo the pool configuration by selecting the Reset from Amplicon Dilution menu item.

If the user wishes to change the barcode to which the sample will be associated to, they can use the Cut and Paste options. A warning appears if the count of barcodes to be pasted exceeds the available barcodes in the target location, barcodes might be overwritten.

The sample ID column is read only.



SB UB Lib Amp

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

Sample and Universal Barcoding	9
Sample Barcode Tag	Volume (µL)
Diluted Amplicon	4
FASTplex Sample Barcode Reagent	6
FASTplex Barcoding Buffer	5
Sample Barcode Stop	Volume (µL)
FASTplex Stop Solution	7.5
Purification of stopped, pooled SB reaction	Volume (µL)
Volume of stopped, pooled SB reaction	90
Volume of Paramagnetic Beads	81
Ethanol Formulation for Each Purification	Volume (µL)
Volume 100% Ethanol	4000
Volume of Nuclease Free Water	1000
Sample Barcode Resuspension	Volume (µL)
FASTplex DNA Suspension Buffer	54
UB reaction set-up	Volume (µL)
Volume of purified SB eluate	48
Volume of UB reagent	4
Volume of Barcoding Buffer	26
UB reaction Stop	Volume (µL)
Volume of Stop Solution	39
Purification of stopping UB reaction	Volume (µL)
Volume of stopped UB reaction	117
Volume of Paramagnetic Beads	117
Universal Barcode Resuspension	Volume (µL)
FASTplex DNA Suspension Buffer	20

Library Amplification	
Library Amplification Mix Recipe	Volume (µL)
Volume of Purified Library Pool	17
Volume of FASTplex Library Amp Mix	75
Volume of FASTplex Library Primer Flex Mix	8
Library Purification	Volume (µL)
Volume of Diluted Library	200
Volume of Paramagnetic Bead(1st Add)	160
Library Resuspension	Volume (µL)
FASTplex DNA Suspension Buffer	35

Lot Tracking

Material	Lot / Batch Number	Expiration Date
FASTplex Sample Barcode Reagent		__/__/____
FASTplex Barcoding Buffer		__/__/____
FASTplex Stop Solution		__/__/____
FASTplex Paramagnetic Beads		__/__/____
FASTplex Univ Barcode P1		__/__/____
FASTplex DNA Suspension Buffer		__/__/____
FASTplex Paramagnetic Beads		__/__/____
FASTplex Library Amp Mix		__/__/____
100% Ethanol		__/__/____
Nuclease Free Water		__/__/____

Notes

-Total number of samples and number of sample barcodes will be based off of the number of Sample IDs input in the Pool Configuration tab.

-Component volumes for sample barcoding purification, universal barcoding reaction, universal barcoding stop reaction, universal barcode purification, as well as library amplification will automatically be calculated based off of the number of sample barcodes per pool and displayed on this tab.

Provides calculations for Sample Barcoding, Universal Barcoding, and Library Amplification steps. The reagent volumes will change depending on the number of samples.

Lot Tracking section of the screen allows the user to enter material information and its expiration date.

Final Quant

gDNA Dilutions | Amp Clean Up | Amplicon Dilution | Plate Layout | Pool Configuration | SB UB Lib Amp | Final Quant | Sample Sheet

MiSeq

Pool Quantitation

Working Solution Recipe	Vol (µL)/Reaction	Vol (µL)
Qubit® dsDNA HS Buffer	199	1990
Qubit® dsDNA HS Dye Reagent	1	10
Total	200	2000

Lot Tracking

Material	Lot / Batch Number	Expiration Date
Qubit® HS Kit		__/__/____
FASTplex DNA suspension Buffer		__/__/____

Recommended: Once made according to the recipe below, read diluted pool to ensure target concentration has been met.

Pool Dilution	Total Number of Pools	1
Readings	-	
Pool Quant Values (ng/µL)	0	
Dilution Concentration and Volume Targets	-	
Desired Target Concentration (ng/µL)	2.1	
Diluted Pool Volume (µL)	100	
Dilution Formulation	-	
Sample Pool Volume for Dilution (µL)	100	
FASTplex DNA Suspension Buffer (µL)	0	
Final Loaded Library Concentration		

Notes

-Once measured, input readings into the Pool Quant Values (ng/µL) section for each pool measured.

-Ensure the target concentration matches the recommended concentration for the platform being used.

-Adjust diluted pool volume if necessary.

-Formulate pool dilutions as detailed on this tab.

-Confirm target concentration has been met once formulation has been completed.

Default Desired Target Concentration (ng/µL) for MiSeq: 2.1

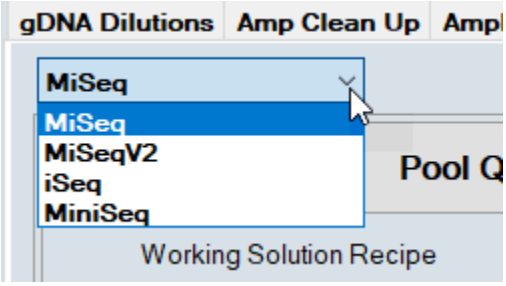
Default Desired Target Concentration (ng/µL) for MiSeqV2: 2.1

Default Desired Target Concentration (ng/µL) for iSeq: 0.056

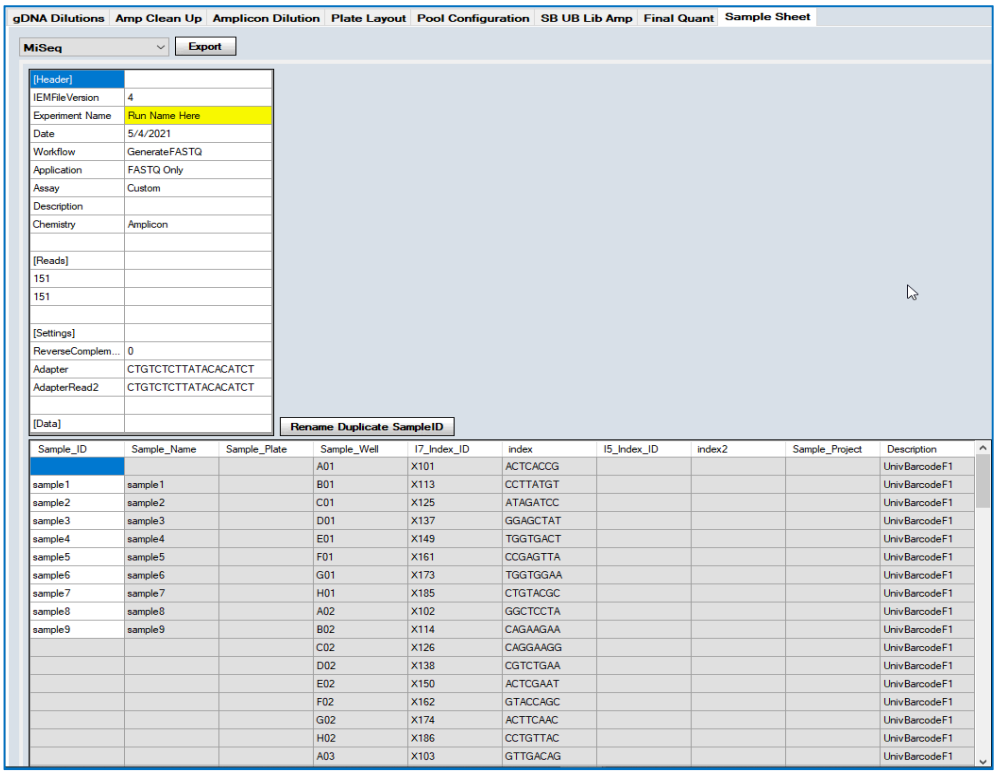
Default Desired Target Concentration (ng/µL) for MiniSeq: 0.53

User will input library concentration in yellow cell, and concentration will be adjusted for sequencing on the Miseq (2.1ng/uL), Miniseq (0.53ng/uL), iSeq (0.56ng/uL) . The calculations /

default values are updated based on the drop-down list that list the different sequencers that are supported as in the below. Users must select one of the 4 drop-down items.



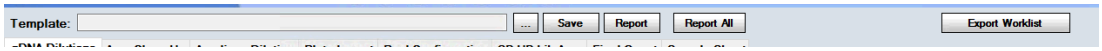
Sample Sheet



Allows users to create a sample sheet that can be used for the sequencing run. The software provides a dropdown list to the user to select the sequencer platform (MiSeq, MiSeq v2, iSeq MiniSeq). This tab is refreshed based on the sequencer selected in the Final Quant tab.

Rename Duplicate Sample ID button renames the duplicate Sample ID's by appending a sequential number to the end of the sample name with a hypen. Both the Sample Name and the Sample ID column values are duplicated in its value

> **NOTE:** Save and Report button from the Sample Sheet perform no action when clicked from the Sample Sheet tab.

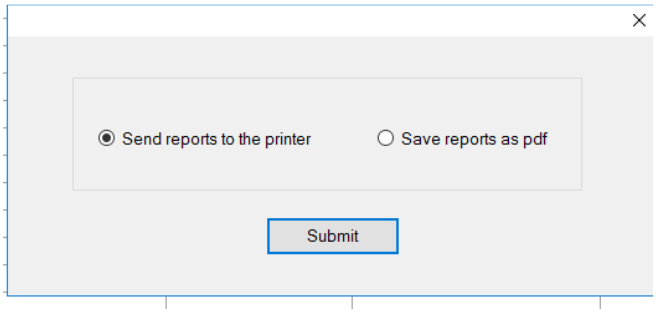


Save button allows the user to save the changes made in each of the tabs below.

User can retrieve the saved data by clicking the Browse button.

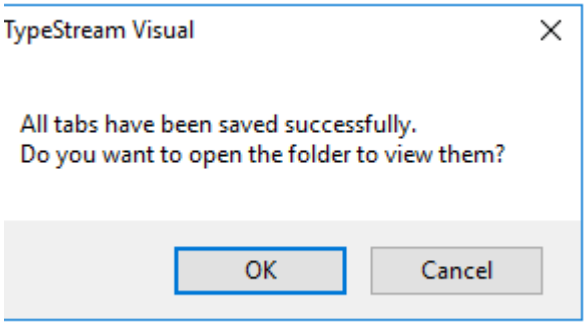
Report button allows the user to generate a report for the current selected tab in the NGS calculator window.

Report All button allows the user to direct the report exports for all the tabs to a printer or generate .pdf.

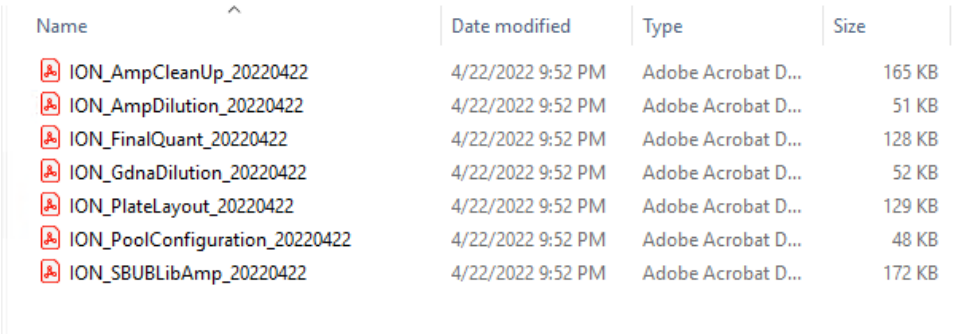


Choosing the Save reports as pdf exports the report to C:\OLI TSV\data\export\NgsCalculatorPdf

User can choose to review the generated reports by clicking OK on the message box.



The pdf generated has the naming convention #instrument name#_#tab name#dateofexport



Name	Date modified	Type	Size
ION_AmpCleanUp_20220422	4/22/2022 9:52 PM	Adobe Acrobat D...	165 KB
ION_AmpDilution_20220422	4/22/2022 9:52 PM	Adobe Acrobat D...	51 KB
ION_FinalQuant_20220422	4/22/2022 9:52 PM	Adobe Acrobat D...	128 KB
ION_GdnaDilution_20220422	4/22/2022 9:52 PM	Adobe Acrobat D...	52 KB
ION_PlateLayout_20220422	4/22/2022 9:52 PM	Adobe Acrobat D...	129 KB
ION_PoolConfiguration_20220422	4/22/2022 9:52 PM	Adobe Acrobat D...	48 KB
ION_SBUBLibAmp_20220422	4/22/2022 9:52 PM	Adobe Acrobat D...	172 KB

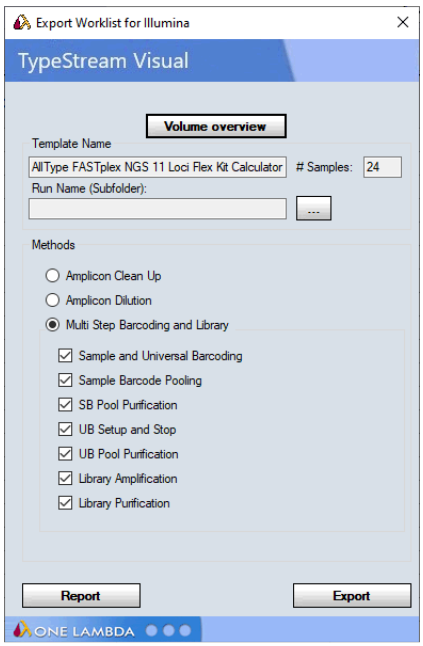
Export Worklist from FASTplex Ion / Illumina Calculator

As described in the previous steps, user can enter or import values (such as “Sample ID”, “Measured Conc. (ng/ µL)”, “Target Dilution Volume (µL)”) into the calculator data grid for Ion or Illumina and save the information. Subsequently, the calculator calculates and displays the required reagent volumes in the related assay steps / tabs.

"Export Worklist" button provides the functionality to export the information present in the calculator to a formatted csv file.

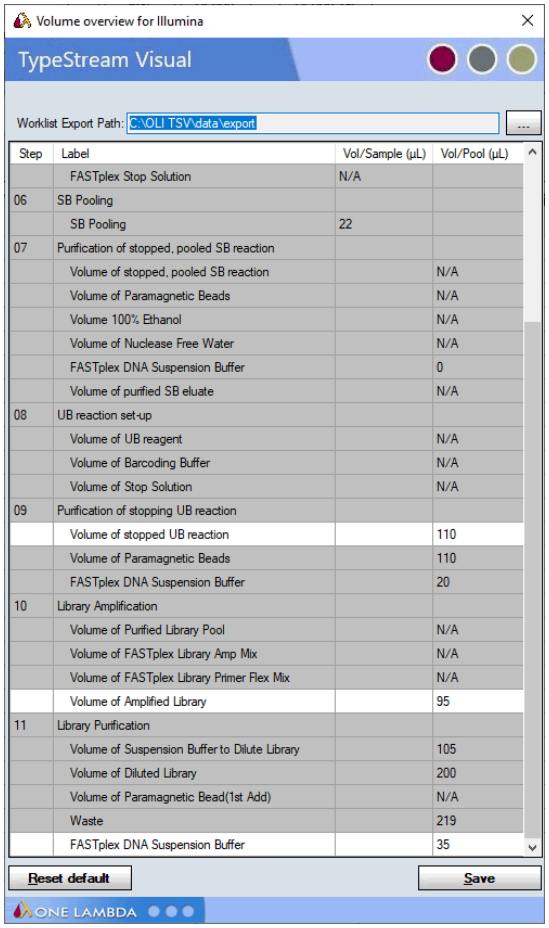
Export Worklist

Export Worklist dialog (for Illumina or Ion) provides the assay volume overview and lets the user export the data for selected assay step(s) and generates reports.



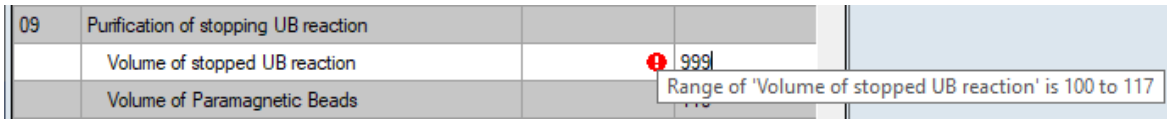
Volume Overview

"Volume overview" button in the Export Worklist dialog lets the user change and save Worklist Export Path and other configurable volumes (white rows). "Reset default" resets the values to default values.



Step	Label	Vol/Sample (µL)	Vol/Pool (µL)
	FASTplex Stop Solution	N/A	
06	SB Pooling		
	SB Pooling	22	
07	Purification of stopped, pooled SB reaction		
	Volume of stopped, pooled SB reaction		N/A
	Volume of Paramagnetic Beads		N/A
	Volume 100% Ethanol		N/A
	Volume of Nuclease Free Water		N/A
	FASTplex DNA Suspension Buffer		0
	Volume of purified SB eluate		N/A
08	UB reaction set-up		
	Volume of UB reagent		N/A
	Volume of Barcoding Buffer		N/A
	Volume of Stop Solution		N/A
09	Purification of stopping UB reaction		
	Volume of stopped UB reaction		110
	Volume of Paramagnetic Beads		110
	FASTplex DNA Suspension Buffer		20
10	Library Amplification		
	Volume of Purified Library Pool		N/A
	Volume of FASTplex Library Amp Mix		N/A
	Volume of FASTplex Library Primer Flex Mix		N/A
	Volume of Amplified Library		95
11	Library Purification		
	Volume of Suspension Buffer to Dilute Library		105
	Volume of Diluted Library		200
	Volume of Paramagnetic Bead(1st Add)		N/A
	Waste		219
	FASTplex DNA Suspension Buffer		35

Error Indicator and tooltip pops up if selected value is out of range.



Report

Button “Report” generates report with reagent, resource calculation and sample information in for selected assay step(s).

FASTplex Reagent and Resource Calculation for Illumina

Amplicon Clean up

Reagents:

Number of samples: 48

Reagent	Volume
FASTplex Paramagnetic Beads	1176µL
80% Ethanol	12800µL
FASTplex DNA Suspension Buffer	3400µL

Preparations:

80 % Ethanol	12800µL
Ethanol	10240µL
Water	2560µL

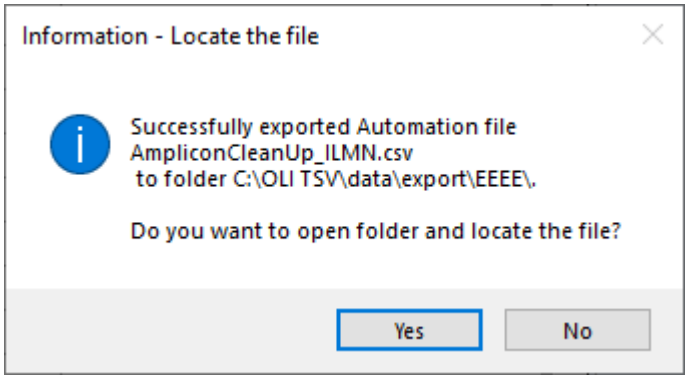
Plates
Amplicon Plate
Nunc Round Bottom (Clean) - 2
ABI Ring Magnet

Sample Information

#	Sample ID	Measured Conc. (ng/µL)	Tar. Dilution Volume (µL)	FASTplex DNA Susp. (µL)
1	1	50	20	20
2	2	55	18.2	21.8
3	3	60	16.7	23.3
4	4	70	14.3	25.7
5	5	80	12.5	27.5
6	6	90	11.1	28.9
7	7	100	10	30
8	8	50	20	20

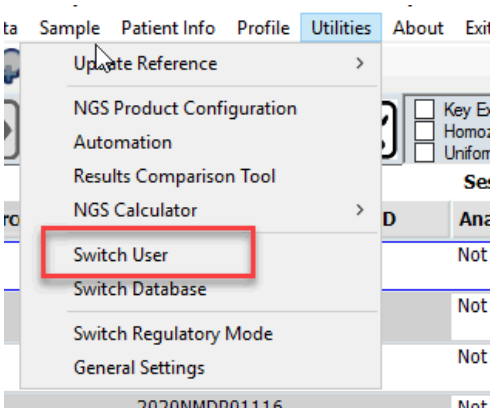
Export

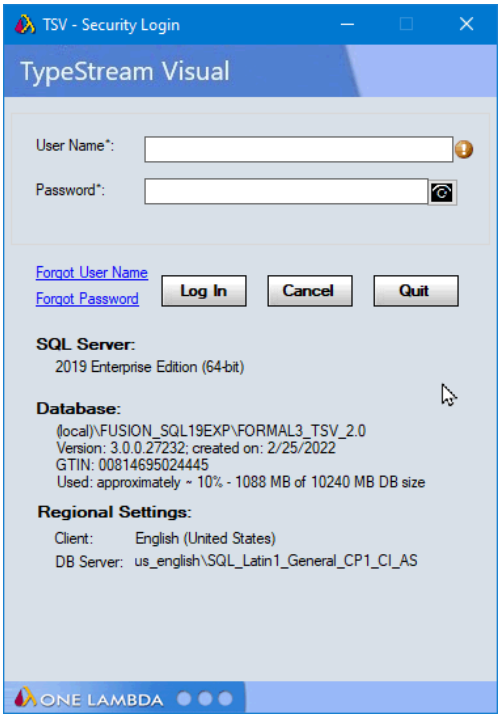
"Export" button exports the formatted csv file under the selected "Run Name" subfolder with the following dialog:



Switch User

TypeStream Visual allows you to switch the active user. From the TypeStream Main Menu, select Utilities → Switch User. The following screen will now appear:



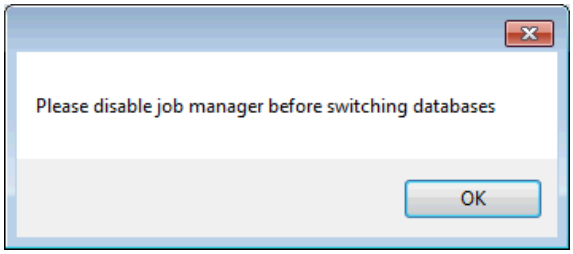


Supply the username and password of the desired user. If the login is successful, the system will log the user in and proceed to the TypeStream Home Screen.

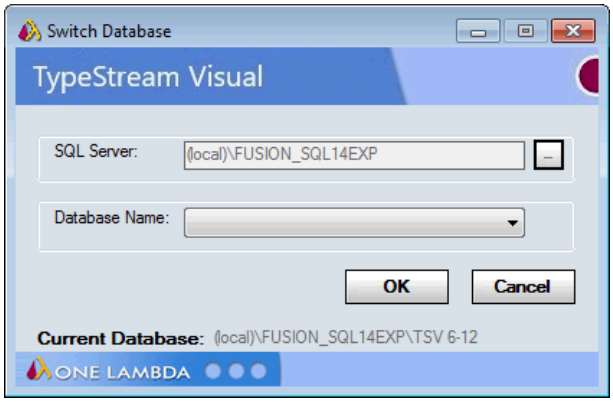
Note: User cannot switch the mode of operation (RUO/IVD) when using the Switch User mode.

Switch Database

TypeStream Visual allows you to switch the active database. From the TypeStream Main Menu, select Utilities → Switch Database. If job manager is currently enabled, the following message will appear:



Disable the job manager and navigate again to Utilities → Switch Database. The following screen will appear:



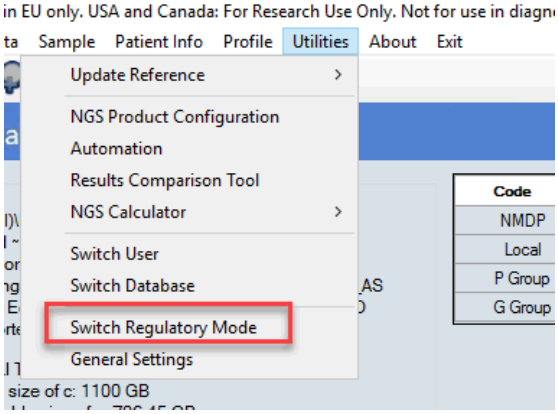
Use the drop down control to select the database name, then click the OK button. If the database choice is valid, the system will attach the database and proceed to the TypeStream Login Screen. Login as you would when first opening the application.

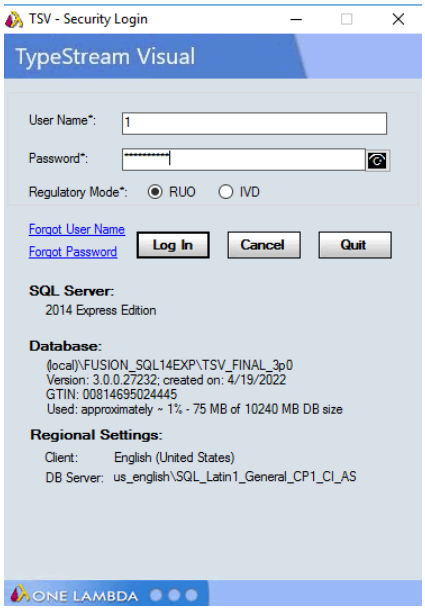
If you click Cancel on the login screen, the application will close but will retain the switched database as the one to which the user is connected.

> NOTE: The database to which you are switching must be from the same release as the current. For example, if you are currently using TSV 2.0, you will not be able to switch to a database from a previous version, e.g., TSV 1.3, without upgrading it first. "Upgrade Database" functionality can be found in the Database Utility.

Switch Regulatory Mode

TypeStream Visual allows you to switch the regulatory mode.



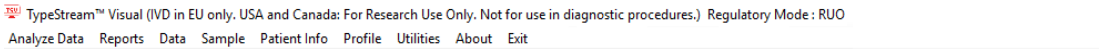


Users can switch regulatory mode when a job is running.

Clicking on Quit will re-login the current user into the application and pop up a confirmation message for the user to take action. This is like when the user would click on "Exit" button from the Home page.

The user can switch to a different user when in the login screen.

The title bar on the home page reflects the regulatory mode the user is logged in.



General Settings

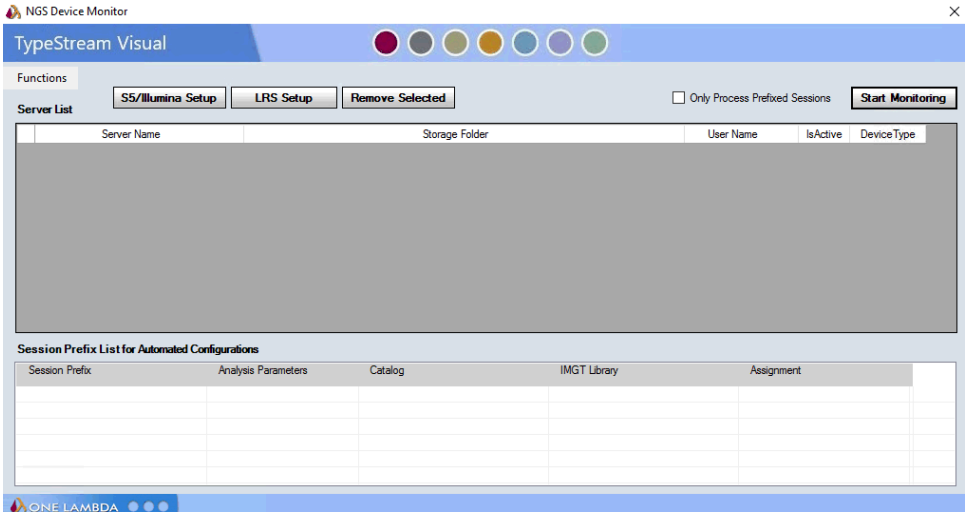
See previous chapters for general settings.

4

Automation

Automation (Auto-Analysis)

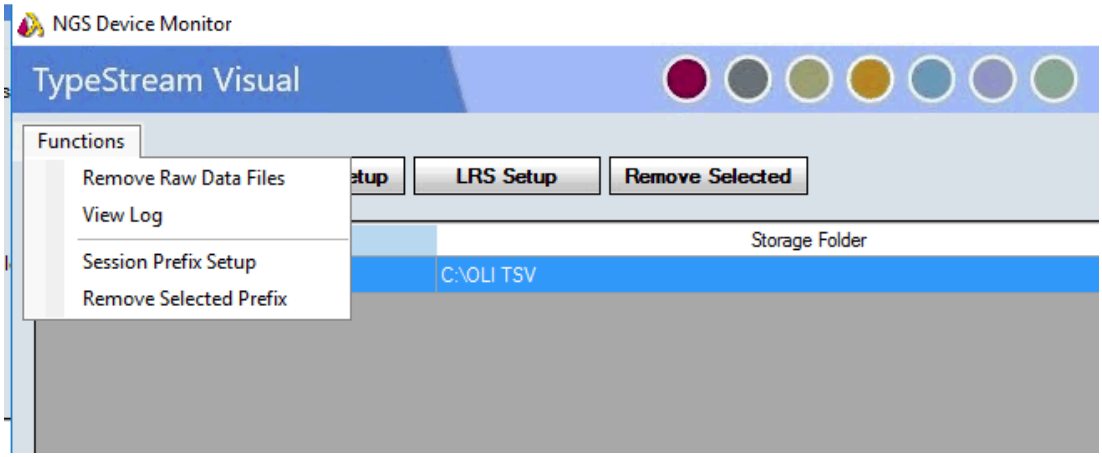
TypeStream Visual can be configured to automatically download and analyze data from Ion S5 , Illumina MiSeq, Illumina MiniSeq , Illumina iSeq sequencers and Long Read Sequencers. To do so select Utilities → Automation from the menu bar. The following NGS Device Monitor screen will display:



All configured servers will be displayed on the server list. All servers are checked 'IsActive' by default. Clicking "Remove Selected" will remove the selected server from the server list.

Ion S5 files will be downloaded to your local drive in order to analyze the data. MiSeq files will be analyzed from the MiSeq output folder. Folder names may include an underscore character.

> **NOTE:** When using automatic analysis, the Automation functionality, it is essential to ensure the Local Storage folder has adequate capacity to hold all the .bam files to be downloaded from the Ion S5.



In addition to setting up the automation monitoring functionality the users have the below options

1. Remove Raw Data files
2. View Log
3. Session Prefix Setup
4. Remove Selected Prefix

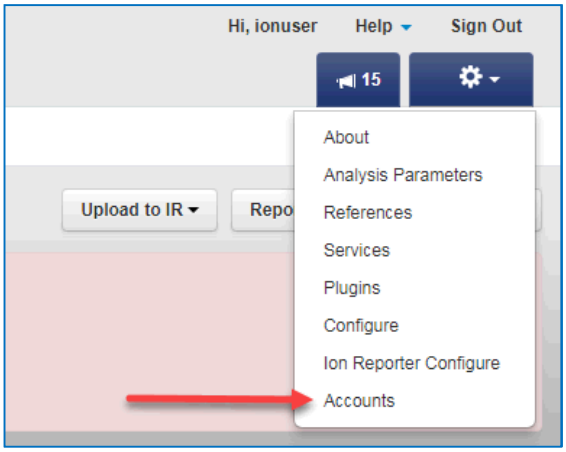
Downloading from Ion S5

Enter the server name, username, and password for the target server. The IP address may be used instead of server name if preferred. Designate a storage folder where the downloaded files will be kept. This folder may be local or in an available networked location.

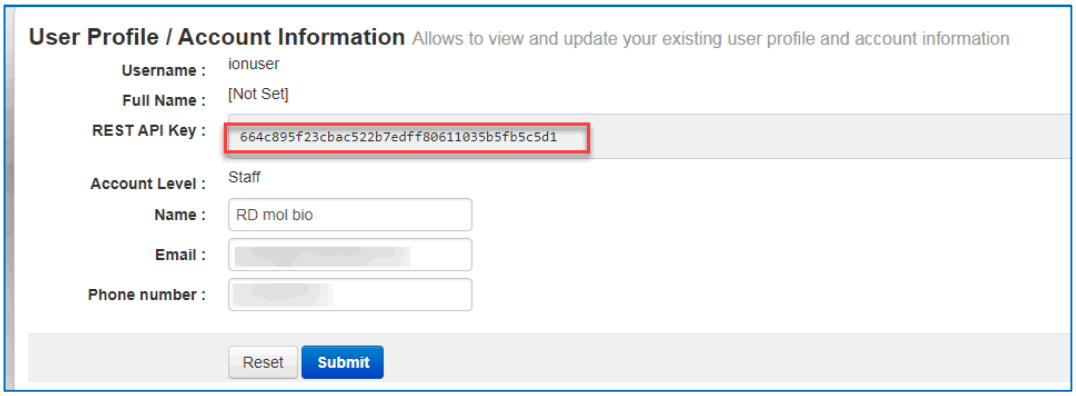
The steps shown here may differ slightly depending on the version of Torrent Server in use.

Obtaining API Key

To obtain the API key from your Ion S5 server, navigate to Accounts from the Torrent Suite web interface.

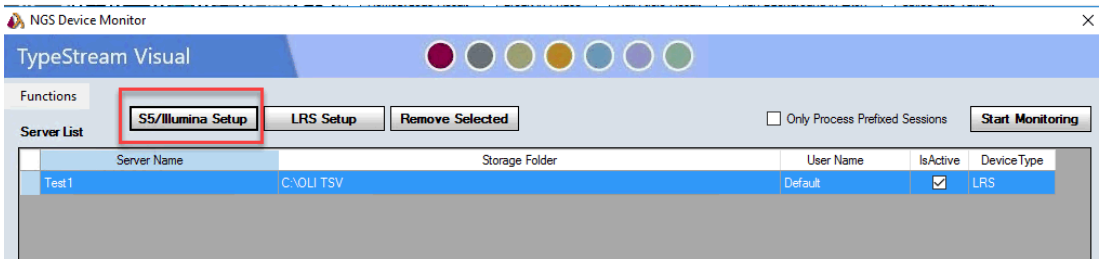


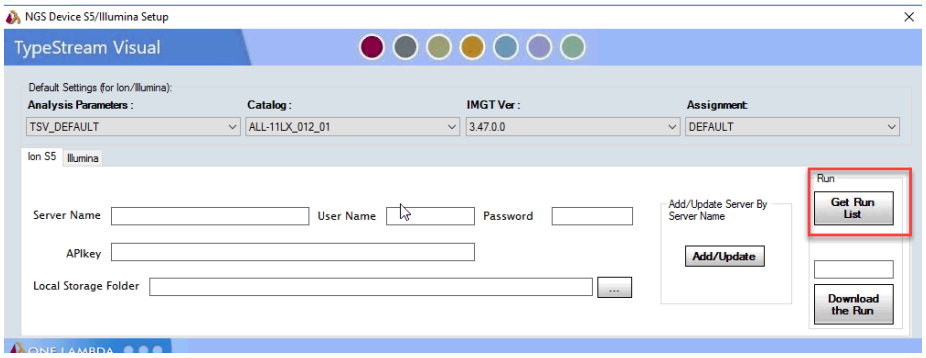
Copy the entire character line from "REST API Key" and paste it into the correct field on the NGS Device Monitor.



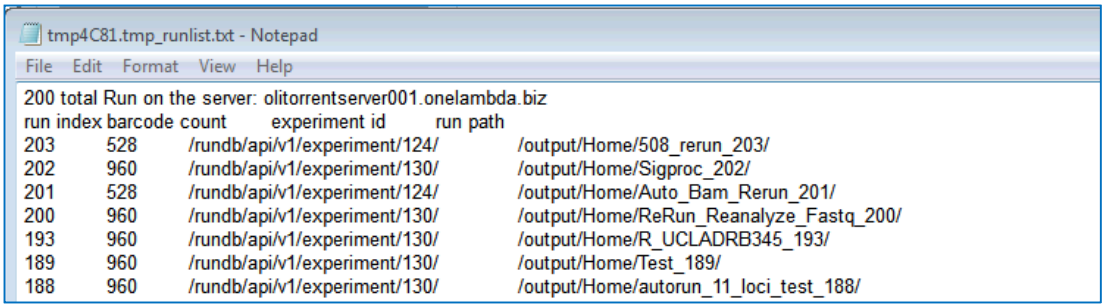
Get Run List

To get a list of all runs on an Ion S5 server, select the server from the server list. (Monitoring does not have to be on.) Click "S5/Illumina Setup"





After several minutes (depending on the size of the server and the number of runs it holds) a text file will open, displaying the number of total runs on the selected server. Following that will be the list of available runs, including run index, barcode count, experiment ID, and run path.

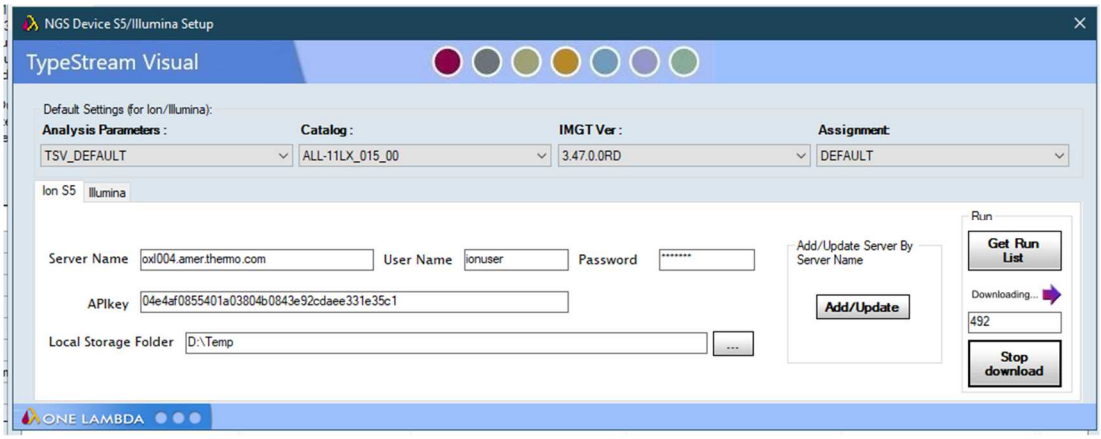


Download a Specific Run

To download and analyze a specific run, enter the run number (first column from the Run List above) into the 'Run' text box. Click 'Download.'

Download Indicator will begin to blink, signifying a download is in process. 'Download' button changes to 'Stop download.'

Download may be stopped at any time. When 'Download' is clicked again, the software will continue to download raw files, picking up where it had left off.

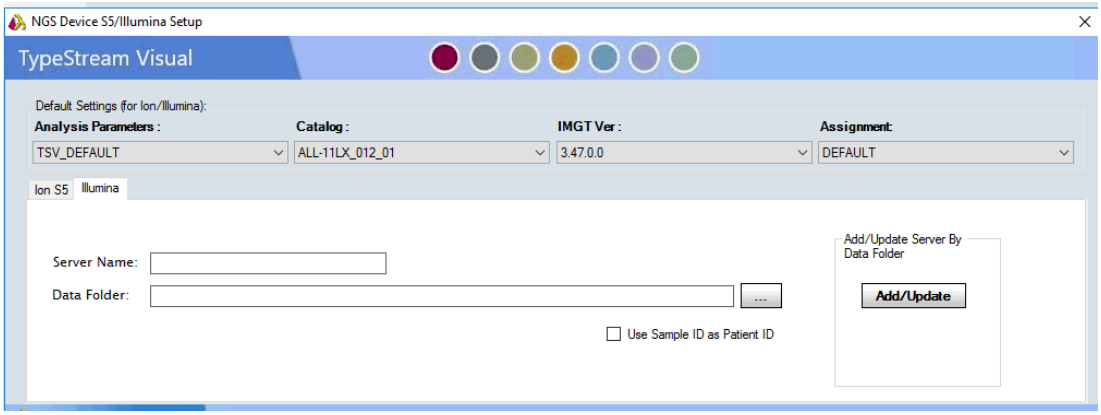


If monitoring is on (see section on Monitoring below), the session will automatically be sent to the engine for analysis when the download is complete. If monitoring is off, the session will begin analysis when 'Start Monitoring' is clicked.

See 'Monitoring' section below for more information on what happens during and after a download.

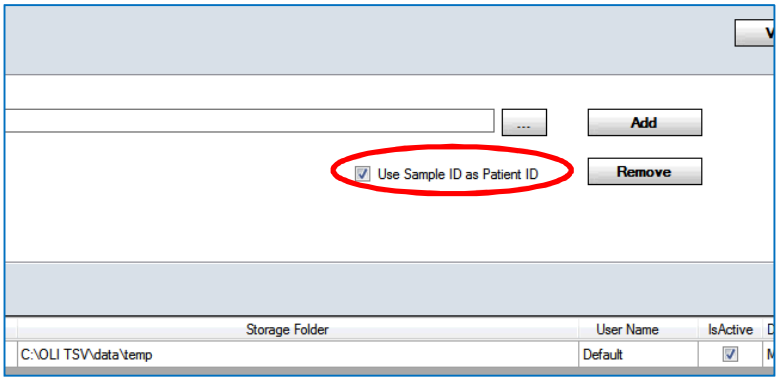
Downloading MiSeq Data

Click the "MiSeq" tab in the NGS Device Manager. The MiSeq window displays as illustrated here. Any servers already configured will display on the server list.

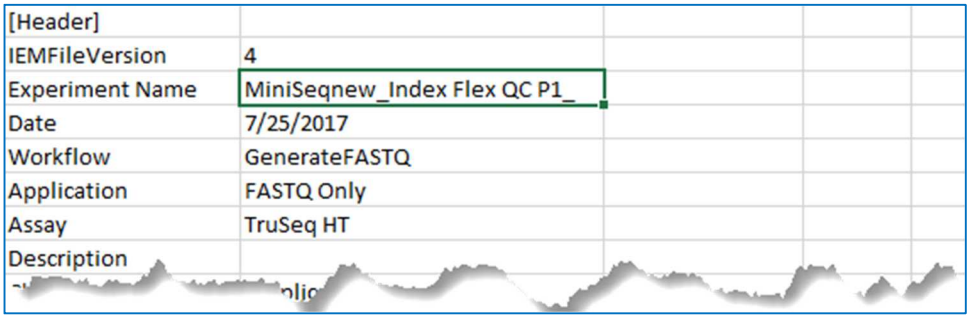


Use the search button (. . .) to navigate to the location of the output folder for MiSeq files. Select the correct folder and click 'Add.' The MiSeq output folder displays on the server list.

User may elect to have the software automatically use the Sample Id as the Patient ID by selecting the checkbox displayed under the Data Folder path.



On the open sample sheet below, the "Experiment Name" is "Index Flex QC P1". That name will be used as session name.



[Header]	
IEMFileVersion	4
Experiment Name	MiniSeqnew_Index Flex QC P1_
Date	7/25/2017
Workflow	GenerateFASTQ
Application	FASTQ Only
Assay	TruSeq HT
Description	

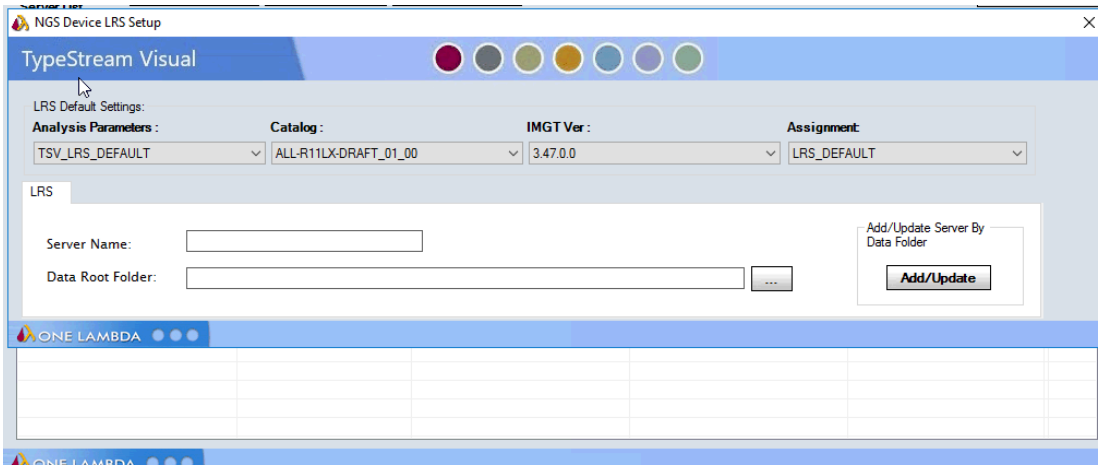
On the open sample sheet below, If the checkbox “Use Sample ID as Patient ID” is checked the “Sample_ID” column values will be used as the Patient ID and “Sample_Name” column values will be used as the Sample ID. If the checkbox “Use Sample ID as Patient ID” is NOT checked, “Sample_ID” column values will be used as the Sample ID and Sample ID will not be disassociated from Patient ID if an association already exists in database.

0	[Data]									
1	Sample_ID	Sample_Name	Sample_Plate	Sample_W	I7_Index_	index	I5_Index_	index2	Sample_P	Description
2	9016-17	9016-17SN	MiSeqNew_Inde	H03	D703	CGCTCATT	D501	TATAGCCT		
3	1073-18	1073-18SN	MiSeqNew_Inde	G03	D703	CGCTCATT	D502	ATAGAGGC		
4	BCK-4	BCK-4SN	MiSeqNew_Inde	E01	D70	ATTACTCG	D504	GGCTCTGA		
5										

Follow folder structure for placement of Sample Sheet:
...\MiSeq\MiSeq_MiniSeq\MiSeq_MiniSeq\190725_M01817_0045_000000000-B2L57\Data\Intensities\BaseCalls\Alignment.

NOTE: When using “Use Sample ID as Patient ID” the checkbox must be checked prior to loading the server path.

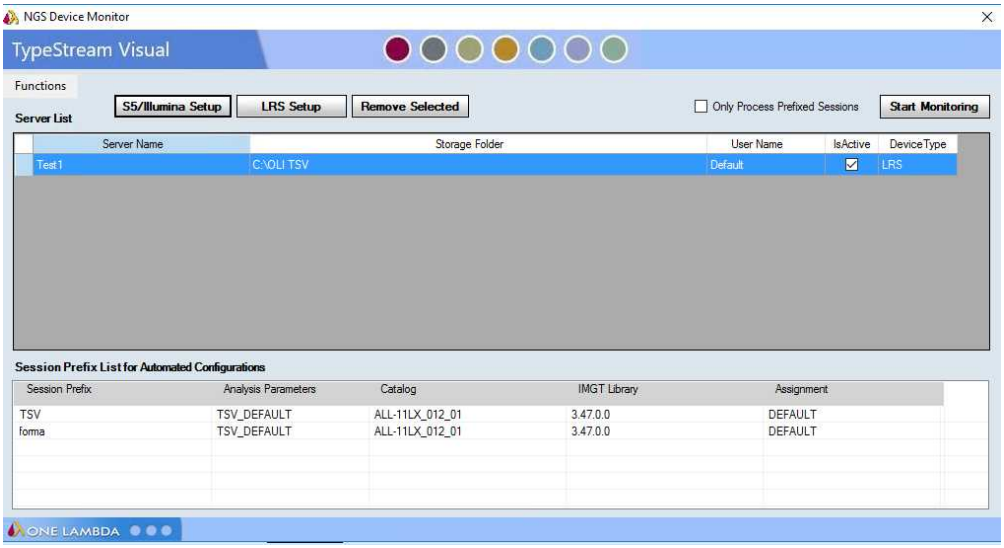
LRS Setup



User can configure TSV to monitor raw data files generated from LRS sequencers. Users may set the data monitoring folder as well as select default analysis parameters, catalogs, IMGT Ver and assignment configurations to be used for analysis.

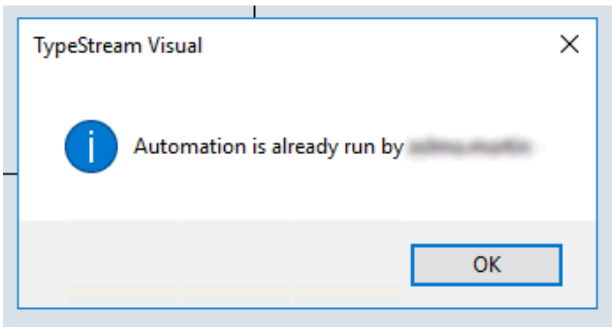
Monitoring

Click the ‘Monitoring’ tab in the NGS Device Monitor. All configured servers display in the server list. Select options for analysis parameters, catalog, and library version. Click ‘Start Monitoring.’



Monitoring indicator begins to blink and 'Start Monitoring' button changes to 'Stop Monitoring.' Every 10 seconds, the software checks each of the active servers to detect new runs. If no new runs are detected when monitoring begins, software will download the most recent two runs that have not been analyzed already.

Only 1 user can start monitoring from one machine. If another user logs into the same instance of the install and tries to start monitoring, the below message appears



By default, the software will auto-apply a machine generated name for the session in the following format: "TSV_S5_[server name]_[run ID]."

If the Sample Sheet contains a blank line, the software will skip that line and continue processing.

If the sample exists in the sample sheet and there is no corresponding fastq files in the watch folder, the session will not be processed.

Using Run Name

Additionally, the user may enable the software to use the Planned Run Name from Gene Studio S5 by careful use of "-" when the session is named in the S5 sequencer. The software will look for the last "-" to extract the session name. For a run with the following name from the S5:

- Auto_User_GSS5PL-0026-122-2019-9-26_ALL-LIBX_STAB_ACC_2106818_PH_467

The software will look for the final "-" and extract the name as such:

- LIBX_STAB_ACC_2106818_PH-467

It then drops the first and last name field in the name, which results in this session name:

- STAB_ACC_2106818_PH

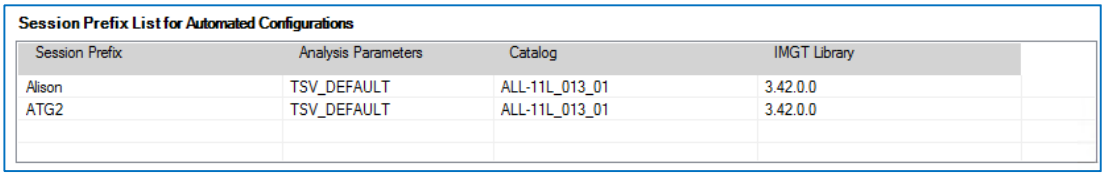
For a MiSeq session, session name will be taken from "Experiment name" on the SampleSheet.csv.

NOTE: When configuring servers for with the Automation functionality, user must be certain that the username and password are correct, as TSV software cannot verify these when entered. If incorrect, new data generated by the sequencer will be noted but not fully downloaded; a .tmp file will display in the folder in its place. The Auto Log will display entries per the following example:

[20180606161037] downloading from server: olitorrentserver001.onelambda.biz run: 203 barcode: IonXpress_021

[20180606161038] Can't download the file. Check web access permission or file path: http://olitorrentserver001.onelambda.biz/output/Home/508_rerun_203/basecaller_results/IonXpress_021_rawlib.basecaller.bam. Failed to download C:\OLI TSV\data\temp\automation\olitorrentserver001\203\IonXpress_021_9086_rawlib.basecaller.bam

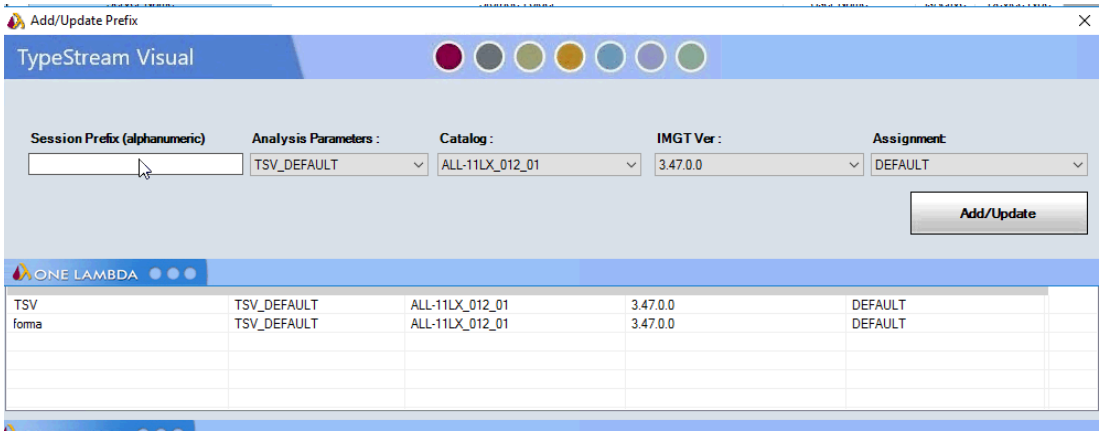
Session Prefix List for Automated Configurations



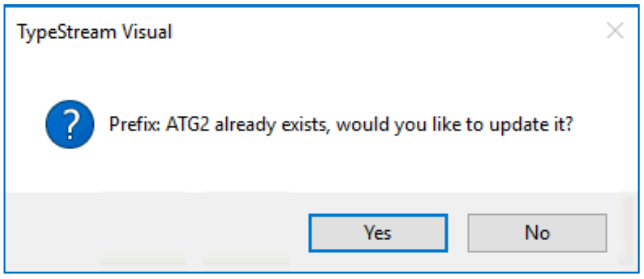
Users can specify the prefix of the run name / session name for processing by TSV automation module. This allows users to specify different analysis configurations based on the session naming convention.

If "**Only Process Prefixed sessions"** checkbox is checked, TSV will only process sessions whose name satisfies the session prefix conditions. If the checkbox is not checked, TSV will first scan through the prefixes, and if it is not found will process sessions using the default settings.

Users can add/update configurations using **Add/Update**



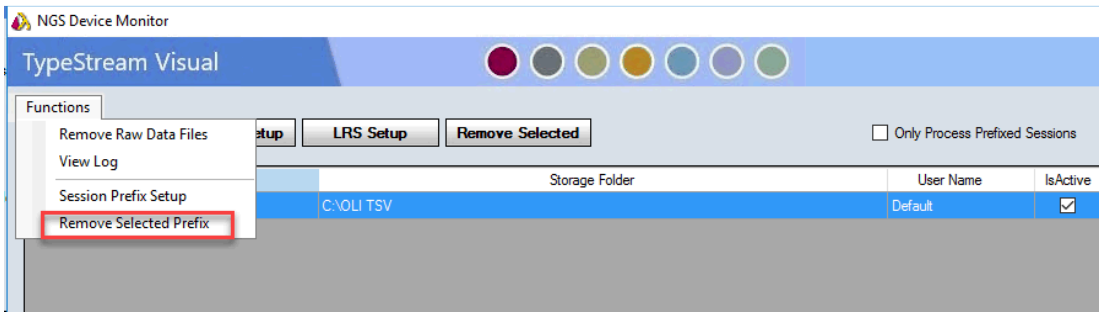
In order to update a current configuration, type in the name of the configuration and update the configurations setting as required. Click on "**Add /Update**" button. The following message appears for confirmation. To create a new configuration, type in a name with a new session prefix.



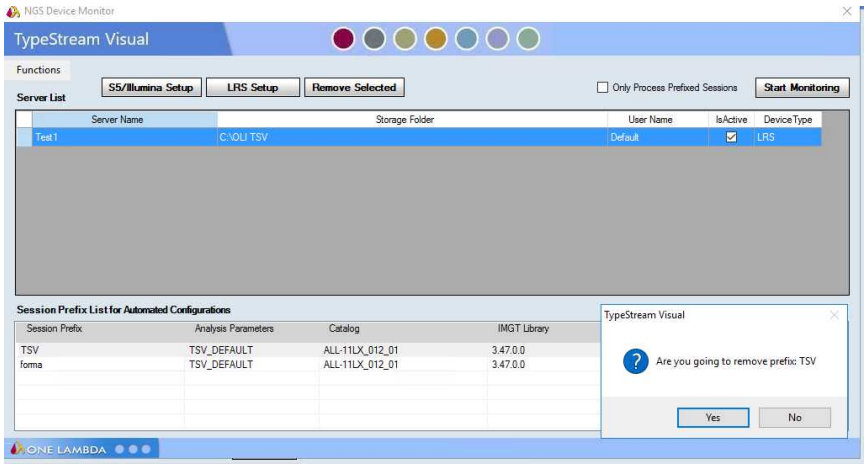
Option Selection

Options selected from 'Analysis Parameters,' 'Catalog,' and 'IMGT Vers' will apply to all sessions downloaded from any active server.

Remove Selected Prefix

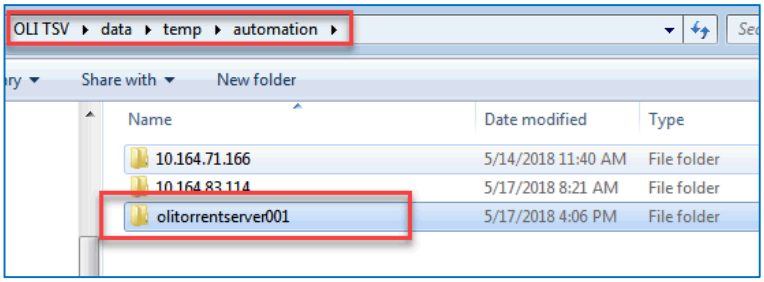


Remove selected prefix function allows users to delete selected session prefix from the configuration.

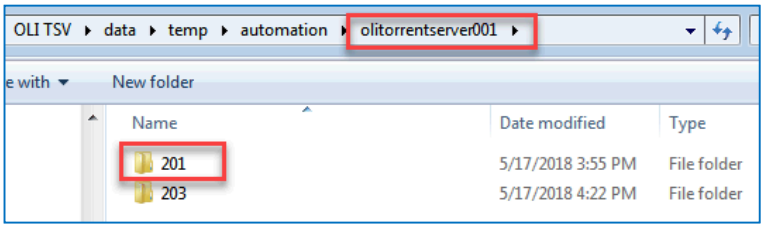


Folder structure

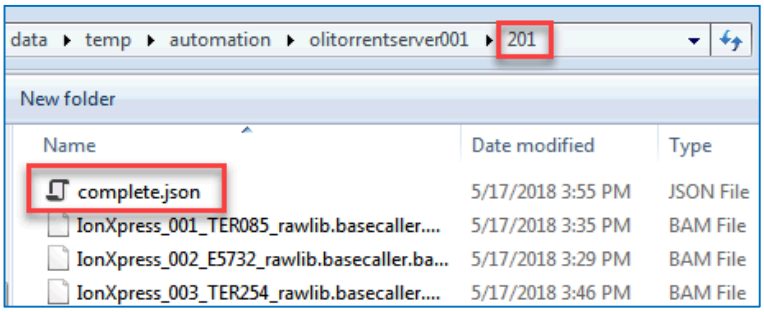
When the software detects a new Ion S5 server, it creates a folder in the storage location with the name of the server.



For each run detected on that server, the software creates a folder with the run ID.



Files continue to download into this folder. While in process, the file currently being downloaded has the extension ".tmp." When the download of all files is complete, the software creates the file "complete.json." This file contains a log of the download and save process.



Folder structure is a little different for MiSeq sessions. There will not be a "completed" file, but the 'submitted.log' file can be found along a path like this:
...\MiSeq\Subfolder\170725_M11111_0045_000000000-B2L57\Alignment_1\12345-10293\fastq

Fastq files for MiSeq runs should be located under the Data\Intensities \Basecalls folder along with the sample sheet. The software assumes that the absence of Sample sheet that the run is a MiSeq run.

Fastq files for MiniSeq runs should be located under\Alignment_1\DateTime folder\fastq

Fastq files for iSeq Runs are in Alignment_1\DateTimefolder\Fastq

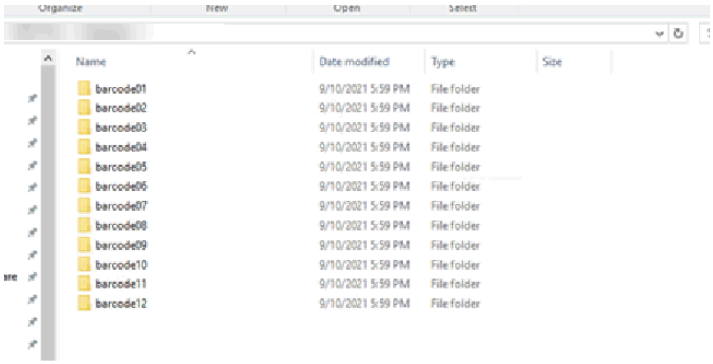
LRS Folder Monitoring Structure

Long-Read Sequencing (LRS) sequencers generates a folder called fastq_pass that contains several barcode subfolders with the below naming convention. The application looks for a file called final_summary_xxx.txt' or duty_time*.csv", or *barcode*.tsv to kick off automation.

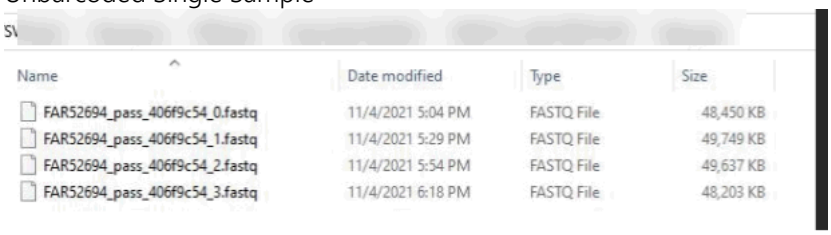
This file trigger TSV to start processing the session by combining the fastq files within each session to process the merged files. The merged files are created as a folder under C:\OLI TSV \data \session folder \TSVMerged. The folder name would be the parent folder to the fastq_pass folder with the "auto_" prefix added to it

The merged folder would contain barcodeNN_NN.NN_merge.fastq for each barcode. Automation merge and session builder merge only works for .fastq file, it does not work for fastq.gz

When the session is submitted to the engine, the software creates the file “submitted.log” and places it into the parent folder.



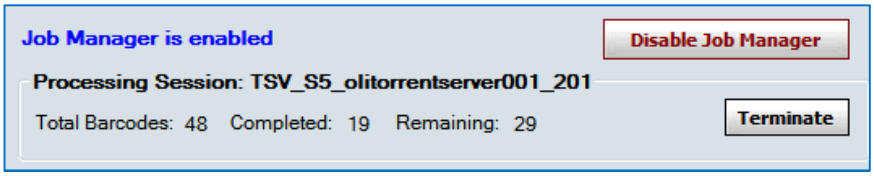
Unbarcoded Single Sample



If it is a non-barcode LRS folder, create a destination file barcode00_00.00_merge.fastq, and generate the merged file by combining the fastq files.

Automatic Session

After completing the download, software sends the session to the Job Manager. When the session is submitted to the engine, the software creates the file “submitted.log” and places it into the folder.



NOTE: If there is inadequate space on the drive, the software will indicate this on the session summary page after the run cycle finishes, and there will be no genotyping. All sessions so affected will need to be rerun manually after adequate space becomes available.

Remove Raw Data Files

Because .bam files are large (typically 1.5 GB to 5 GB per file), user may find it necessary to delete the original raw data files for sessions that have finished analysis in TypeStream Visual in order to save space on the hard drive. To do so, make sure the server whose files you want to remove is *Active* on the server list. Click "Remove Raw Data Files."

> **NOTE:** When using the "Remove Raw Data Files" button within the Automation functionality, software will delete completed sessions on the MiSeq output folder as well as the downloaded S5 files. If you do not want the MiSeq files deleted, simply make the MiSeq server inactive on the server list.
>
> Additionally, the software will only delete files for sessions in the current database. Those sessions in other databases will not be removed.

Software will check each of the subfolders for the selected server for the presence of the files "complete.json" and "submitted.log." It will also verify that the analysis has been performed by checking to see if the session name appears in the database and the run is complete. If these criteria are met, software will remove all raw data files from the folder, leaving in their place a small file "removed.txt." This file contains the time stamp for the removal of the files.

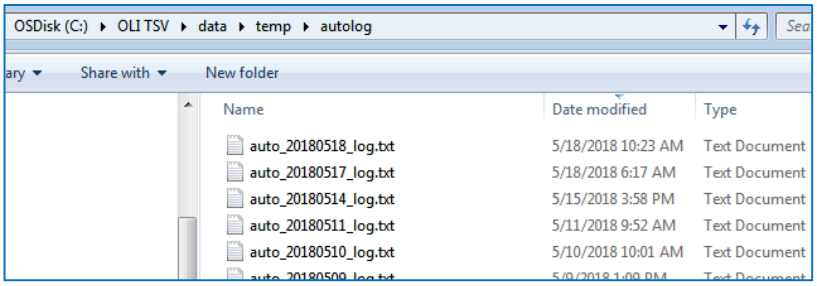
Reanalyzing after Deletion

After deleting the raw data files, session can still be reanalyzed using the following process:

1. Go to Analyze Data → NGS on the menu bar to start a session the normal way.
2. Click Add Fastq/BAM File
3. Navigate to C:\OLI TSV\data\session\NGS\[session name]\[barcode output folder]
4. Select 'mappedReads.bam' and click Open
5. File displays on the create session page. User will have to supply a Sample ID.
6. Repeat this for each barcode to be reanalyzed.
7. Click 'Submit.'

View Log

TypeStream Visual software creates a daily log for all activity on the NGS Device Monitor. Clicking "View Log" brings up today's log file. To view log files from other days, navigate to C:\OLI TSV\data\temp\autolog and double-click on the desired date.



An automatic download will display download start, each of the files downloaded, and the submission to job manager.

```
auto_20180517_log.txt - Notepad
File  Edit  Format  View  Help
[20180517082156] Start download from server: 10.164.83.114 run: 234 barcode #: 10
[20180517082156] downloading from server: 10.164.83.114 run: 234 barcode: IonXpress_004
[20180517083336] downloading from server: 10.164.83.114 run: 234 barcode: IonXpress_001
[20180517084031] downloading from server: 10.164.83.114 run: 234 barcode: IonXpress_003
[20180517085141] downloading from server: 10.164.83.114 run: 234 barcode: IonXpress_005
[20180517092003] downloading from server: 10.164.83.114 run: 234 barcode: IonXpress_002
[20180517093702] downloading from server: 10.164.83.114 run: 234 barcode: IonXpress_004
[20180517095632] downloading from server: 10.164.83.114 run: 234 barcode: IonXpress_005
[20180517100940] submit TSV_S5_10.164.83.114_234
```

A manual download will specify that it is a manual download and indicate the save location for the files.

```
auto_20180517_log.txt - Notepad
File  Edit  Format  View  Help
[20180517152027] Start: manual download of run 201
[20180517152030] Start download from server: olitorrentserver001.onelambda.biz run: 201 barcode #: 528
[20180517152030] downloading from server: olitorrentserver001.onelambda.biz run: 201 barcode: IonXpress_021
[20180517152044] save to C:\OLI TSV\data\temp\automation\olitorrentserver001\201\IonXpress_021_9086_rawlib.basecaller.bam
[20180517152044] downloading from server: olitorrentserver001.onelambda.biz run: 201 barcode: IonXpress_045
[20180517152100] save to C:\OLI TSV\data\temp\automation\olitorrentserver001\201\IonXpress_045_9086_rawlib.basecaller.bam
[20180517152100] downloading from server: olitorrentserver001.onelambda.biz run: 201 barcode: IonXpress_004
[20180517152119] save to C:\OLI TSV\data\temp\automation\olitorrentserver001\201\IonXpress_004_BCK_rawlib.basecaller.bam
```

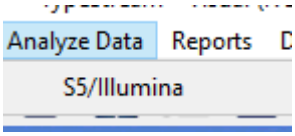
If a manual download is stopped while in progress, the log will display the log line "Abort: manual download of run [ID]." When started again, the download will pick up where it left off.

5

Create Session and Analyze Data

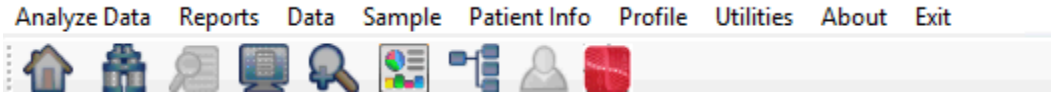
Open Create Session Page

From the top left corner of the screen, navigate to Analyze Data → S5/Illumina (applies to IVD and RUO mode).



Page displays for creating a new session.

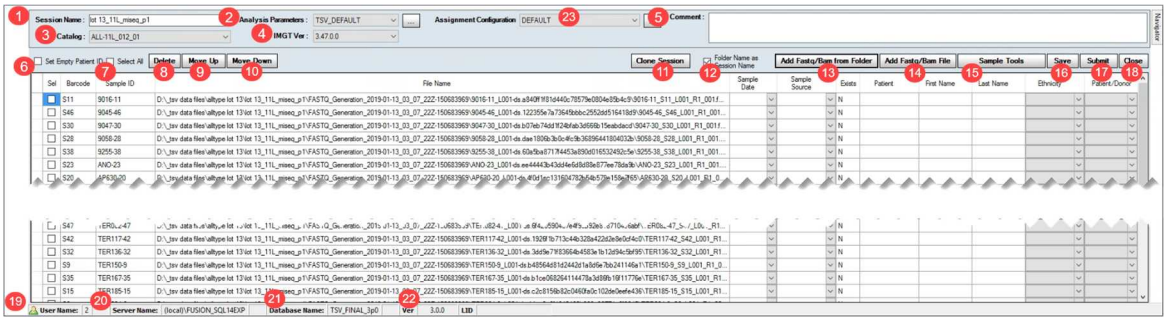
Optionally, clicking the Analyze S5/Illumina icon will bring up the same page.

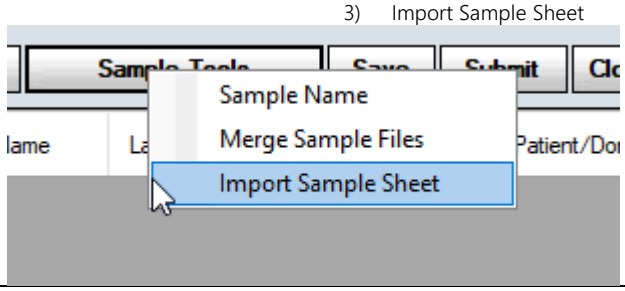


Required Files

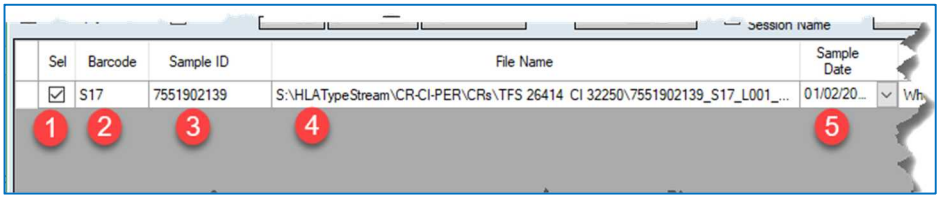
If either catalog files or an IMGT library have not yet been downloaded, the software will warn the user and not allow a session to be created until that task has been done.

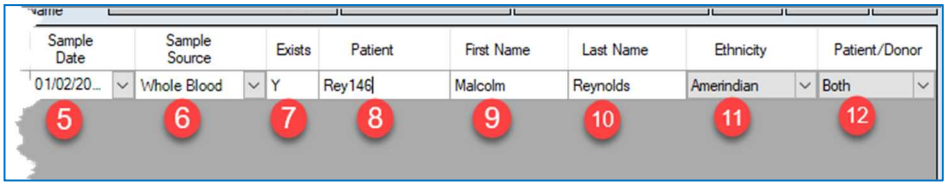
Session creation page displays as shown below.



	Item	Description
1	Session Name	Session name as entered on the session import page. User may overwrite the session name automatically assigned by the software.
2	Analysis Parameters	The parameter set selected by the user. Software comes with default settings for both 9-loci and 11-loci. User may also create new parameter sets to suit specific needs.
3	Catalog dropdown selector	Select from any of the catalogs in the database
4	IMGT Ver	Select from any of the IMGT library versions in the database
5	Comment	Optional User comment field. Comments entered here will display on the session summary.
6	Set Empty Patient ID	When checked, TSV will use the Sample ID to populate any Patient ID fields that are blank.
7	Select All	Selects all the files in the session grid
8	Delete	Deletes all selected files
9	Move Up	When a sample is selected in the grid, use this button to move it up in the list. (Software will analyze in the order displayed.)
10	Move Down	When a sample is selected in the grid, use this button to move it down in the list.
11	Clone Session	Clicking this button brings up a list of analyzed sessions in the database. User may select sessions or individual samples for reanalysis.
12	Folder Name as Session Name	Checking this box prior to loading files will enable the software to use the folder name as the session name.
13	Add Fastq/Bam from Folder	Will load multiple files by selecting the folder.
14	Add Fastq/Bam File	Opens a navigation window to load files.
15	Sample Tools	From here select to either load sample names from a .csv file or merge files or folders prior to analysis. Right click on the Sample Tools button will provide the below menu items 1) Sample Name 2) Merge Sample Name 3) Import Sample Sheet 
16	Save	Saves the session as entered to the Navigator; does not send to the engine
17	Submit	Send the session to the engine for analysis
18	Close	Closes the session in the import screen. Does not save any save on the grid.
19	Username	Name of logged in user
20	Server Name	Name of the SQL instance to which you are attached.
21	Database Name	Name of the database currently in use.
22	Ver	Version of TypeStream Visual
23	Assignment Settings	The assignment setting selected by the user.

Grid columns:





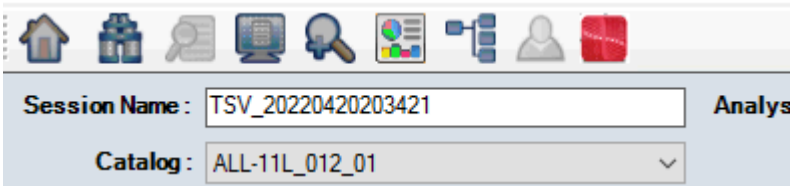
	Item	Description
1	Sel (checkbox)	Selection checkbox – select samples for deletion or to move up or down in the grid. Selection does not affect submission to the engine; all samples on the grid are submitted.
2	Barcode	Barcode number automatically derived from the file name.
3	Sample ID	In most cases will be derived from sample name. If not, can be manually entered or modified.
4	File Name	Displays the path to the raw data files.
5	Sample Date	User may manually enter the date sample was collected
6	Samples Source	Source of collected sample
7	Exists	Will display 'Y' if the sample ID already exists in the active database. Will display 'N' if the sample ID does not exist in the active database.
8	Patient	Patient ID. If sample ID exists in the database and is associated to a patient, patient ID displays here. Can be manually entered.
9	First Name	Patient first name
10	Last Name	Patient last name
11	Ethnicity	Select ethnicity from dropdown list
12	Patient/Donor	Select from 'Patient', 'Donor', or 'Both'

Create a session

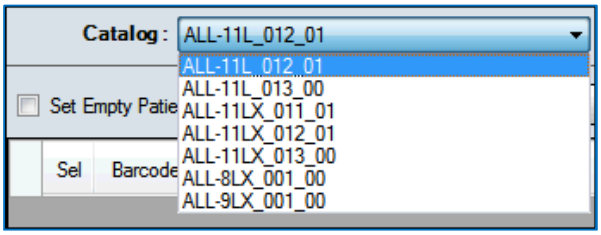
1. Enter session name

   Software automatically enters a session name which includes date and time stamp, but user may type in any alpha-numeric up to 75 characters. If two sessions have the same user-supplied session name, the second session will overwrite the first. For that reason, if choosing not to use the system-generated session names, care must be taken to give unique names to all sessions.

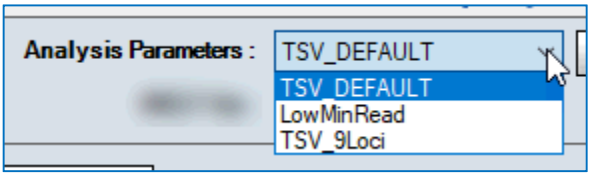
   Please Note: in naming sessions and samples, TypeStream Visual does not support the use of non-English Unicode characters.



2. Select a catalog – Catalog selection needs to match the SKU name for the assay used. For AllType NGS 11 Loci Amplification reagents, use catalog beginning with 'ALL.' By default, the system will select the last catalog used in analysis.

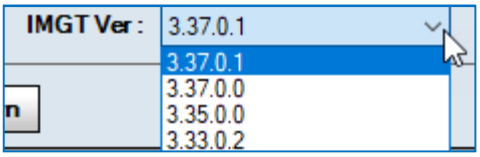


3. Analysis parameters
    a. select an existing parameter set
    b. or create a new one by first clicking the ellipsis. *(See "Utilities" for more information.)*

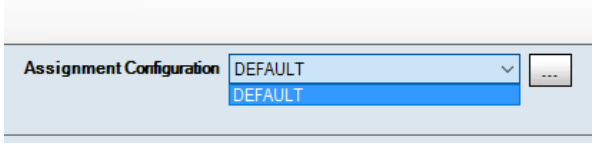


    c. By default, the system will select the last analysis parameter used in analysis

4. Select library:



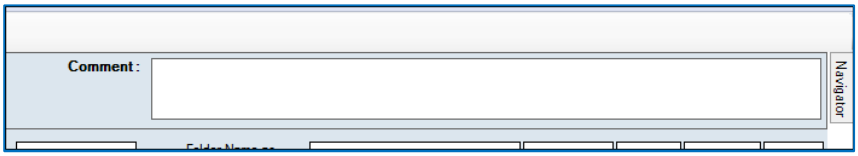
5. Select Assignment Configuration:



By default, only the DEFAULT assignment configuration is displayed in the drop-down. Any newly created assignment configuration will be added to this list.

6. Enter comment (optional)

Comments entered here will appear on the session summary page of the analyzed session and on the Genotype Summary Report (.pdf). By default, the software will select the last library used in analysis.



Load Files

It is recommended that users follow standard naming conventions for input files for TypeStream Visual. Files coming from Ion Torrent, S5 should use one of the following:

IonXpress_barcode.samplename_otherinfo.bam
IonXpress_barcode.samplename_otherinfo.fastq

MiSeq filenames (pairend files) should follow MiSeq filename convention, typically in one of the following forms:

Samplename_S#_L###_R1_###.fastq
Samplename_S#_L###_R2_###.fastq

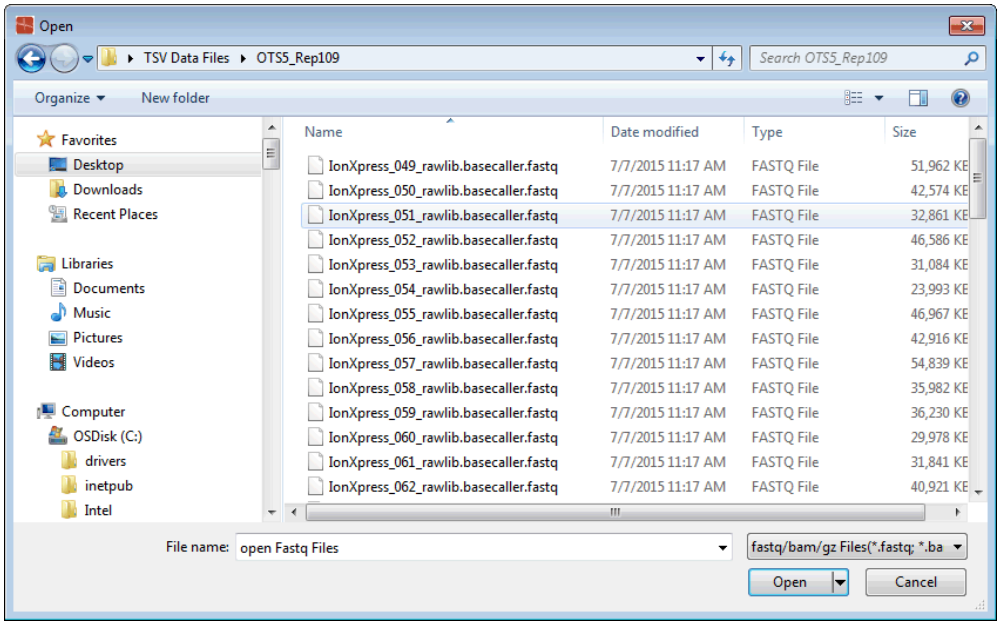
There are three buttons which enable the loading of data files.

- 'Add Fastq/Bam File' is the most commonly used to load files from any source.
- 'Add Fastq/Bam from Folder' when files exist in separate folders. TypeStream Visual will create a separate file for each folder.
- 'Fastq<>Sample Name' is used to populate sample names when the name cannot be derived from the file or file name.

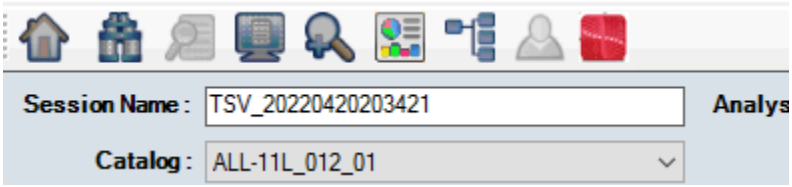
Add Fastq/Bam

To load most standard files for analysis, click button 'Add Fastq/BAM file'

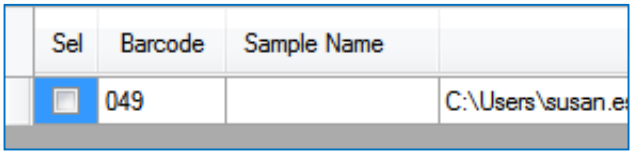
Navigation pane will display. Navigate to the location of the data files, select and click Open. System will accept .bam, .fastq, and .gz files. The path to the selected files will appear on the grid on the session page.

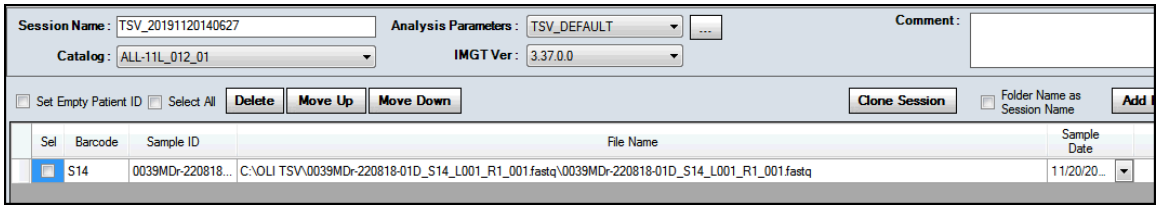


The software will automatically assign a time-stamped session name. This name can be changed to user's preference.



The system requires Sample Name to be populated. If the Sample Name column is blank, it can be manually entered. Please refrain from using blanks or dashes when naming.

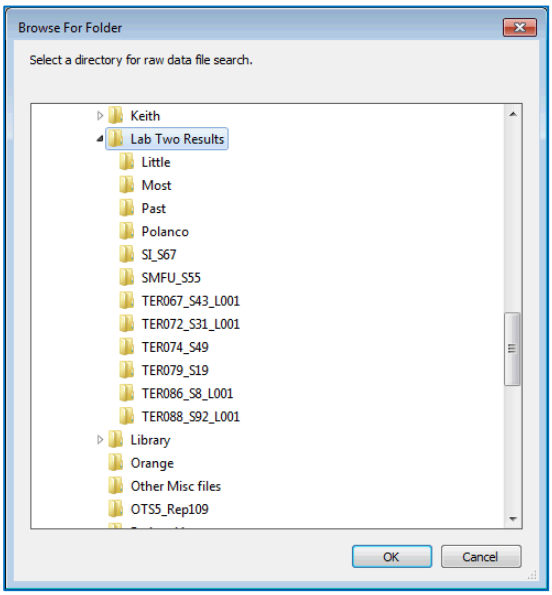




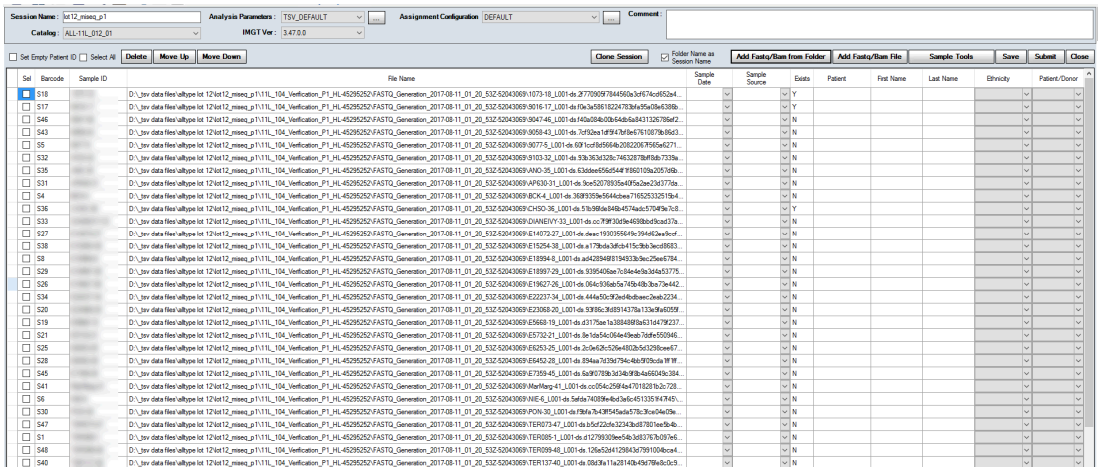
Click 'Submit' or 'Save' button. 'Submit' will send the session directly to the engine for analysis. 'Save' will keep session for later analysis.

Add Fastq/Bam from Folder

In the illustration below, one folder has multiple subfolders containing typing results. TypeStream Visual will load the contents of each of the subfolders by selecting the folder "Lab Two Results" below.



Each folder is represented by a single entry in the grid.

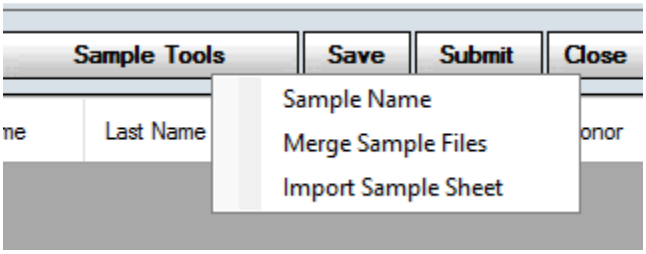


Click 'Save' or 'Submit.'

Note: Avoid use of diacritic characters (e.g. 'à') in folder names when submitting FASTQ files in TSV.

Sample Tools

Right clicking the Sample Tools button (formerly labelled "Fastq<>Sample Name") displays Sample Name, Merge Sample Files and Import Sample Sheet menu items.



Sample Name

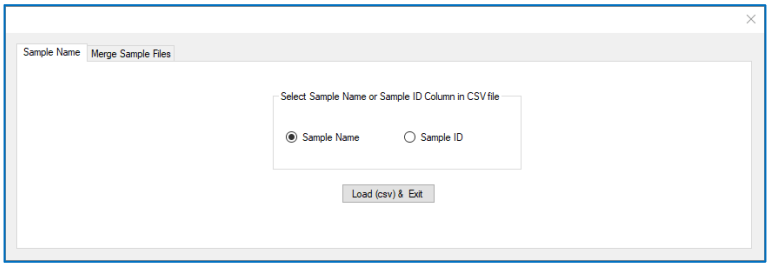
If the user has a large number of files to load but the sample names cannot be derived from the file or file name, they can be uploaded in bulk via a .csv file. User must construct the .csv file containing the barcode numbers and Sample Name, or optionally Sample ID.

	A	B	C	D
1	CSV Version (required)	1		
2	Barcode	Control Type	Sample Name (required)	Sample ID
3	IonXpress_049		McNutt	
4	IonXpress_050		Eubank	
5	IonXpress_051		Likovich	
6	IonXpress_052		Harker	
7	IonXpress_053		Badertscher	

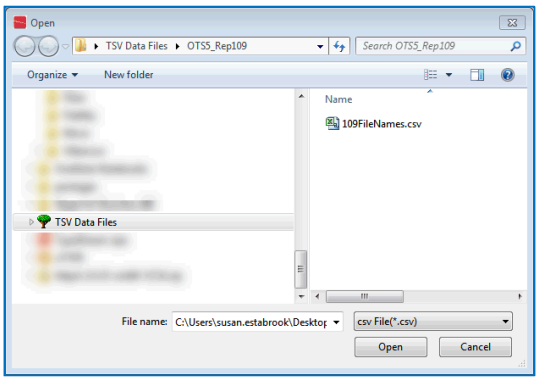
Load the files using the 'Add Fastq/Bam File' as described earlier. Files will display without sample names.

Sel	Barcode	Sample ID	File Name	Sample Date	Sample Source	Exists	Patient	First
	049		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	050		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	051		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	052		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	053		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	054		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	055		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	056		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	057		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	058		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	059		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	060		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	061		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	062		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	063		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		
	064		C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N		

Click 'Sample Tools' option the user can select Sample Name or Sample ID.



Click Load. Navigate to location of the .csv file containing the sample names for the files.



Click Open. The sample names are populated for each file.

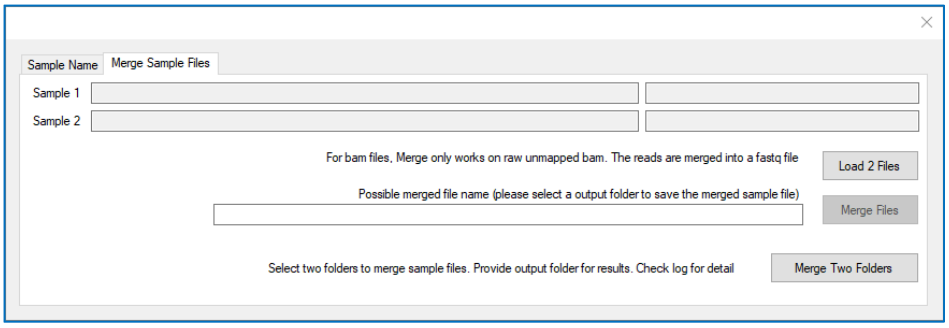
Sel	Barcode	Sample ID	File Name	Sample Date	Sample Source	Exists	Patient
	049	McNutt	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	McNutt
	050	Eubank	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Eubank
	051	Likovich	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Likovich
	052	Harker	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Harker
	053	Badertscher	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Badertscher
	054	Cave	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Cave
	055	Laubney	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Laubney
	056	Hise	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Hise
	057	Widup	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Widup
	058	Ward	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Ward
	059	Thompson	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Thompson
	060	Dreier	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Dreier
	061	Mollencupp	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Mollencupp
	062	Gregory	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Gregory
	063	Lawtner	C:\Users\susan.estabrook\Desktop\TSV Data Files\OTS5_R...			N	Lawtner

Regardless of the method of loading, any file may be removed prior to submitting for analysis

simply by check the check box in the first column and clicking 'Delete' button.

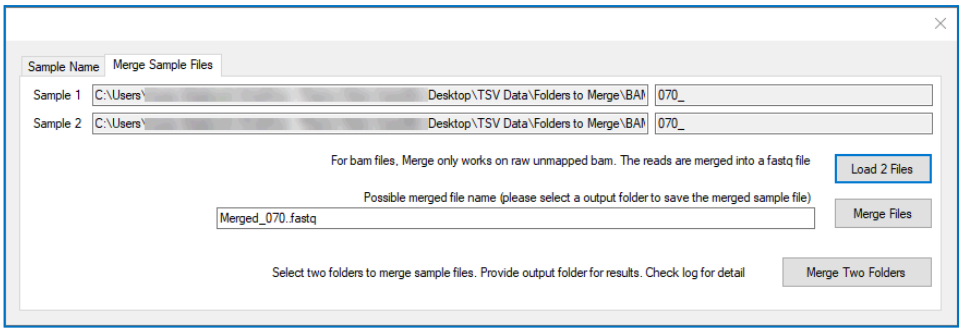
Merge Sample Files

Merge Sample Files tab allows the user to select files or folders to merge prior to analysis.

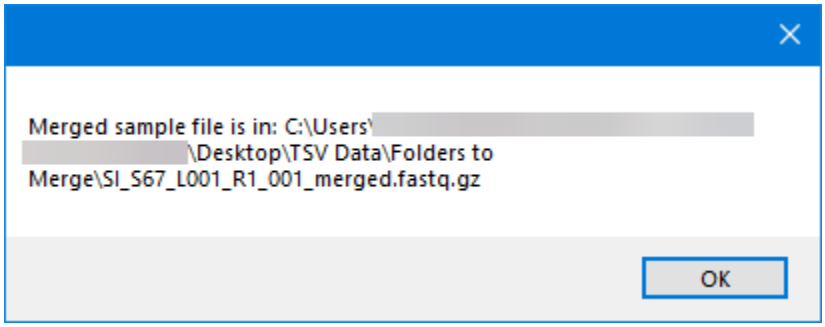


To load the files, do the following:

1. Click 'Load 2 Files' button
2. Navigation pane displays. Navigate to and select the first file.
3. Click 'Open.' Navigation pane immediately displays again.
4. Navigate to and select the second file.
5. Click 'Open.' The software displays both selected files in the text boxes along with the path. It will also suggest a possible name for the merged files.

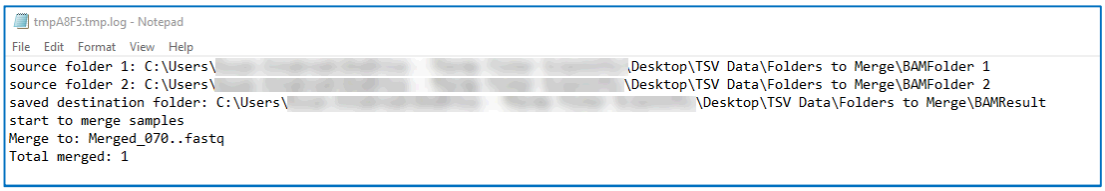


6. 'Possible merged file name…' is an editable text field where user may change the name as desired.
7. Click 'Merge Files.' Navigation pane opens once more. Select an output folder and click 'OK.'
8. TypeStream displays confirmation that the merge was successful. Merge file is in the designated folder.



The process to merge folders is very similar. Click 'Merge Two Folders' button. Select Folder 1 and Folder 2 in the same way you selected individual files. The navigator to select the output folder will come up immediately after selecting Folder 2.

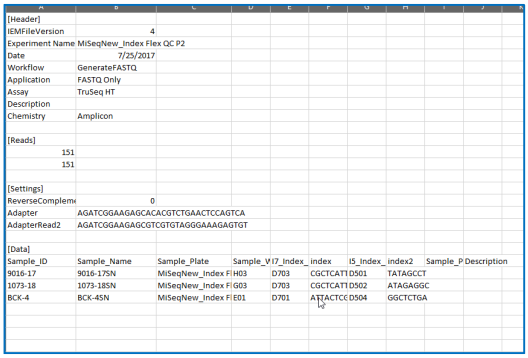
On clicking 'OK' on the last navigation pane, a results file will display in Notepad, giving the paths for both source folders and destination folder, plus the name of the merged file and # merged.



Import Sample Sheet

This feature allows the user to associate the sample names in the import grid to the patient id information in the sample sheet. The user should first import the raw data files into the session import grid followed by using the Import Sample Sheet to import the sample / patient associations.

The patient Id column is populated with the Sample_ID column information by comparing the Sample_Name and the Sample_Well column with the Sample ID and the Barcode column in the session import grid. If there is no match with the Sample ID and the barcode, the patient id column is left unpopulated.



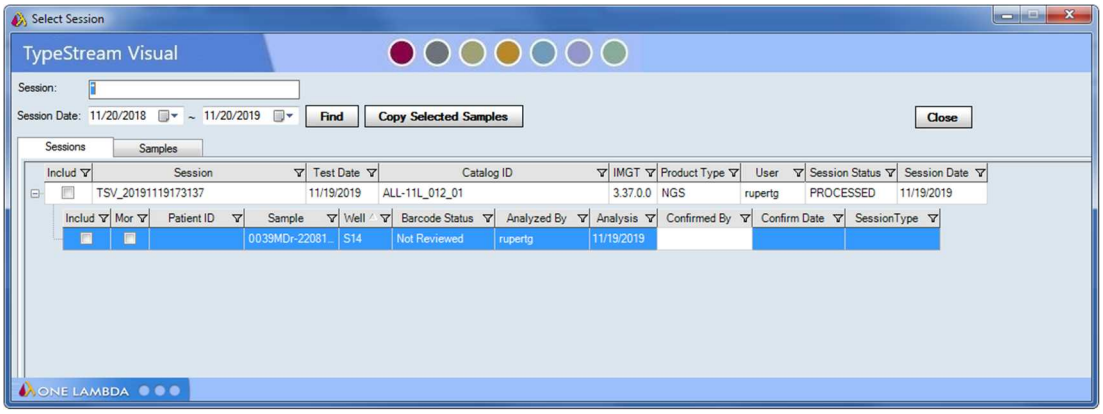
[Header]									
IEMFileVersion	4								
Experiment Name	MiSeqNew_Index Flex QC P2								
Date	7/25/2017								
Workflow	GenerateFASTQ								
Application	FASTQ Only								
Assay	TruSeq HT								
Description									
Chemistry	Amplicon								
[Reads]									
151									
151									
[Settings]									
ReverseComplem	0								
Adapter	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA								
AdapterRead2	AGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGT								
[Data]									
Sample_ID	Sample_Name	Sample_Plate	Sample_W	I7_Index_	index	I5_Index_	index2	Sample_P	Description
9016-17	9016-17SN	MiSeqNew_Index F	H03	D703	CGCTCATT	D501	TATAGCCT		
1073-18	1073-18SN	MiSeqNew_Index F	G03	D703	CGCTCATT	D502	ATAGAGGC		
BCK-4	BCK-4SN	MiSeqNew_Index F	E01	D701	ATTACTCG	D504	GGCTCTGA		

TSV validates the file based on the below criteria -

1. The extension of the file has to be either "csv"
2. The 20th row should contain the header and the header should have "Sample_ID" in the 1st column, "Sample_Name" in the 2nd column and "Sample_Well" in the 4th column.

Clone Session

A previously-run session, or any combination of sessions or samples, can be run again to compare results. Sessions can be run using the same or a different analysis configuration. To clone a session, click "Clone Session" button at the top of the screen. The following screen displays, from which the user may select any or all of the sessions.



The session opens in the import screen as if it were a new session. Session Name, Analysis Parameters, Catalog, and IMGT version can all be modified for the new session. Users have more flexibility in analysis to obtain desired results.

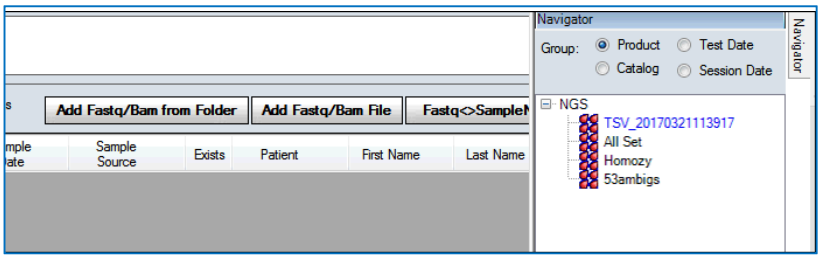
NOTE: Although users are able to select sessions and samples that have been analyzed using different catalogs, the created session will use only the catalog selected. Some results may differ.

NOTE: After selecting sessions and/or samples for the new session you MUST CLICK 'Copy Selected Samples" in order to send them to the create session page.

Save a Session

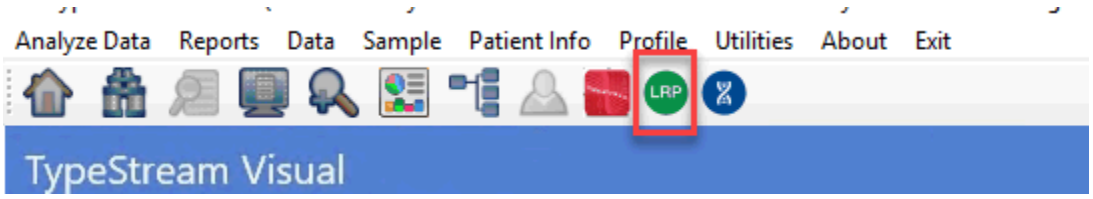
The situation may arise where the user has loaded the path to the raw data files and selected other variables but chooses not to analyze right away. Instead of submitting to the engine right away, clicking "Save" will put the session name into the navigator without submitting it to analysis.

For any file saved but not analyzed, the name of the file will display in the Navigator in Blue.

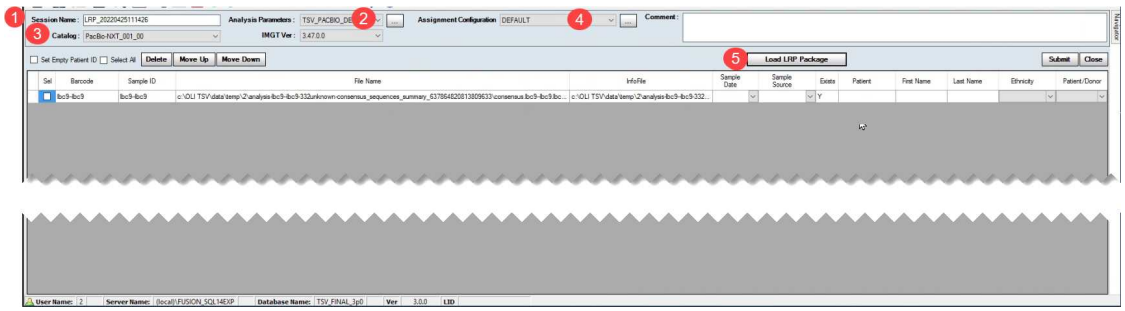


NOTE: This functionality is not available for LRP sessions. Because of the input structure, the software is currently unable to save the path to the raw data.

Create Session for LRP

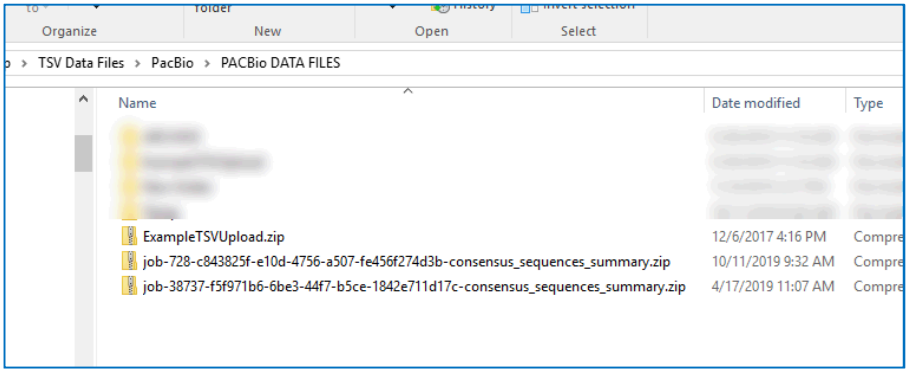


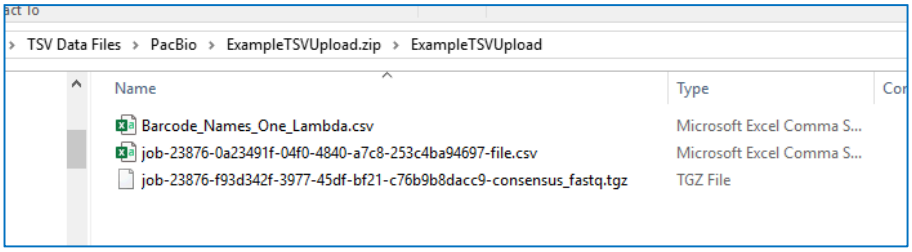
Clicking the icon for 'LRP Session Builder' will bring up a screen which is largely the same as for Ion S5 and Illumina but differs in important ways. Those ways are highlighted below.



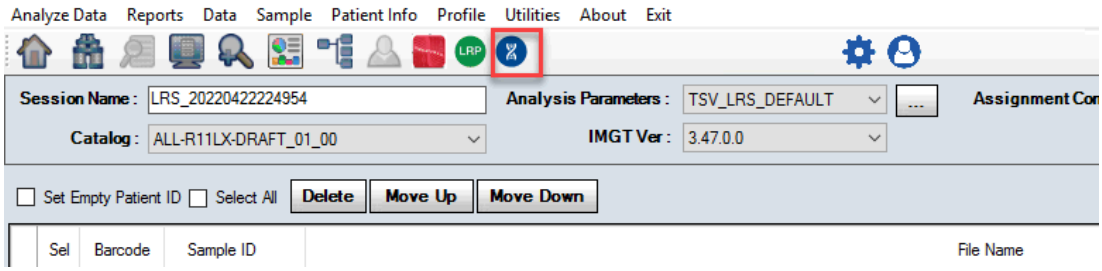
	Item	Description
1	Session Name	Session names are preceded by "LRP_" followed by the time stamp. They can be modified or replaced prior to analysis
2	Analysis Parameters	The software contains a separate set of default parameters for LRP. See Utilities for more information.
3	Catalog dropdown selector	Only LRP catalogs may be used; only LRP catalogs will display
4	Assignment Configuration	By default, only the DEFAULT assignment configuration is displayed in the drop-down. Any newly created assignment configuration will be added to this list.
5	Load LRP Package	This button will allow navigation to the LRP data files. Only whole 'packages' can be downloaded.

LRP packaged files are zipped files containing all data from the LRP sequencer.

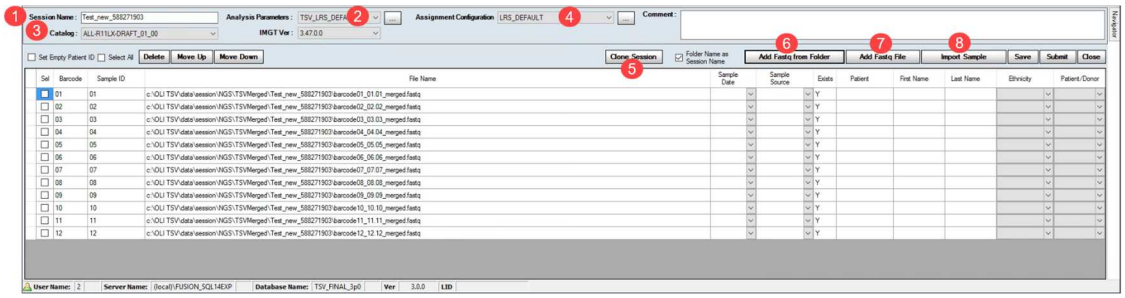




Create Session for LRS



Clicking the icon for 'LRS Session Builder' will bring up a screen which is largely the same as for Ion S5 and Illumina but differs in important ways. Those ways are highlighted below.

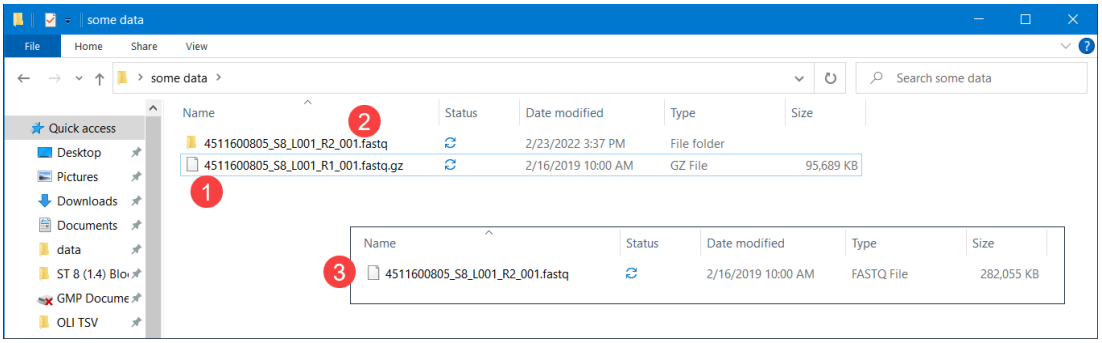


	Item	Description
1	Session Name	Session names are preceded by "LRS" followed by the time stamp. They can be modified or replaced prior to analysis
2	Analysis Parameters	The software contains a separate set of default parameters for LRP. See Utilities for more information.
3	Catalog selector	Only LRS catalogs may be used, and only LRS catalogs will display in the dropdown list.
4	Assignment Config.	Selects one of the predefined or custom Product Configurations created and saved on the Product Configuration menu. By default only LRS_DEFAULT assignment configuration is displayed.
5	Clone Session	Clicking on this button will allow the user to create a session by selecting samples from one or more sessions that have already been imported into the database. Samples for which a barcode does not exist in the original folder location will be skipped in the new session creation.
6	Add Fastq Folder	Imports the contents of an entire folder of fastq sequencer data files for analysis.
7	Add Fastq File	Imports the contents of a single sequencer data file for analysis. There can be several Fastq files associated with a barcode or just one.

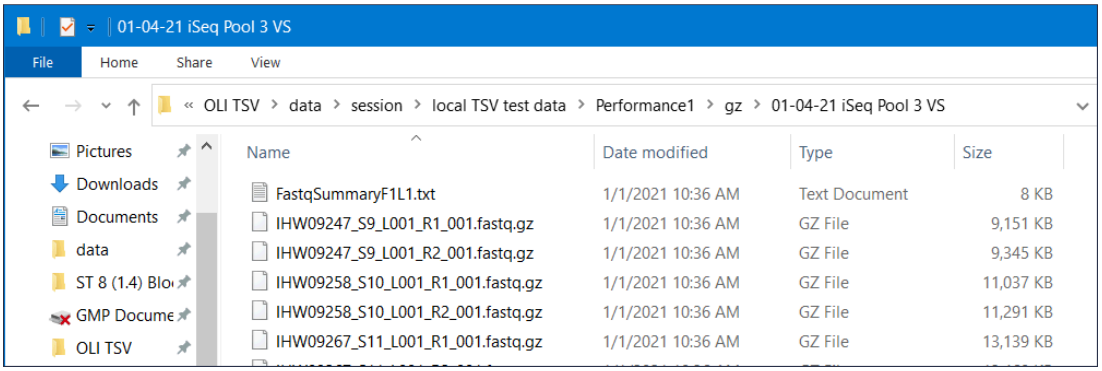
8	Import Sample	This button allows the user to navigate to a .csv file whose format is as below. Selecting the sample import file replaces the sample id and the patient ID in the sample import grid by matching the barcode id in the .csv file. The updated values are highlighted in yellow on the sample import grid. **Required Columns** - Barcode#, Sample ID, Patient ID A B C D Session ID SessionNano Flow Cell 2323 Barcode # Sample ID Patient ID 1 1 2 2 3 3 4 4 5 5 6 6 7 7 The session name is updated to the session ID value in the .csv file.

LRS.fastq.gz packaged files are zipped files containing all Long-Read Sequencing data.

A typical .fastq.gz file (1) will contain a folder inside it (2) containing individual .fastq data files (3). There can be one or many .fastq data files inside a compressed folder.



You can select a folder containing many .fastq.gz files using the "Add Fastq Folder" button:



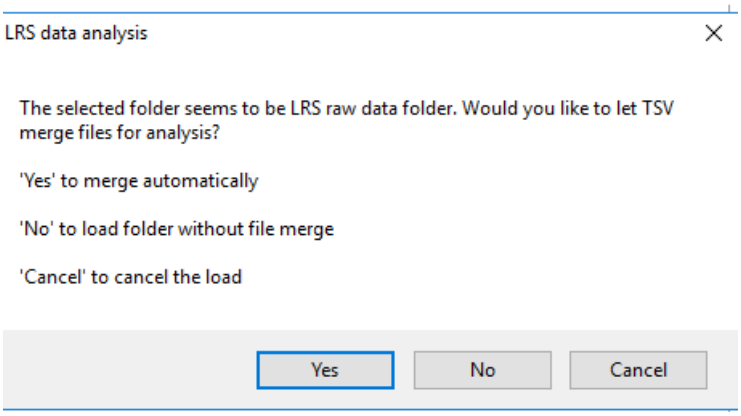
When such a folder is selected, the LRS input module loads all the files into the Importer:

Sel	Barcode	Sample ID	File Name	Sample Date	Sample Source	Exists	Patient
☐	S9	IHW09247	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09247_S9_L001_R1_001.fastq.gz			N	
☐	S10	IHW09258	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09258_S10_L001_R1_001.fastq.gz			N	
☐	S11	IHW09267	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09267_S11_L001_R1_001.fastq.gz			N	
☐	S12	IHW09277	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09277_S12_L001_R1_001.fastq.gz			N	
☐	S13	IHW09279	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09279_S13_L001_R1_001.fastq.gz			N	
☐	S14	IHW09302	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09302_S14_L001_R1_001.fastq.gz			N	
☐	S15	IHW09326	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09326_S15_L001_R1_001.fastq.gz			N	
☐	S16	IHW09353	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09353_S16_L001_R1_001.fastq.gz			N	
☐	S17	IHW09364	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09364_S17_L001_R1_001.fastq.gz			N	
☐	S18	IHW09365	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09365_S18_L001_R1_001.fastq.gz			N	
☐	S19	IHW09368	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09368_S19_L001_R1_001.fastq.gz			N	
☐	S20	IHW09369	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09369_S20_L001_R1_001.fastq.gz			N	
☐	S21	IHW09370	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09370_S21_L001_R1_001.fastq.gz			N	
☐	S22	IHW09378	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09378_S22_L001_R1_001.fastq.gz			N	
☐	S23	IHW09394	D:\OLI TSV\data\session\local TSV test data\Performance1\gz\01-04-21 iSeq Pool 3 VS\IHW09394_S23_L001_R1_001.fastq.gz			N	

Select the desired files for processing, submit the session, and like the other products, the Home Page and Navigator will then open to show sessions being processed.

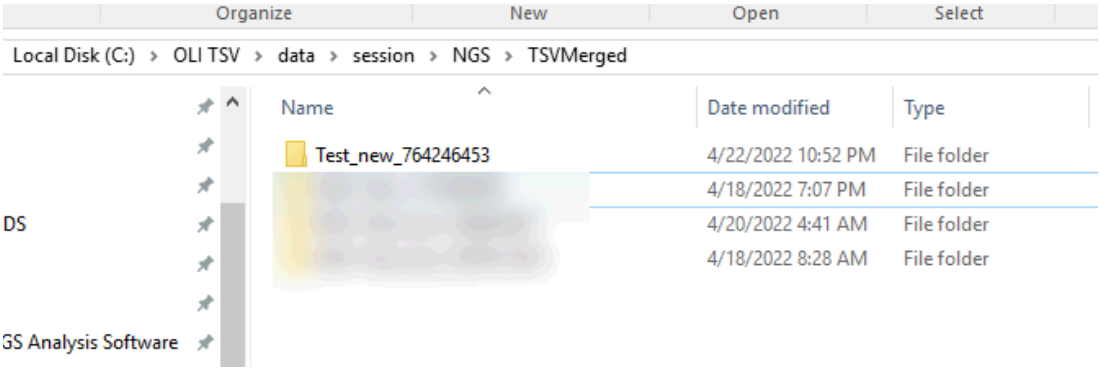
Note: Many times, barcode input folders from sequencing will be contained within a **fastq_pass** folder. To select all barcode data files, select the **fastq_pass folder** and click OK. The contents of all the barcode folders inside this master folder will be read into the importer.

TSV may then offer to merge the barcode data files into a single file:



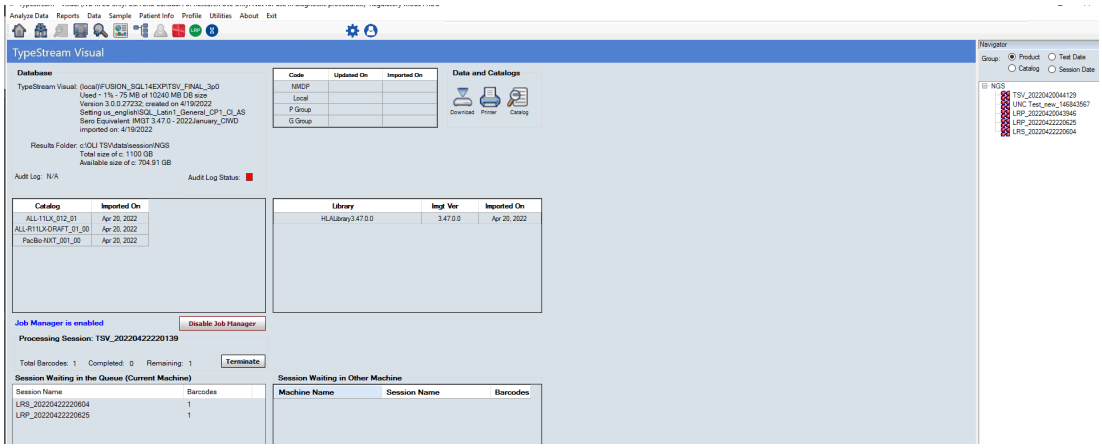
If you answer Yes, the merged files are created under TSVMerged folder under the **C:\OLI TSV\data\session\NGS** folder. If the same folder already exists there is no remerge of the fastq files.

Once the files are created, they will reside here under the **TSVMerged folder:**

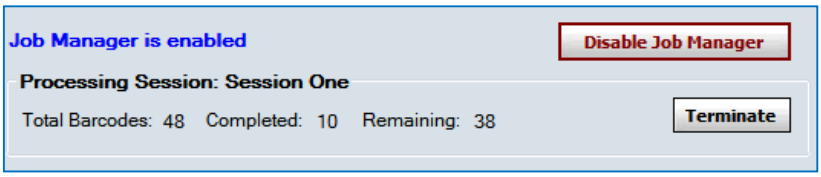


Job Manager

A session sent to the engine will appear in left column of the Job Manager under "Sessions Waiting in the Queue." Sessions submitted subsequent to this will appear in the right column under "Session Waiting in Other Machine."



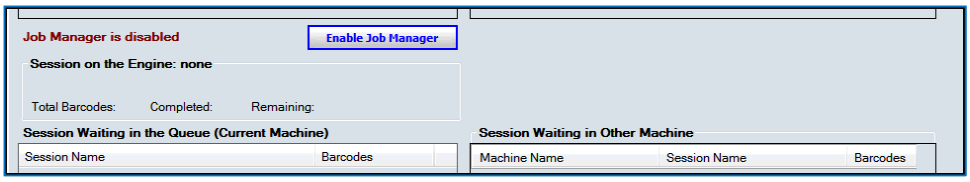
Job Manager displays the name of the session on the engine, total number of barcodes in the session, how many have been analyzed, and how many remain.



There is limited functionality with respect to the queue waiting on other machine. User on current machine cannot change the analysis order, remove from queue, or terminate sessions on the other machine. It is there for informational purposes only.

Disable/Enable Job Manager

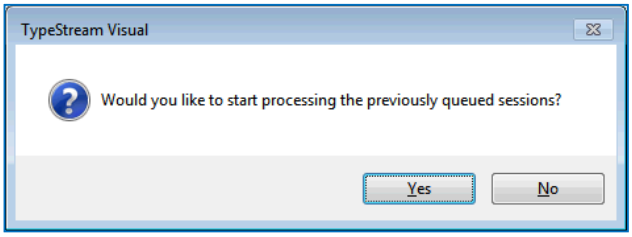
"Disable Job Manager" will stop the engine and return the current session to the queue. The number of barcodes successfully analyzed will display. To continue processing, click "Enable Job Manager."



The Job Manager will automatically be disabled when the application is closed or the computer is shut down.

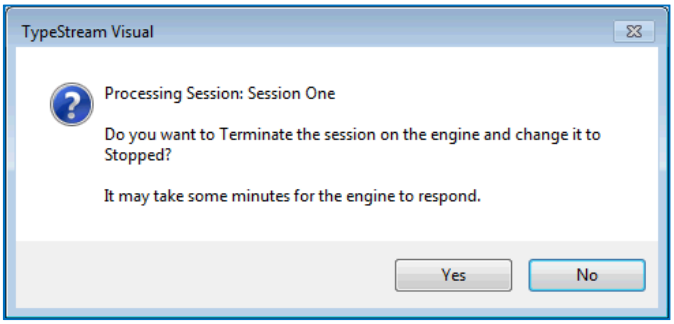
When the application is re-opened, user will be asked if the session running at last shutdown

should be started again. If "No" is selected, sessions will remain in the queue and job manager will remain in 'disabled' state.



Terminate a session

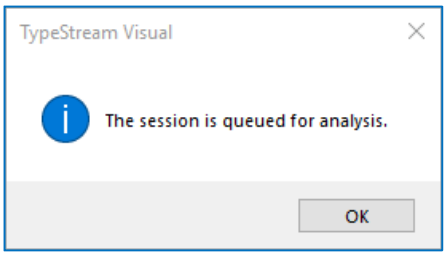
"Terminate" button will end the analysis process for the session on the engine. Software will confirm the termination.



That session will then appear in Navigator in red text. The engine will proceed with analysis on the next session in the queue.

A terminated session can be returned to the engine by doing the following:

- Click on the session name in the Navigator – the session opens in summary screen. Each sample will display status of "Not Reviewed," "In Process," or "Not Submitted."
- Click the **Functions** button and select "Resubmit the Session". *(See more information in Chapter 6.)*
- Software will send the session back to the queue and give confirmation to the user.



Session Queue

The session Queue consists of two separate panels:

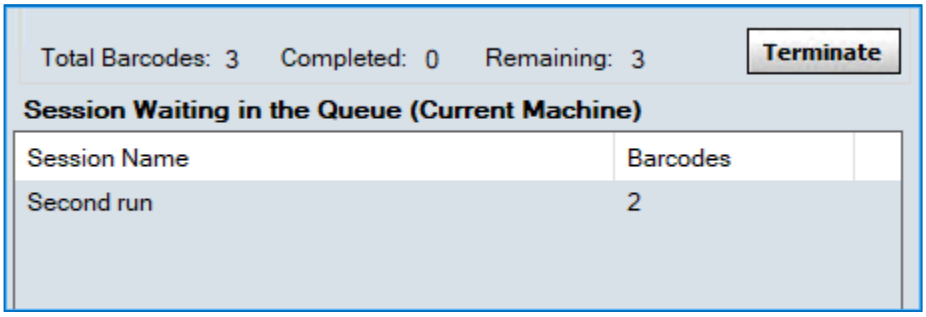
- "Sessions Waiting in the Queue (Current Machine)" and
- "Session Waiting in Other Machine." This second panel enables multiple users connected to the same database to see what sessions the other user have waiting.

Sessions Waiting in the Queue (Current Machine)

Sessions in the queue display with Session Name, and the total number of barcodes.

Both IVD and RUO mode sessions that are queued up for analysis are displayed in the Sessions Waiting in Queue list.

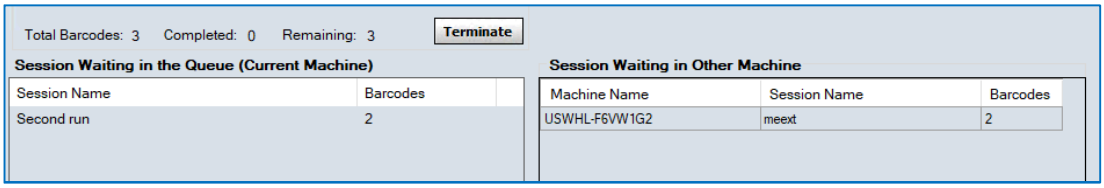
The order of sessions waiting in the queue can be modified by dragging and dropping the session name to another position. This must be done while the engine is disabled.



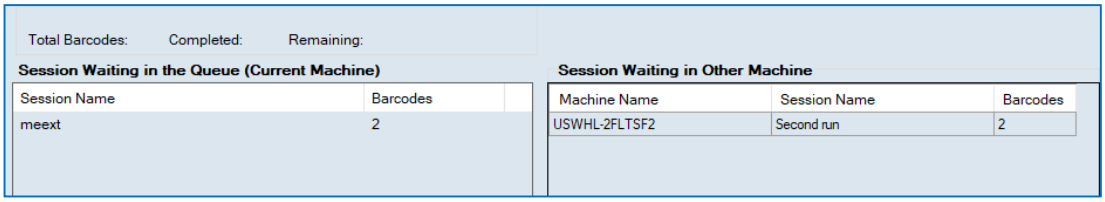
Session Waiting in Other Machines.

Sessions in this queue display the session name, machine name, and number of barcodes for sessions connected to the same database where the sessions are running on a different machine.

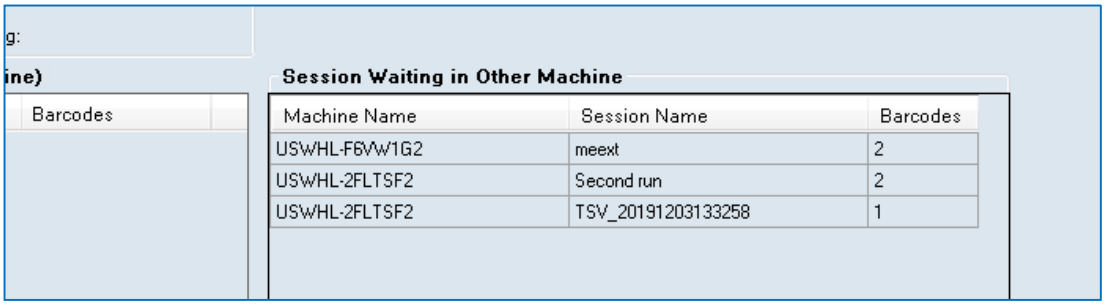
As with the current machine queue, when the session goes to the engine, it is removed from the queue list.



The other machine will display the reverse of this machine:

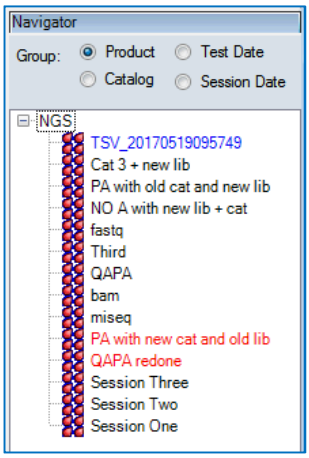


"Session Waiting in Other Machine" can accommodate multiple other machines and multiple sessions on the same machine.



Navigator

All sessions display in the Navigator. A session that was Saved but not Submitted on the Import page displays in blue font. A session terminated from the engine displays in red font.



Sessions in the Navigator can also be sorted by Test Date, Session Date, Product or Catalog.

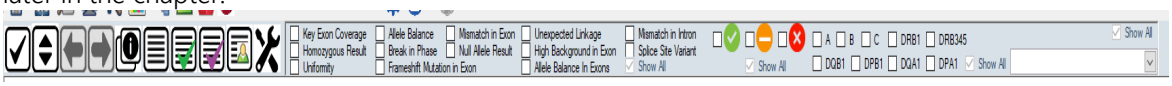
6

View Analysis

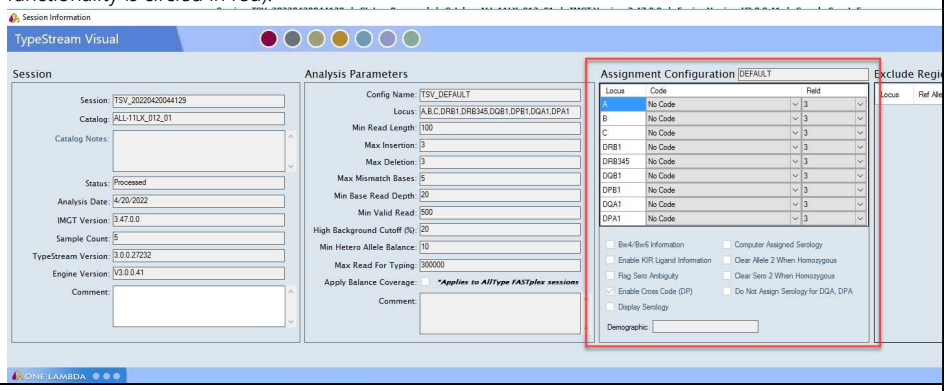
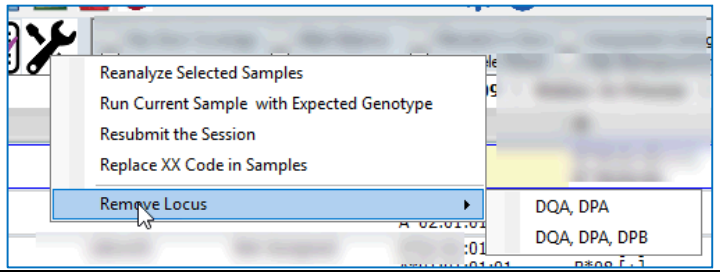
Session Summary

The Session Summary window displays the results of the TypeStream Visual analysis for all samples. This window can display in either 'collapsed' or 'expanded' view to show differing levels of detail.

At the top of the page, whether in collapsed or expanded view, are a set of functions and filters for use after analysis. What displays here is a high-level explanation. More detailed information follows later in the chapter.

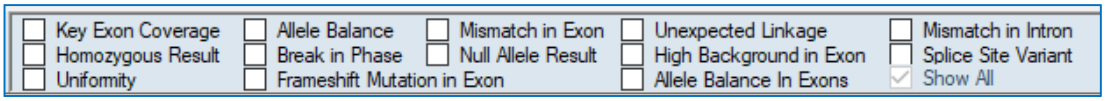


	Hover Tooltip	Description
1	Toggle Select All	Will select or de-select all samples in a session
2	Session Detail View / Session Summary View	This button will toggle between 'collapsed' (session summary view) and 'expanded' (session detail view). The icon above indicates that the samples are currently in collapsed view and clicking this will expand them. The icon to go from expanded to collapsed looks like the following and will replace the icon at position 2. When moving from one session to another, the view will be in collapsed mode. If the session contains only one sample, the session summary view defaults to a Detail View.

	Hover Tooltip	Description
3	Sample Navigation	These buttons help the user to navigate to other samples. Click right arrow to go to the next sample; click left arrow to go to the previous sample.
4	Show session information	Clicking this will display a window showing information pertaining to this session, including analysis parameters used, catalog and library used, sample count, TypeStream version, engine version, and the locations of any excluded regions. The regions that were excluded for current session will be checked. Analysis Parameters display in the same order as in the configuration window. **New in v3.0** The Session Information Window now includes Assignment Configuration information (new functionality is circled in red). 
5	Save Assignment to Selected Samples.	Clicking this button assigns the software-generated genotypes to all loci that have been selected using the checkbox. In case of a NO CALL or highly ambiguous (having 100 or more) genotype ambiguity, an assignment will not be made. Assigned genotypes will display in **BOLD** on the sample row of session summary.
6	Mark Selected Samples as Reviewed	When supervisor or technologist reviews the assigned genotypes, clicking this button will mark them as Reviewed. Reviewed genotypes display in GREEN BOLD in collapsed view; locus will have green background in expanded view. Only samples that have been assigned will be reviewed.
7	Mark Selected Samples as Confirmed	This requires supervisor-level status and confirms that all assigned and reviewed genotypes are approved. Confirmed genotype display in PURPLE BOLD in collapsed view; locus will have purple background in expanded view. Only samples that have been reviewed will be confirmed.
8	Bulk Patient Assign	This button allows the selected samples to be assigned to the patient in bulk, instead of individually.
9	Functions	This button opens a selection panel for further operations on the session or sample. *See Functions section below for more information.* 

Filtering for Health Metrics

The health metrics discussed in the 'Utilities' section of a previous chapter can be filtered here for easy viewing. Refer to that section and later in this chapter for information on the specifics of each filter.

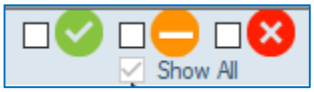


Note: Frameshift mutation in Exon and Allele Balance in Exons does not apply to LRP sessions.

> **NOTE:** 'Frameshift mutation in Exon' and 'Allele Balance in Exons' are not available for LRP sessions.

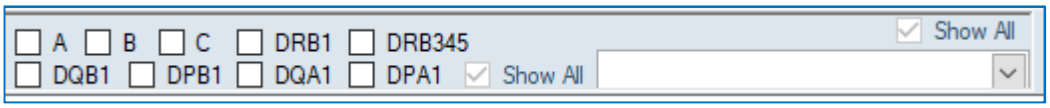
Filtering for Health Metric Level

In NGS Configuration, each of the health metrics above was weighted with the level of severity of the metric. Use the filters below for a quick view. The filtering of the samples is at the barcode level.

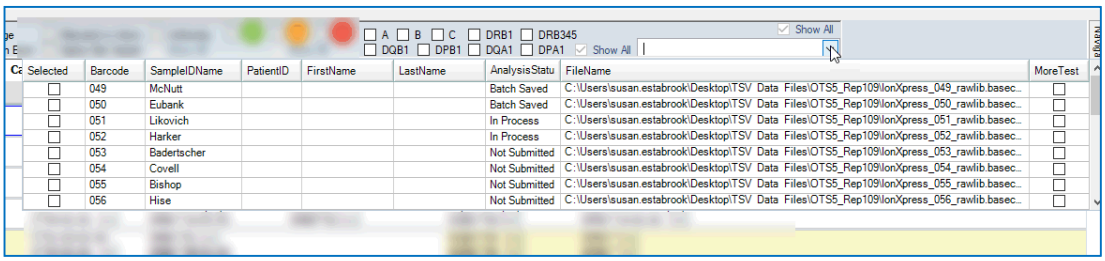


Filtering for Locus and Barcode

Loci may be filtered to view single loci or combinations (e.g. DRB1 + DRB345). Can also be used in combination with barcode, or any other filter option.



Clicking the dropdown for barcode display all barcodes in the session and includes related information as well as current analysis status.



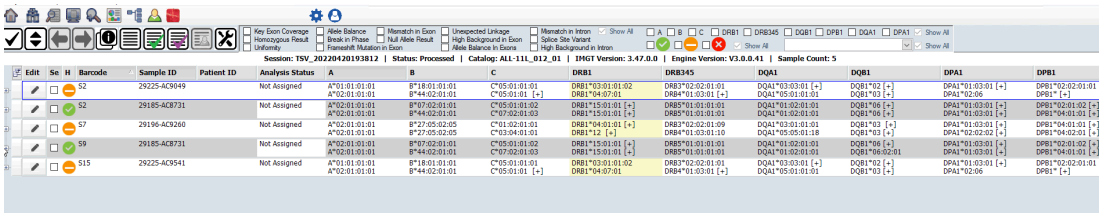
Session Summary View – collapsed

When first selected from the Navigator, sessions open in Session Summary View. This is a high-level overview in which you see the following:

- Above the grid are listed the session name, session status, catalog used, IMGT library version used, engine version, and sample count.
- Each sample is shown on a separate summary row, displaying health level, Barcode, Sample ID, Analysis Status, and all loci represented in the data.
- Summary rows are alternately shaded with gray, making it easier to distinguish on a large table.
- Health level for the barcode represents the highest (most severe) rating from

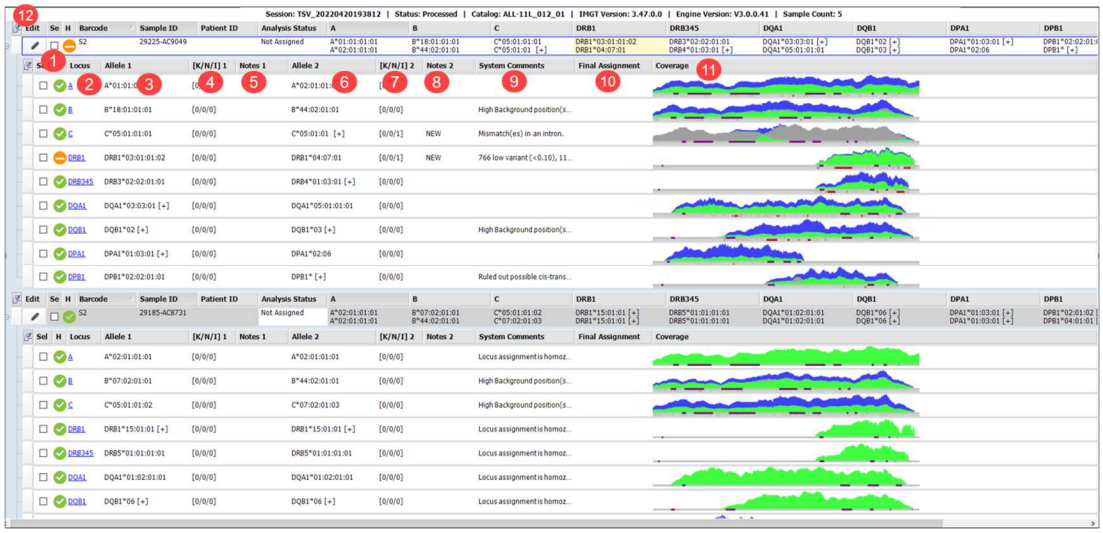
the individual samples.

- Software-derived genotyping displays for each locus.
- Any failure of a metric will be highlighted in yellow.



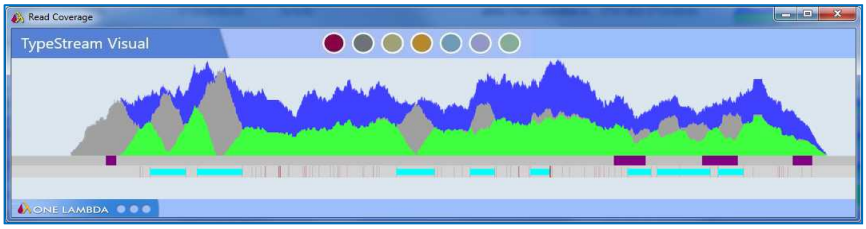
Session Detail View – expanded

To view the individual loci and get more detailed information click "Session Detailed View" button. This will expand all samples and all loci will be visible. Or click "+" on barcode to display individual loci for only one sample. The grid expands as shown below.



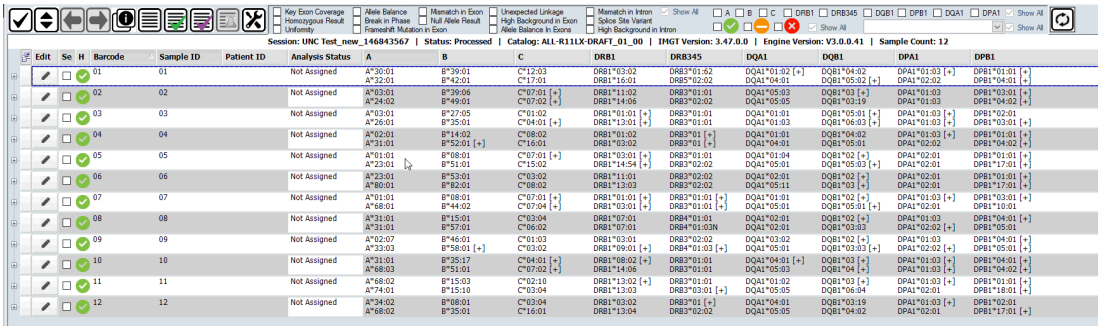
With all rows expanded, grid displays barcode list with the data columns listed below. Please note that the selection checkbox on the far left is for selecting loci for functions (e.g. 'Assign All') and has nothing to do with what displays in the analysis panel.

	Item	Description
1	Locus Health icon (H)	Health – health metric and severity as established in Utilities. Each locus will display the health icon that represents the highest number (most severe) of all the failed metrics.
2	Locus	All loci present in the sample display here. Locus field displays in green when the locus is saved on the analysis page and purple when it is confirmed on the analysis page.
3	Allele 1	Displays the software-determined genotyping. • [+] indicate there are ambiguous alleles. Hover over this indicator to view the allele list. • "r" indicates a rare allele if the software has been configured to display allele frequency • Cis/trans ambiguities are shown in purple with both genotypes displaying.
4	[K/N/I] 1	Mismatch count for allele 1. K=mismatches is key exons; N=mismatches in non-key exons; I=mismatches in introns.
5	Notes 1	Notations regarding the allele call for allele 1 appear here, and may include NEW, Low Coverage, NO CALL.

6	Allele 2	The software-generated top allele call for allele 2.
7	[K/N/I] 2	Mismatch count for allele 2.
8	Notes 2	Notations regarding the allele call for allele 2.
9	System Comments	System comments include any failed metrics that were configured to so display, or various other conditions relating to insertion, high background frequency, or other notable aspects of the analysis.
10	Final Assignment	When the user saves a final assignment on the analysis page, the final assignment displays here. On the illustration above, only A locus has been saved.
11	Coverage	Histogram of read coverage of the locus. Left click on the histogram displays a large size version for more clarity:  Elements of the histogram are as follows: • Green area = allele 1 • Blue area = allele 2 • Gray area = both alleles • Dark purple banding = exons • Light purple banding = introns
12	Notepad	The notepad icon is visible on the session summary grid header when the catalog notes has information related to the assay to alert the user. This icon is invisible when there is no information present in the catalog. Clicking on the icon displays the information to the user.

All column widths on the locus level can be resized by the user. To retain the resized columns, go to Home page before selecting another session to view.

LRS Session Summary View – collapsed

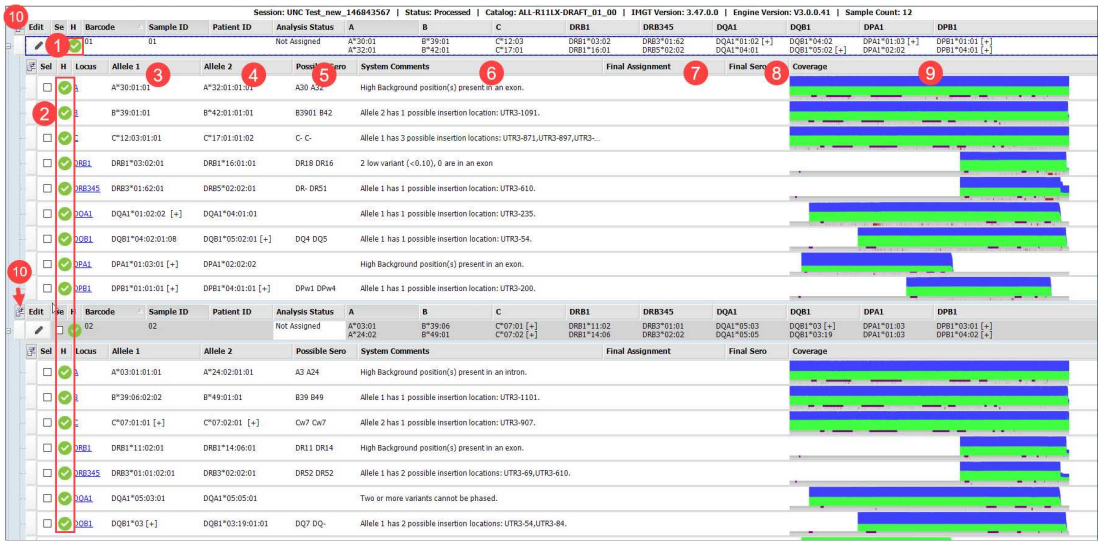


When first selected from the Navigator, sessions open in Session Summary View. This is a high-level overview in which you see the following:

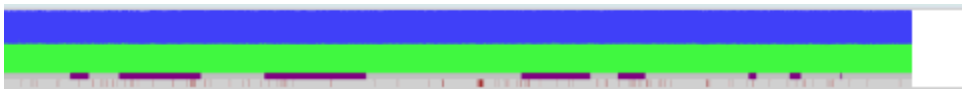
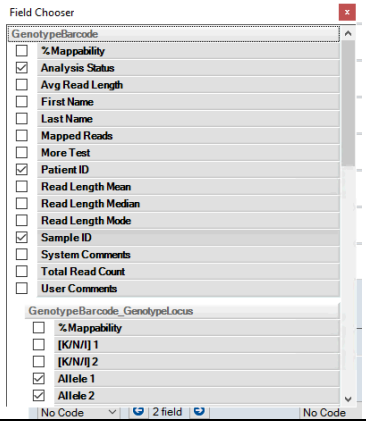
- Above the grid are listed the session name, session status, catalog used, IMGT library version used, engine version, and sample count.
- Each sample is shown on a separate summary row, displaying health level, Barcode, Sample ID, patient ID, Analysis Status, and all loci represented in the data.
- Summary rows are alternately shaded with gray, making it easier to distinguish on a large table.

- Health level for the barcode represents the highest (most severe) rating from the individual samples.
- Software-derived genotyping displays for each locus. The display resolution is 2 field resolution. User can click on the icon to toggle between low resolution (2 field) and high resolution view (3 field/ 4 field resolution) as in non – LRS sessions.
- Any failure of a metric will be highlighted in yellow.

LRS Session Summary View – expanded



	Item	Description
1	Locus Health icon (H)	Health – health metric and severity as established in Utilities. Each locus will display the health icon that represents the highest number (most severe) of all the failed metrics.
2	Locus	All loci present in the sample display here. Locus field displays in green when the locus is saved on the analysis page and purple when it is confirmed on the analysis page.
3	Allele 1	Displays the software-determined genotyping. • [+] indicate there are ambiguous alleles. Hover over this indicator to view the allele list. • "r" indicates a rare allele if the software has been configured to display allele frequency • Cis/trans ambiguities are shown in purple with both genotypes displaying.
4	Allele 2	The software-generated top allele calls for allele 2.
5	Possible Sero	The software-generated possible sero value for the given locus. In case the allele is not found in the serological database used, the sero assignment is not displayed. The assignment setting would display this allele as "locus_0"
6	System Comments	System comments include any failed metrics that were configured to so display, or various other conditions relating to insertion, high background frequency, or other notable aspects of the analysis.
7	Final Assignment	When the user saves a final assignment on the analysis page, the final assignment displays here. On the illustration above, only A locus has been saved.
8	Final Sero	Displays the serological assignment for the given locus. This column is blank when there is no final sero assignment.

9	Coverage	Histogram of read coverage of the locus. Left click on the histogram displays a large size version for more clarity:  Elements of the histogram are as follows: • Green area = allele 1 • Blue area = allele 2 • Gray area = both alleles • Dark purple banding = exons • Light purple banding = introns
10	Field Chooser	Users can select additional columns to be displayed from the field chooser. 

Note: The notepad icon is visible on the session summary grid header when the catalog notes has information related to the assay to alert the user. This icon is invisible when there is no information present in the catalog. Clicking on the icon displays the information to the user.

Allele display

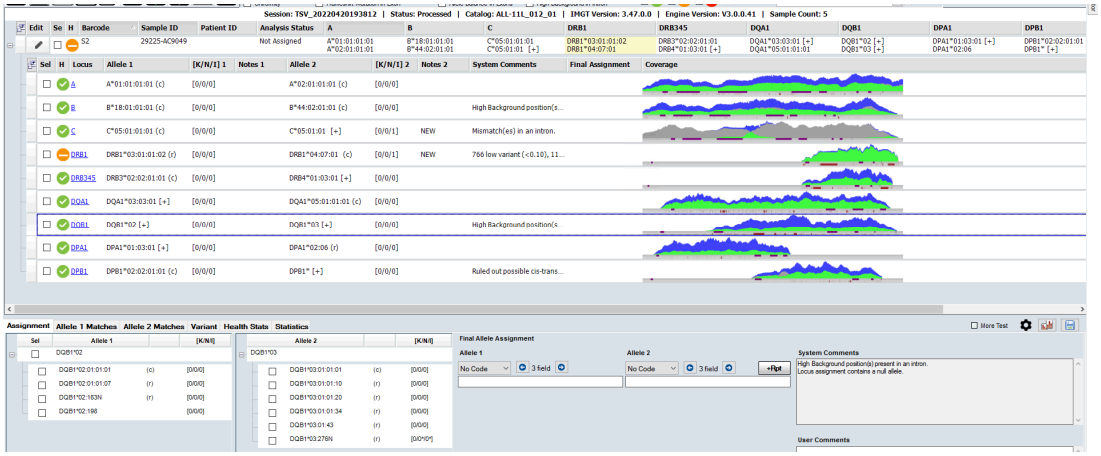
TypeStream visual will display locus results based on the latest IMGT library in the database. A typical heterozygous allele displays with top software-generated genotypes and accompanying data as described above. For a cis/trans ambiguity, the software will fully display both genotypes on the summary detail page, and the data will be shaded with a purple background.

Sel	H	Locus	Allele 1	[K/N/I] 1	Notes 1	Allele 2	[K/N/I] 2	Notes 2	Final Assignment
		A	A*01:01:01:01	[0/0/0]		A*02:01:01:01	[0/0/0]		

Final Assignment	Mapped Reads	Min Coverage	Max Coverage	Total Reads	Coverage
	10829	246	683	10983	

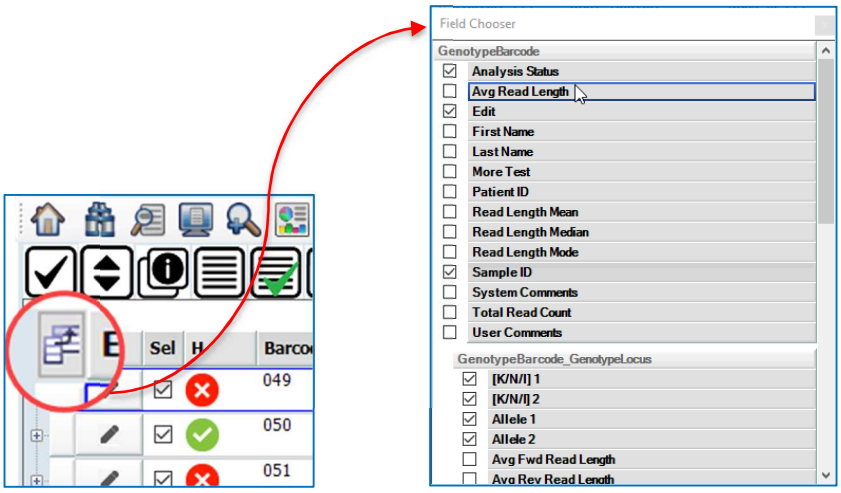
Applying the demographic filter, each of the alleles in the session summary row are suffixed with c, wd, i or r to represent common, well documented, intermediate or rare allele respectively. Ambiguous alleles do not get a demographic designation. The assignment tab displays the frequency for each of the alleles in the child rows.

Alleles with a frequency of 1 are represented as a c, alleles with a frequency of 2 are represented as a wd, and alleles with a blank are represented as an r.

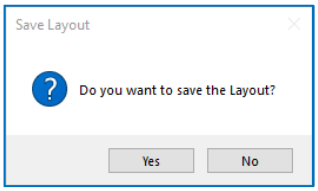


Field Chooser

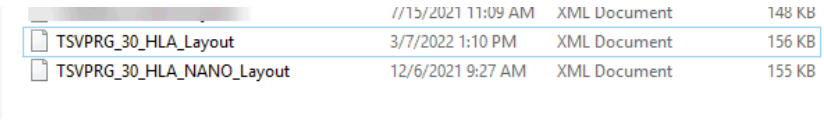
User may include more columns in the grid by clicking the icon in the top left corner of the grid. Field Chooser window displays. The top part of the chooser shows options available for the collapsed mode, the bottom part shows options for the expanded mode (locus level). Select the desired options by checking the checkbox and exit the field chooser to save them. The information is system specific.



After making selections, use the 'x' in the upper right corner to remove the Field Chooser. A message will display confirming that the layout should be saved.



To clear all field selections and return to default settings, navigate to C:\OLI TSV\data\temp and remove the file "TSVPRG_XX_HLA_Layout.xml."



When using TSV 3.0, the field chooser layout file is saved as “TSVPRG_30_HLA_Layout.xml” and TSVPRG_30_HLA_NANO_Layout.xml for LRS sessions.

For LRS session, to clear all field selections and return to default settings, navigate to C:\OLI TSV\data\temp and remove the file “TSVPRG_30_HLA_NANO_Layout.xml.”

Fields that are available at the barcode level:

%Mappability, Analysis Status Avg Read Length, Edit, First Name, HistoTrac, Last Name, Mapped Reads, More Test, Patient ID, Read Length Mean, Read Length Median, Read Length Mode, Sample ID, System Comments, Total Read count, User Comments

Fields that are available at the locus level:

%Mappability, [K/N/I] 1, [K/N/I] 2, Allele 1 , Allele 2, Avg Fwd Read Length, Avg Rev Read Length, Avg Frag Length, Avg Read Depth, Avg Read Length, Confirmed Date, Confirmed User, Coverage, Final Assignment, Final Sero, Fwd Read Count, Mapped Reads, Max Coverage, Ma Read Depth, Min Coverage, Notes 1 , Notes 2, Rev Read Count, Reviewed Date, Reviewed User, Sel, System Comments, Total Reads, User Comments

Assign, Review, Confirm

Using these three buttons, it is possible to assign, review, or confirm genotyping for all samples or selected samples with the click of a button.

Session: B-109 | Status: Processed | Catalog: ALL-11LX_007_01 | IMGT Version: 3.37.0.1 | Engine Version: V2.0.0.51 | Sample Count: 18

Sel	H	Barcode	Sample ID	Analysis Status	A	B	C	DRB1	DRB345	DQB1	DPB1
☐	✕	049	McNutt	Confirmed	A*02:10 A*11:02:01	B*40:01:02 B*46:01:01	C*07:02:01 C*08:01:01	DRB1*08:03:02 DRB1*09:01:02/09:31	DRB4*01:03:02 DRB4*01:03:02	DQB1*03:03:02/03:3 98...	DPB1*05:01:01/135:01 DPB1*14:01:01/834:01
☑	✕	051	Likovich	Confirmed	A*01:01:01 A*01:01:01	B*08:01:01/08:20 7...	C*07:01:01 C*07:01:01	DRB1*03:01:01/03:14 7...	DRB3*01:01:02 DRB3*01:01:02	DQB1*02:01:01/02:1 09/02:148...	DPB1*03:01:01/727:01/ DPB1*04:01:01/350:01
☐	✕	056	Hise	Reviewed	A*29:02:01 A*29:02:01	B*44:03:01/44:46 6N B*44:03:01/...	C*16:01:01 C*16:01:01	DRB1*07:01:01/07:79 DRB1*07:01:01	DRB4*01:01:01/01:75/0 1:83 DRB4*01:01:01	DQB1*02:02:01/02:1 56/02:02:09/02:11...	DPB1*02:01:02 DPB1*02
☐	✕	057	Zirpola	Reviewed	A*02:01:01 A*02:01:13	B*44:02:01/44:19 N B*44:02:01/4...	C*05:01:01 C*05:01:01	DRB1*14:54:01/14:12 2 DRB1*14:54:01/1...	DRB3*02:02:01 DRB3*02:02:01	DQB1*05:03:01/05:0 3:18/05:03:19/05:...	DPB1*04:02:01 DPB1*04
☐	✕	058	Thatcher	Assigned	A*24:02:01 A*24:02:01	B*07:02:01/07:02 :71/07:02:62/07...	C*07:02:01 C*15:02:01	DRB1*14:07:01 DRB1*15:01:01/15:...	DRB3*02:02:01 DRB5*01:01:01	DQB1*05:03:01/05:0 3:18/05:03:19/05:...	DPB1*04:01:01/350:01 D

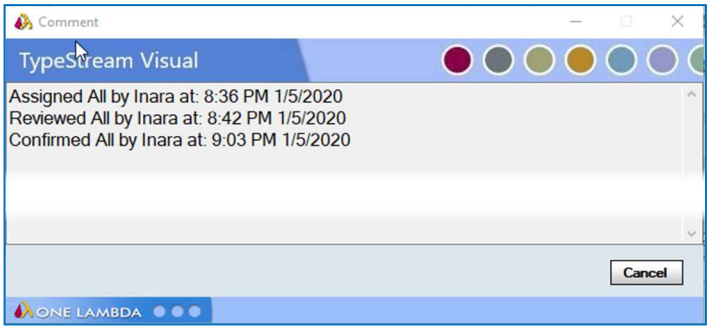
In the example above, barcode 58 has had all loci assigned using the Assign button. The genotypes display in bold and Analysis Status displays “Assigned.”

Barcodes 56 and 57 were first Assigned, then Reviewed using the Review button. The genotypes display in bolded green and Analysis Status displays “Reviewed” and has a green background.

Barcodes 49 and 51 were first Assigned, then Reviewed, and then Confirmed using the Confirm button. The genotypes display in bolded purple and Analysis Status displays “Confirmed” and has a purple background.

By design, samples cannot be confirmed before they are reviewed and cannot be reviewed before they are assigned.

All assignments, reviews, and confirmations are tracked and can be accessed via “Assignment History” on the Analysis Panel.



There are several instances in which the assignments will not be made by the software.

- In the case of a cis/trans ambiguity, the software will not select one genotype over the other
- A highly ambiguous allele having 100 or more ambiguities
- A NO CALL allele

Session: B-109 | Status: Processed | Catalog: ALL-11LX_007_01 | IMGT Version: 3.37.0.1 | Engine Version: V2.0.0.51 | Sample Count: 18

Sel	H	Barcode	Sample ID	Analysis Status	A	B	C	DRB1	DRB345	DQB1	DPB1
☐	✓	050	Eubank	Not Assigned	A*02:01:01 A*02:01:01	B*27:05:02 B*27:05:02	C*01:02:01 C*01:02:01	DRB1*01:01:01/01:01 :32/01:01:33/01:10...		DQB1*05 [+] DQB1*05 [+]	DPB1*04:01:01 DPB1*04:01:01
☐	✗	053	Badertscher	Not Assigned	A*03:01:01 A*03:01:01	B*35:01:01/35:44 7...	C*01:02:01 C*04:01:01	DRB1*01:01:01/01:01 :32/01:01:33/01:10...		DQB1*04:02:01/04:0 2:18/04:51/04:52/...	DPB1* [+] DPB1* [+]
☑	✓	063	Schudlo	Assigned	A*02:01:01 A*02:07:01	B*46:01:01 B*46:01:01	C*01:02:01 C*01:02:01	DRB1*08:03:02 DRB1*08:03:02		DQB1*06:01:01/06:0 1:15/06:01:25/06:...	DPB1*02:02:01 DPB1*02:02:01
☑	✗	064	Grapes	Not Assigned	A*01:01:01/01:17 /01:194/01:23:0...	B*08:01:01/08:20 7 B*44:02:01/44...	C*05:01:01 C*07:01:01	DRB1*04:04:01 DRB1*04:09	DRB4*01:03:01/01:107/ 01:83 DRB4*01:03:02	DQB1*03 [+] DQB1*03 [+]	DPB1*20:01:01 DPB1*532:01/891:01
☑	✗	065	Greene	Not Assigned	A*02:07:01 A*24:02:01/24:0...	B*07:02:01/07:02 :62 B*15:01:01	C*03:03:01 C*07:02:01	DRB1*15:01:01/15:17 1 DRB1*15:01:01/1...	DRB5*01:01:01 DRB5*01:40	DQB1*03 [+] DQB1*06 [+]	DPB1*02:02:01/779:01/496:01 DPB1*04:01:01/04:01:01N/806:01:01

Notice the following for the table above:

- Barcode 50 has been confirmed but has NO CALL for DRB345 and a highly ambiguous DQB1. Because of the high ambiguity, the software did not make an assignment for DQB1, and the alleles are neither bold nor in purple. Additionally, Analysis Status retains its "Not Assigned" value because the assignments are not complete.
  Barcode 53 has a NO CALL for DRB345. DPB1 is a cis/trans ambiguity and was therefore not assigned by the software. Analysis Status again retained its "Not Assigned" value.
  Barcode 63 has a NO CALL for DRB345. As this was expected due to linkage association, and all other loci have been assigned, the Analysis Status has been changed to "Assigned."
  Barcode 64 and 65 both have highly ambiguous DQB1 alleles and have therefore not been assigned. Although the other loci have been assigned, and, for barcode 64, reviewed, the Analysis Status remains "Not Assigned."

Note that this process displays genotypes to the number of fields specified in Assignment Settings in NGS Configuration. *(See "Utilities" for more information.)*

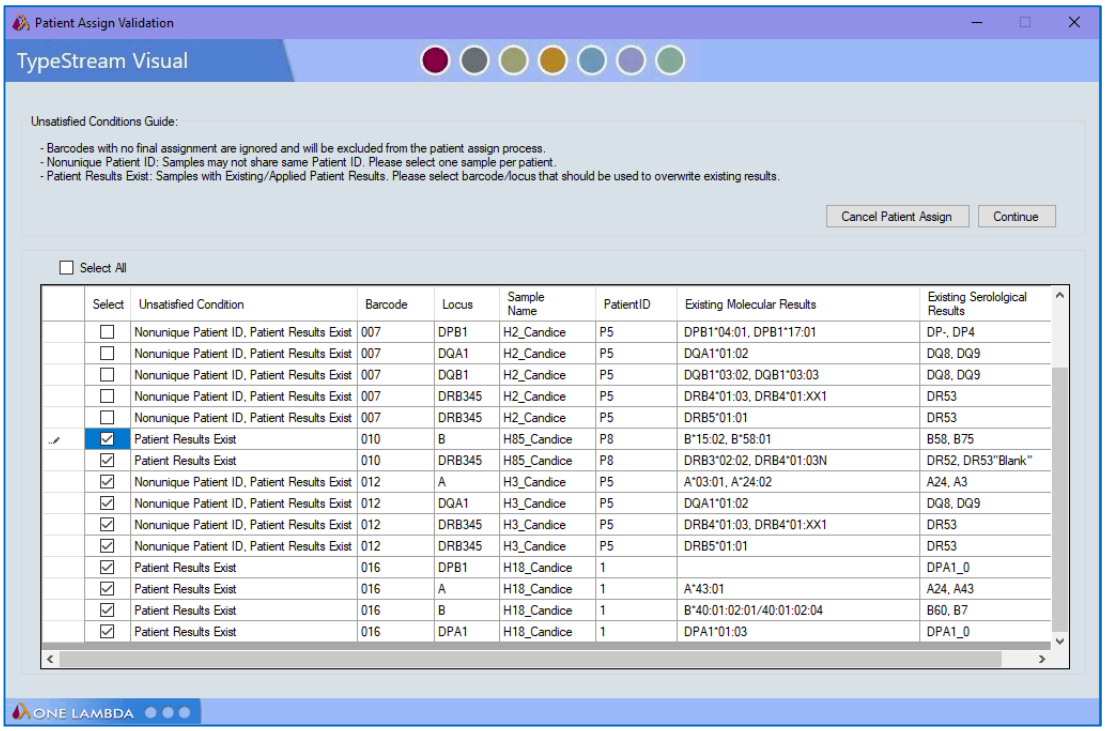
Note also that using this process will not save genotypes to the patient record. That must be done manually on the Analysis Panel.

Bulk Patient Assign

The following conditions need to be met for the bulk Patient Assign to succeed:

- Selected barcodes must have patient association
- Patient associations must be unique among selected barcodes
- At least one barcode has final assignment

When the "Bulk Patient Assign" button is pressed, TSV first validates the selected barcodes to guarantee that no two barcodes have the same patient ID associated with them. Barcodes that do not meet this condition will be displayed in a grid on a pop-up dialog with patient ID and patient results, if they exist. The user is expected to select one barcode per patient in the grid. In case patient results exist, by selecting a barcode in this pop-up grid the user also allows the replacement of existing patient results.

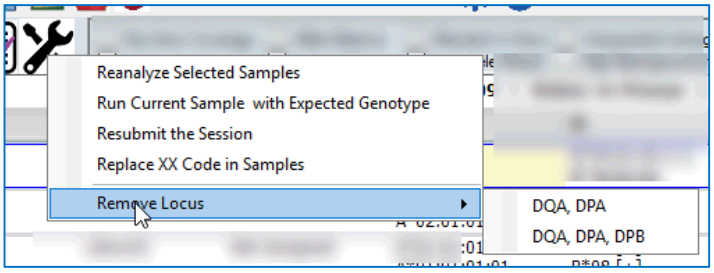


Select	Unsatisfied Condition	Barcode	Locus	Sample Name	PatientID	Existing Molecular Results	Existing Serololgical Results
☐	Nonunique Patient ID, Patient Results Exist	007	DPB1	H2_Candice	P5	DPB1*04:01, DPB1*17:01	DP-, DP4
☐	Nonunique Patient ID, Patient Results Exist	007	DQA1	H2_Candice	P5	DQA1*01:02	DQ8, DQ9
☐	Nonunique Patient ID, Patient Results Exist	007	DQB1	H2_Candice	P5	DQB1*03:02, DQB1*03:03	DQ8, DQ9
☐	Nonunique Patient ID, Patient Results Exist	007	DRB345	H2_Candice	P5	DRB4*01:03, DRB4*01:XX1	DR53
☐	Nonunique Patient ID, Patient Results Exist	007	DRB345	H2_Candice	P5	DRB5*01:01	DR53
☑	Patient Results Exist	010	B	H85_Candice	P8	B*15:02, B*58:01	B58, B75
☑	Patient Results Exist	010	DRB345	H85_Candice	P8	DRB3*02:02, DRB4*01:03N	DR52, DR53"Blank"
☑	Nonunique Patient ID, Patient Results Exist	012	A	H3_Candice	P5	A*03:01, A*24:02	A24, A3
☑	Nonunique Patient ID, Patient Results Exist	012	DQA1	H3_Candice	P5	DQA1*01:02	DQ8, DQ9
☑	Nonunique Patient ID, Patient Results Exist	012	DRB345	H3_Candice	P5	DRB4*01:03, DRB4*01:XX1	DR53
☑	Nonunique Patient ID, Patient Results Exist	012	DRB345	H3_Candice	P5	DRB5*01:01	DR53
☑	Patient Results Exist	016	DPB1	H18_Candice	1		DPA1_0
☑	Patient Results Exist	016	A	H18_Candice	1	A*43:01	A24, A43
☑	Patient Results Exist	016	B	H18_Candice	1	B*40:01:02:01/40:01:02:04	B60, B7
☑	Patient Results Exist	016	DPA1	H18_Candice	1	DPA1*01:03	DPA1_0

Next, software will look for existing patient results for patients associated with the selected barcodes. If patient results are found but, whether they may be replaced, has not yet been determined during the previous dialog, found results will be displayed in a similar pop-up dialog to allow the user to choose barcodes patient results of which may overwrite the existing results.
On this dialog, the user will have the option to either cancel out of "Patient Assign All" or to make zero or more selections and press Done to continue the operation. Only the selected samples will overwrite existing patient results. The rest will be skipped.

Functions

TypeStream Visual contains number of functions for further operations on analyzed data that are available directly from the Summary Page, whether in expanded or collapsed mode. Just click on the tools icon and select the option you wish to use.



Reanalyze Selected Samples

'Reanalysis' will open a new session for any selected barcode directly from the summary page. Select a single or multiple barcodes or the entire session, click 'Reanalysis,' and the application opens the selected barcode(s) in a new session. Session Name, Analysis Parameters, Catalog, and IMGT version can all be modified for the new session.

Run Current Sample with Expected Genotype

Formerly known as "Retype Current Barcode" this tool can help user who feel that the software may have not used the correct reference allele in its analysis.

In a regular run, the software first estimates candidate alleles based on the raw read sequences. The sequences from the candidate alleles are used to map reads. The mapped reads then are used to construct consensus sequence for genotyping.

When the estimated candidate alleles are too different from the target alleles, it causes a read mapping problem; the consensus sequence may then result in a wrong genotype or none.

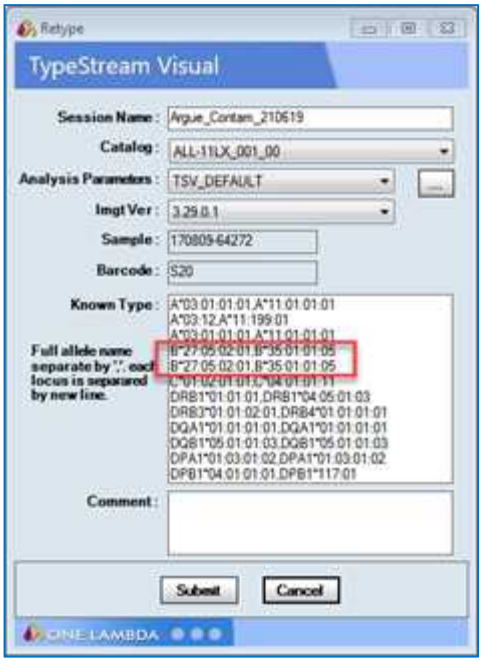
By using this function, the user can provide an expected genotype, i.e., sample was previously typed by different method. With the expected genotype, the software does not need to use candidate alleles as a mapping reference. Instead, it uses the user-provided alleles as a reference for downstream mapping and typing.

Usually, the resulting genotype should be close to the given genotype. If it is completely different, either the given genotype is not expected, or the software is mis-mapping the reads.

User may select the 'Rerun Current Barcode with Expected Typing' option, manually enter the correct type, and submit for reanalysis, which may use the same parameters and library or may change

The known type format is very restricted, and the software will pre-fill the typing as determined in original analysis. The user needs only to edit the alleles for which the typing call is in question and leave the rest as is. The software does not verify if the allele name entered is valid; any invalid allele name will be ignored, i.e., using DRB1*04:01:01:01 and not DRB1*04:01,which may lead to a mistype.

In the example below, B locus has two genotypes. If the user clicks submit with the window as is, B locus will retype with only the first B locus genotype

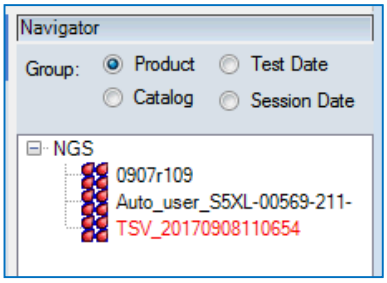


If user wants the software to leave B locus alone and only change, for example, the C locus, she will change it to the following and then hit submit:

Using this method, the B locus will still display as multiple genotypes, as displayed above. When a sample is run with an expected genotype, a system comment is included "Sample analyzed with a user-defined type reference: C*01:02:02 + C*04:01:01:11".

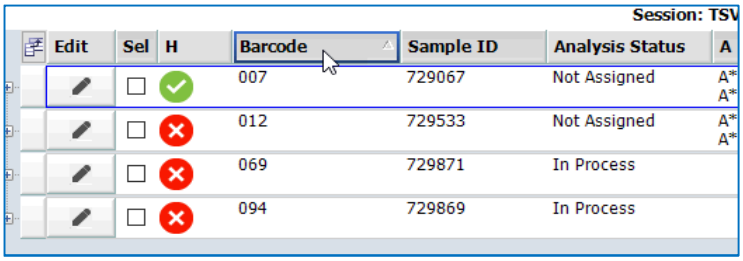
Resubmit the Session

Resubmit option is available only for a session that was only partly analyzed. When a session analysis has been terminated using the 'Terminate' button, the session displays in the Navigator in red text.



Selecting the session opens the session summary page. Go to Functions > Resubmit the Session.

Each of the samples and barcodes in the session displays with the status of 'Not Assigned,' 'In Process,' or 'Not Submitted.'



Selecting 'Resubmit the Session' will send the session back to the engine to continue analysis where it left off. Only sessions with at least one failed sample can be resubmitted.

User can resubmit the session only from the same machine that it was originally created from.

Replace XX Code

Following the upload of an updated NMDP file, clicking this button will replace any "XX" placeholders in final assignment with updated NMDP code. Status of the sample and locus is irrelevant when replacing XX Code.

Remove Locus

User has the option of removing DQA1, DPA1 and/or DPB1 analysis results from the session. This ability is most useful when 9-loci data has been analyzed with 11-loci settings. In this case DQA1 and DPA1 will display as NO CALL, when in actuality there is no data and therefore even NO CALL is a wrong call.

To rectify this situation, go to 'Functions → Remove Locus → DQA, DPA.' The two loci will be removed from the summary and will not display as a NO CALL.

Similarly, if 11-loci analysis was using for an 8-loci sample, go to 'Functions → Remove Locus → DQA, DPA, DPB. All three loci will be removed from all samples in the session.

Note: One the loci have been removed, they cannot be brought back.

Filters

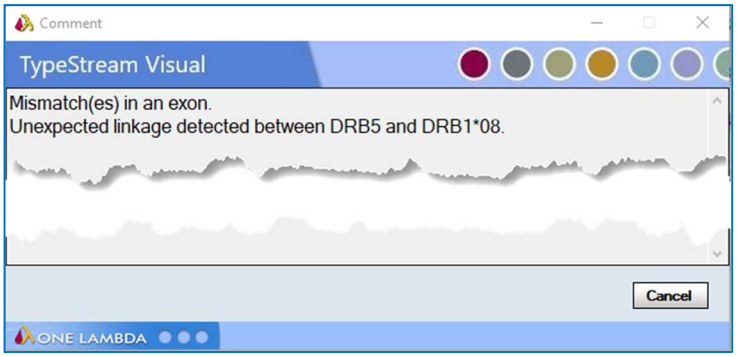
The filter panel covers several categories of filters. Filters and filter types can be used in any combination the user wishes to see.

Health Metrics

Loci failing the named metrics display on the summary page. For more detail on any of these metrics, click the locus or the barcode to access the analysis page.

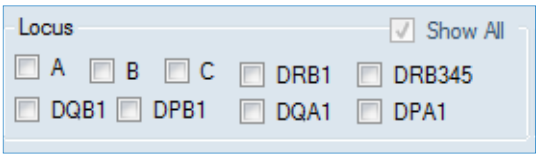
Filter	Description
Key Exon Coverage	For exons 2 & 3 (Class I) and exon 2 (Class II), if the percentage of bases covered for a given exon drops below 100%, the test is flagged.
Homozygous Result	User may display only homozygous samples with this filter.
Allele Balance	The degree to which one allele is represented in the data compared to the other. If the allele balance ratio is ≤ 0.2, the test is flagged.
Break in Phase	User may display only samples that contain at least two consecutive variants that couldn't be phased (or that don't have sufficient read coverage to determine phase) with this filter.
Mismatch in Exon	If a mismatch towards the reference sequence is present in an exon, the test is flagged.
Null Allele Result	User may display only samples that contain a novel position which indicates the new allele could have a null expression with this filter.
Unexpected Linkage	User may display only samples that contain DRB1/DRB345, DRB1/DQB1, or B/C typings that do not match known association rules with this filter
High Background in Exon	User may display only samples with a high background position in a key exon with this filter. High background due to deletions or insertions are not flagged by the software unless the percentage of reads is greater than 50% for the insertion/deletion.
High Background in Intron	**New in v3.0** Metric is flagged when there are high Background position(s) present in an intron. Option to have System Comments contain a notice is available as a checkbox like other Health Metrics.
Mismatch in Intron	User may display only samples that contain an intronic mismatch with this filter
Splice Site Variant	In the case of a possible splice site mutation, if an expressed intron (excluding UTR) does not start with "GT" or end with "AG" the software will raise the associated health metric flag. If 'include in system comment' is selected in the health metric configuration, the software will place "Possible splice site variant at [position number]" warning in the System Comments pertaining to that test.
Uniformity	The degree to which the read depth across a sequenced region remains consistent. When the CV for the uniformity calculation is ≥ 1, the test is flagged.
Frameshift Mutation in Exon	This flag is raised when there is a frameshift mutation due to novel insertion(s) or deletion(s) in an exon. Default value is >0
Allele Balance in Exons	This flag is raised when there is an allele imbalance in the exons. The default threshold for allele balance in exons in <20.

Notice of health metrics missed displays in system comments.



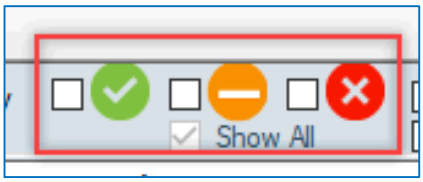
Locus Filters

Loci may be filtered by any single locus or a combination of loci.

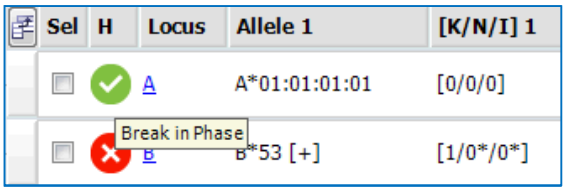


Health Level

Referring to Health Metrics filters (following), the color-coded icons display the level of health metrics that do not meet the standard. User may alter the default severity standards in the NGS Configuration window, as well as whether it displays in system comments.

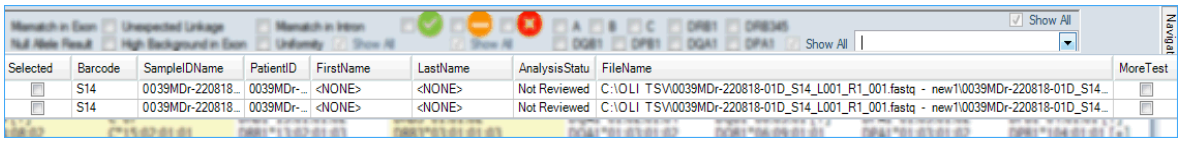


Hovering over a Health Metric icon for a locus will display the missed metrics in a tooltip.



Barcode Filter

Clicking the dropdown selector for Barcode displays all barcodes available in the session. Select any combination of barcodes, then click anywhere off the grid to examine the barcodes.



Elements of the Locus Row

Allele 1 and Allele 2

Allele 1 and Allele 2 display with the best typing to the highest level of homology. "[+]" indications the existence of ambiguities associated with the typing.

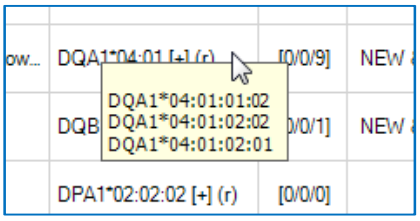
K/N/I values

K/N/I values display for each of the top possible genotypes and indicate the number and location of mismatches to the reference allele. K = mismatch in a key exon, N = mismatch in a non-key exon, and I = mismatch in an intron or UTR. The addition of a star (*) next to a number indicates that there are unknown bases present.

Ambiguities

The display of "[+]" next to the allele name indicates the presence of ambiguous alleles. Hovering over the "[+]" will display a tooltip listing the all the associated ambiguous alleles. The maximum number of alleles that are displayed in the tooltip and in the analysis detail grid is 30 if the ambiguity is due to low coverage. If there are more than 30 alleles generated, a system comment is included as below

"***Allele 1:*** "# allele ambiguity found due to low coverage, top 30 are reported without resolving positions. Try rerunning this sample and locus with a lower minimum read depth to possibly resolve ambiguity.". "



Note:	The display order of the alleles in the tooltip is the same as the display of alleles in the assignment tab.

Rare Alleles

A rare allele is indicated with "(r)" next to the allele name if the software has been configured to do so. On Analysis Panel, this designation will display for all rare alleles on the allele list.

	DPB1	DPB1*04:02:01 (r)	[0/0/1]	NEW	DPB1*104:01:01 [+] (r)	[0/0/1]	NEW

Notes

Notes fields display for each allele and are can display a number of important attributes about the results, including 'NEW,' 'Low Coverage,' 'NO CALL.'

NEW – Novel Allele Identifier

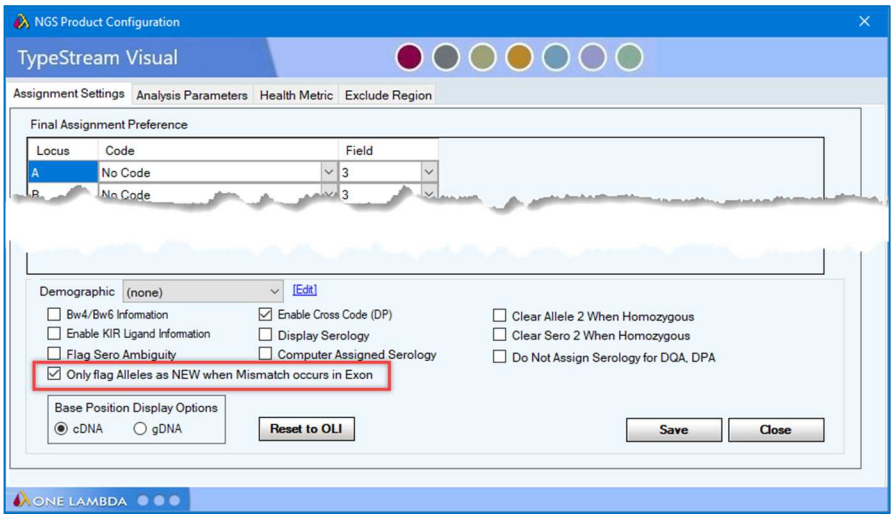
Due to the increased coverage of genes offered by NGS, users may run across scenarios in which the top results display is shown to contain mismatches in key exons, non-key exons, or

intronic regions. When this occurs, the word **NEW** is tagged in the Notes field. The list of allele pairs listed under Allele 1 and Allele 2 columns represent the closest match allele.

C*07:01:01	[0/0/1]	NEW

While further investigation by the user into such samples is required for confirmation, such cases can represent a scenario in which a previously uncharacterized allele is present in the sample tested. In such cases, users should ensure they are working with the most up-to-date library.

User has the option of having 'NEW' display only when the base mismatch occurs in an Exon. To do this, go to Utilities → NGS Product Configuration. On the Assignment Settings tab, check the box "Only flag Alleles as NEW when Mismatch occurs in Exon."



☐ ✓	C	C*01:02:01:01	[0/0/0]	C*03:03:01 [+]	[0/0/1]	NEW	15183	391

When the option is checked, below would be the impact on screen

☐ ✓	C	C*01:02:01:01	[0/0/0]	C*03:03:01 [+]	[0/0/1]	15183

There is no "NEW" added to the Notes column even though there is a mismatch in the non-key exon.

Low Coverage

When read coverage on a region is below a preset threshold (see Analysis Parameters), it may cause ambiguities in the genotype. When this occurs, **Low Coverage** displays in the Notes field.

DPB1* [+]	[1/1/3]	Low Coverage

NO CALL

When there are not enough reads of a particular locus to meet the minimum requirement (see Analysis Parameters), the software will not determine a genotype and instead will display the words "NO CALL."

✓	DRB345			NO CALL			NO CALL

In such a case, system comments will contain more specifics on the reads.

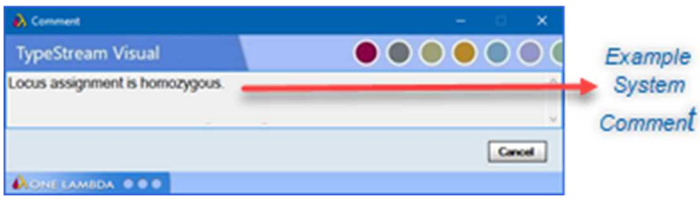
System Comments
Not enough reads to process DRB345 locus, only detected 27 reads

Sel	H	Locus	Allele 1	[K/N/I] 1	Notes 1	Allele 2	[K/N/I] 2	Notes 2	System Comments
☐	✕	DQA1			NO CALL			NO CALL	No reads found for locus DQA1.

NOTE: If an expected locus is reported as a "NO CALL" and the "Total Read Count" value for the barcode is the same as the "Max Read for Typing" analysis parameter (or exactly double for paired end samples.) It is recommended that the user rerun with an increased value for the "Max Read for Typing" parameter. This will allow the software to analyze more reads from the raw data and may detect enough for the locus to provide a typing.

System Comments

This is an un-editable text field (and pop-up dialog box, if user clicks in the place within the System Comments area in the Analysis screen) where the software spells out the possible areas of interest for the user. The warnings and informative texts are comprised of both the user-selected messages from Health Metrics configuration and other warnings as described below.



Message	Meaning
High Insertion Count	The system comments will include insertion information, including location, if the software finds the insertion count is more than 20% of the total base count at a base location. Up to 5 such insertion locations can be listed.
Low Variant Count	One or more variant positions have an Allele Balance of less than 10%. The number of variants that are in Exon is regions is also displayed as part of the system comments.
Key Exons Not Adequately Covered	Key exons are not adequately covered.
Alleles Not Balanced	Software has detected that alleles are not balanced/

Alleles Not Balanced In Exons	Software has detected that alleles are not balanced.
Ruled Out Possible Cis-Trans Allele Pair	Software has ruled out a possible Cis-Trans allele pair.
Possible Novel Variant	Possible novel variant is present in a splice site.
High Background	High background positions are present in an exon (or intron, as of TSV 3.0).
Mismatches	Mismatches are present in an exon (or intron as of TSV 3.0).
No reads found for locus	No reads are found for a locus
Break In Phase	Two or more variants cannot be phased.
Locus Assignment Homozygous	Locus assignment is homozygous.
Unexpected Linkage	The genotype calls for two loci do not match the expected linkage data. See Linkage Table below for expected linkage between locus groups.
No Expected Genotype	When there is no genotyping call for a locus, and none is expected based on linkage disequilibrium data. See Linkage Table below for expected linkage between locus groups.
Frameshift Mutation in Exon	Frameshift mutation due to novel insertion(s) or deletion in an exon.
Uniformity	Read depth is not uniform across the gene
Null Allele	Locus assignment contains a null allele
Ignored Regions	System comment will include the base range that was selected for exclusion during session creation.
Error messages	When there is an analysis error the system comment will indicate the reason. Possible reasons include: locus not found in provided catalog file, failed to load library, not enough reads found for locus, no reference found for locus.
Ruled out null allele	When the DQB1*03:276N allele can be ruled out of the DQB1*03:01:01 ambiguity string the system comment will indicate the reason. The reasons could be either a heterozygous position was found in exon 1 or a mismatch position was found in the intron. The position will be listed in the comment.

Linkage table

Following is a table of expected linkage between locus groups. When an allele from the lead group column appears in a genotype, the software will look for a corresponding allele from the expected group. If such is not found, the software displays a warning in system comments. The warning specifies what linkage was expected and not found.

New in v3.0

DRB1 Group	Expected DRB345 group
DRB1*01	None - or - DRB5
DRB1*03	DRB3
DRB1*04	DRB4

DRB1*07	DRB4
DRB1*08	None
DRB1*09	DRB4
DRB1*10	None
DRB1*11	DRB3
DRB1*12	DRB3
DRB1*13	DRB3
DRB1*14	DRB3
DRB1*15	DRB5
DRB1*16	DRB5
DRB1 Group	**Expected DQB group**
DRB1*01	03 - or – 05
DRB1*03	02 - or – 04
DRB1*04	03 - or - 04 - or – 05
DRB1*05	
DRB1*06	
DRB1*07	02 - or – 03
DRB1*08	03 - or - 04 - or – 06
DRB1*09	02 - or – 03
DRB1*10	05
DRB1*11	02 - or - 03 - or – 06
DRB1*12	03 - or – 05
DRB1*13	02 - or - 03 - or - 05 - or – 06
DRB1*14	03 - or – 05
DRB1*15	02 - or - 05 - or – 06
DRB1*16	03 - or – 05
DRB1*17	
DRB1*18	

DRB1 Group	**Expected DQA group**
DRB1*01	01 - or – 05
DRB1*03	04 - or – 05
DRB1*04	01 - or – 03
DRB1*05	
DRB1*06	
DRB1*07	02
DRB1*08	01 - or - 04 - or - 05 - or – 06
DRB1*09	03
DRB1*10	01
DRB1*11	01 - or – 05
DRB1*12	01 - or - 05 - or – 06
DRB1*13	01 - or - 02 - or – 05
DRB1*14	01 - or – 05
DRB1*15	01

DRB1*16	01 - or – 05
DRB1*17	
DRB1*18	

The BC linkage table, and associated linkage warning, now reflects all b-locus specificities.

B Group	Expected C group
B*07	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 15 - 16 - 17 - 18
B*08	01 - 03 - 04 - 05 - 06 - 07 - 12
B*13	01 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 16 - 18
B*14	02 - 04 - 06 - 08 - 14 - 15 -16 -18
B*15	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 14 - 15 - 16 - 17 - 18
B*18	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 14 - 15 - 16 - 18
B*27	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 14 - 15 - 16
B*35	01 - 02 - 03 - 04 - 06 - 07 - 08 - 12 - 14 - 15 - 16 - 17
B*37	01 - 02 - 04 - 05 - 06 - 07 - 08 - 14 - 15 - 16
B*38	01 - 03 - 06 - 07 - 12 - 16
B*39	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 15 - 16
B*40	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 14 - 15 - 16
B*41	04 - 06 - 07 - 08 - 16 - 17
B*42	04 - 07 - 08 - 15 - 17
B*44	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 14 - 15 - 16 - 17 - 18
B*45	02 - 04 - 05 - 06 - 15 - 16 - 17
B*46	01 - 04 - 07 - 08 - 15
B*47	04 - 06 - 07 - 12 - 17
B*48	01 - 03 - 04 - 08 - 12 - 16
B*49	02 - 03 - 04 - 05 - 06 - 07 - 12
B*50	02 - 04 - 05 - 06 - 07 - 12 - 15 - 17
B*51	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 14 - 15 - 16 - 17 - 18
B*52	01 - 03 - 04 - 07 - 12 - 15 - 16
B*53	01 - 02 - 03 - 04 - 05 - 06 - 07 - 08 - 12 - 15 - 16 - 17 - 18
B*54	01 - 03 - 06 - 07 - 08 - 14
B*55	01 - 03 - 04 - 06 - 07 - 08 - 12 - 15
B*56	01 - 03 - 04 - 07 - 12
B*57	01 - 02 - 03 - 04 - 06 - 07 - 08 - 12 - 15 - 16 - 17 - 18
B*58	01 - 02 - 03 - 04 - 06 - 07 - 08 - 12 - 16 - 17
B*59	01
B*67	07 - 12
B*73	15
B*78	01 - 02 - 16
B*81	07 - 08 - 15 - 18
B*82	02 - 03 - 04

C Group	Expected B group
C*01	07 - 08 - 13 - 15 - 18 - 27 - 35 - 37 - 38 - 39 - 40 - 44 - 46 - 48 - 51 - 52 - 53 - 54 - 55 - 56 - 57 - 58 - 59 - 78

C*02	07 - 14 - 15 - 18 - 27 - 35 - 37 - 39 - 40 - 44 - 45 - 49 - 50 - 51 - 53 - 57 - 58 - 78 - 82
C*03	07 - 08 - 13 - 15 - 18 - 27 - 35 - 38 - 39 - 40 - 44 - 48 - 49 - 51 - 52 - 53 - 54 - 55 - 56 - 57 - 58 - 82
C*04	07 - 08 - 13 - 14 - 15 - 18 - 27 - 35 - 37 - 39 - 40 - 41 - 42 - 44 - 45 - 46 - 47 - 48 - 49 - 50 - 51 - 52 - 53 - 55 - 56 - 57 - 58 - 82
C*05	07 - 08 - 13 - 15 - 18 - 27 - 37 - 39 - 40 - 44 - 45 - 49 - 50 - 51 - 53
C*06	07 - 08 - 13 - 14 - 15 - 18 - 27 - 35 - 37 - 38 - 39 - 40 - 41 - 44 - 45 - 47 - 49 - 50 - 51 - 53 - 54 - 55 - 57 - 58
C*07	07 - 08 - 13 - 15 - 18 - 27 - 35 - 37 - 38 - 39 - 40 - 41 - 42 - 44 - 46 - 47 - 49 - 50 - 51 - 52 - 53 - 54 - 55 - 56 - 57 - 58 - 67 - 81
C*08	07 - 13 - 14 - 15 - 18 - 27 - 35 - 37 - 39 - 40 - 41 - 42 - 44 - 46 - 48 - 51 - 53 - 54 - 55 - 57 - 58 - 81
C*12	07 - 08 - 13 - 15 - 18 - 27 - 35 - 38 - 39 - 40 - 44 - 47 - 48 - 49 - 50 - 51 - 52 - 53 - 55 - 56 - 57 - 58 - 67
C*14	14 - 15 - 18 - 27 - 35 - 37 - 40 - 44 - 51 - 54
C*15	07 - 14 - 15 - 18 - 27 - 35 - 37 - 39 - 40 - 42 - 44 - 45 - 46 - 50 - 51 - 52 - 53 - 55 - 57 - 73 - 81
C*16	07 - 13 - 14 - 15 - 18 - 27 - 35 - 37 - 38 - 39 - 40 - 41 - 44 - 45 - 48 - 51 - 52 - 53 - 57 - 58 - 78
C*17	07 - 15 - 35 - 41 - 42 - 44 - 45 - 47 - 50 - 51 - 53 - 57 - 58
C*18	07 - 13 - 14 - 15 - 18 - 44 - 51 - 53 - 57 - 81

Linkage table association is based on
http://www.ctht.info/resourceslinks.htm
Tables 8, 12, and 13 were used, rare and extremely rare associations were not included

and https://www.haplostats.org/haplostats?execution=e1s1

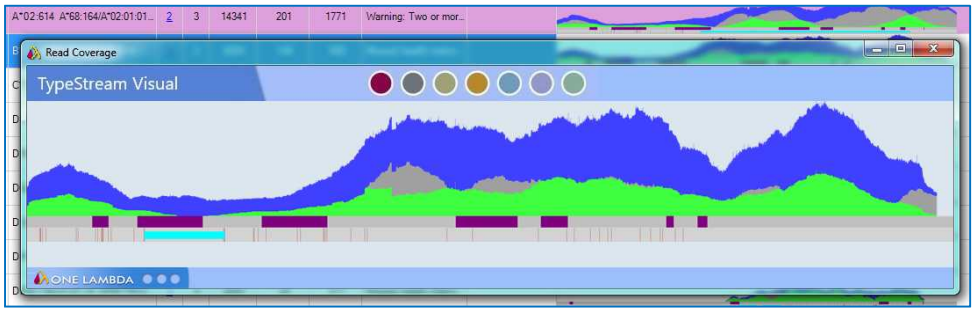
Note: Linkage association for DRB1*01 is listed as "None – or – DRB5." It should be noted that this association is very rare.

Final Assignment

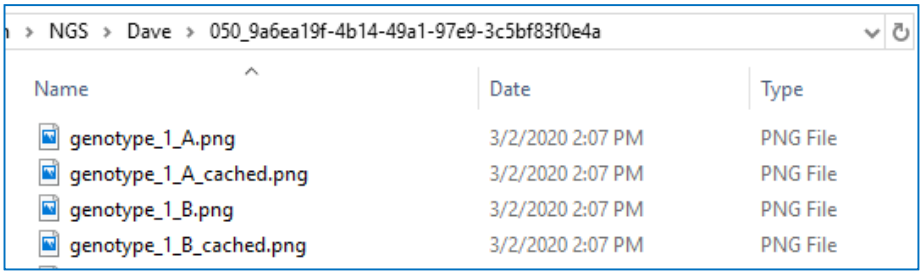
The final assignment will not display in the final assignments field until a user, technologist or supervisor, selects a final assignment and clicks "Assign" on the analysis panel. From that point, it will display in session detail mode, with or without the analysis panel in display. More information about Final Assignment in the next section.

Histogram

Clicking on the histogram in Session Detail View will bring up a larger-scale view.



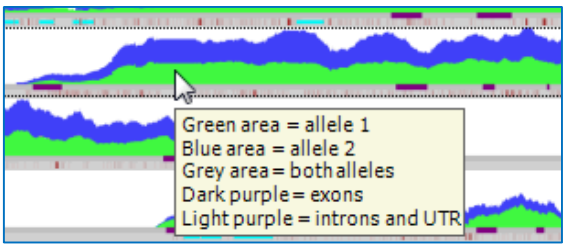
NOTE: in the interest of faster histogram display, the histogram files exist in two versions in the session directory: 1). The original .png file and 2). A 'cached' version which is smaller and quicker to load.



Elements of the histogram are as follows:

- Green area = allele 1
- Blue area = allele 2
- Gray area = both alleles
- Dark purple banding = exons
- Light purple banding = introns
- Light blue banding = unphased region between heterozygous positions
- Dark orange 'tick marks' = heterozygous positions

Hovering over a histogram on session summary will display a tooltip



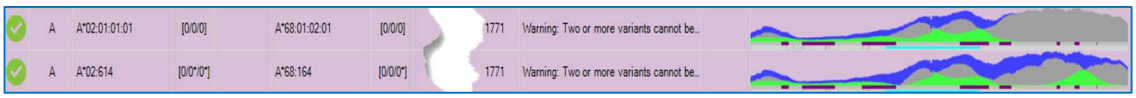
Homozygous genotypes

Homozygous calls are immediately identifiable by their single-color shading in the histogram.

These alleles are also filterable using the warning flag functionality (see above).

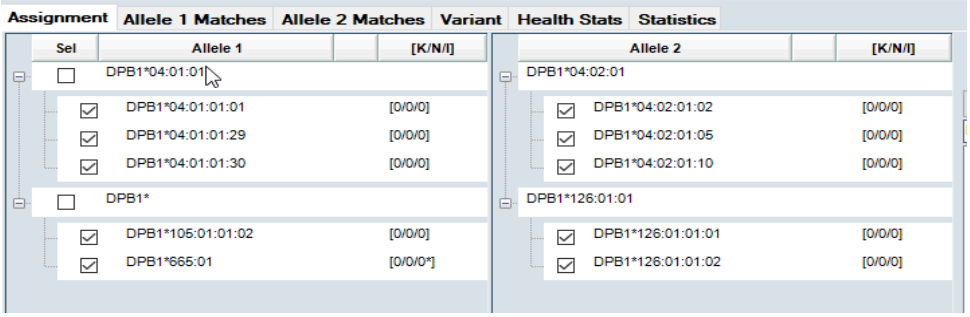
Cis-Trans Ambiguities

If two positions required to resolve a cis-trans ambiguity span a distance that exceeds a kit's maximum read length, the specific cis-trans ambiguity will persist in the data. Both genotypes will display and background will be shaded purple.



The software will not assign a genotype to this allele if "Assign All" functionality is used to assign type. On the Analysis page, the two pairs of genotypes are displayed separately. The user may then select the final genotype. The tooltip for each row displays the alleles that

correspond to the alleles for the selected cis-trans pair.



NOTE: In cases where phase[1] cannot be established between exons, and the phase break correlates to a known cis-trans pair, the software will report both pairs of alleles. An intronic or non-key exon mismatch in only one pair will not lead to elimination of the pair from the reported genotypes as a means of accounting for novel alleles where an understanding of the exon phase is required.

[1]Phase: When there is at least one mapped read bridging the distance between two variant positions, the positions are known as "in phase." Phase breaks are caused when no mapped reads can be found which will bridge that distance.

Suffixes used with allele names

There are additional optional suffices that may be added to an allele to indicate its expression status. Alleles that have been shown not to be expressed, 'Null' alleles have been given the suffix 'N'. Those alleles that have been shown to be alternatively expressed which may have the suffix 'L', 'S', 'C', 'A', 'Q', or 'X'.

Suffix	Definition
N	An allele that has been shown not be expressed, or is 'Null'.
L	Indicates an allele which has been shown to have 'Low' cell surface expression when compared to normal levels.
S	Used to denote an allele specifying a protein which is expressed as a soluble 'Secreted' molecule but is not present on the cell surface
C	Indicates an allele product which is present in the 'Cytoplasm' but not on the cell surface.
A	Indicates 'Aberrant' expression where there is some doubt as to whether a protein expressed.
Q	Used when the expression of an allele is 'Questionable' given that the mutation seen in the allele has previously been shown to affect normal expression levels.
X	At times the software may make a heterozygous call where the only variant identified is novel, and the typing call results in the same closest matching allele for both the Allele 1 and Allele 2 consensus. In this case, the software will report a heterozygous allele call and the read viewer will display the closest allele sequence with an 'X' appended to the allele name.

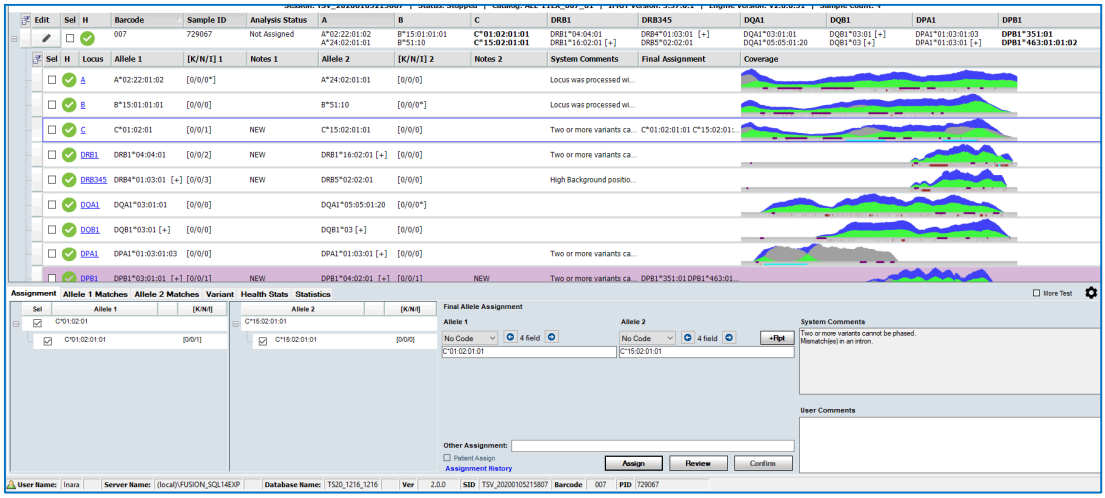
Analysis Panel

To view your analyzed files, you can do one of the following actions.

1. From collapsed mode, click on the locus genotypes for the locus you wish to view. Analysis panel opens for that locus.

2. From expanded view, click on the locus row anywhere except the locus itself or the

histogram. The analysis panel opens on the bottom half of the page with the selected locus highlighted. It is subdivided into panels; the borders between the panels can be repositioned so the user can focus on a chosen section. Here the C locus is highlighted in the top window, and the pertinent information is displayed below in the lower window.

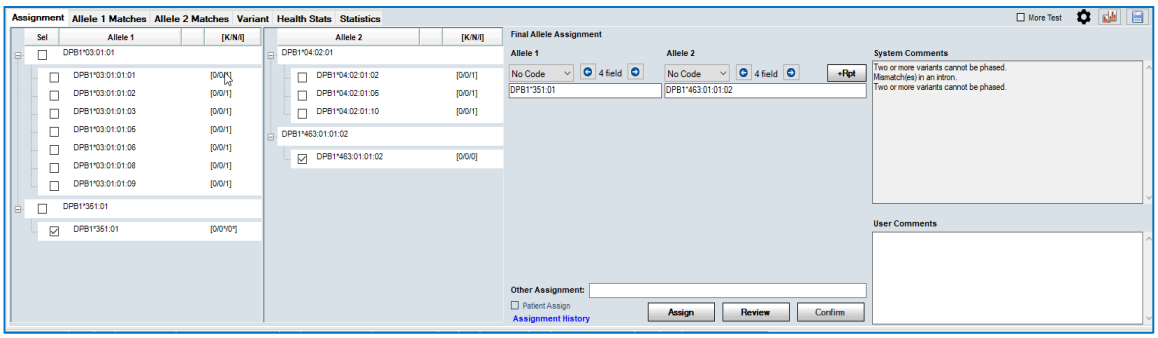


The Analysis Panel consists of six tabs displaying different but related information for the user.

Assignments – displays possible and final allele assignments plus system and user comments
Allele 1 Matches and Allele 2 Matches – displays ambiguities, resolving positions, and close match list per allele.
Variant – shows all variant positions with consensus bases, counts and percentages of variation, and whether each variant is phased. Also show allele balance bar graph.
Health Stats – displays status and numerical values for all Health Metrics
Statistics – displays values for Mapped Read Metrics and Locus Coverage

NOTE: Navigating to the analysis panel for a given sample, the status bar is refreshed to include the current User Name, Server Name, Database Name, Version of the application, Session ID (SID), Barcode, Local ID (LID), Patient ID (PID) information.

Assignments tab

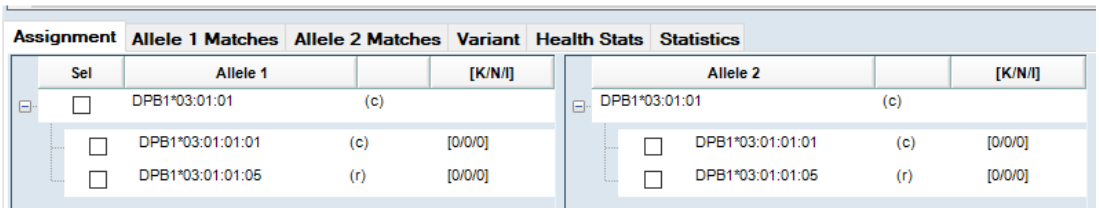


The assignments tab provides the user with a complete list of all ambiguities. On the right-hand side, both allele 1 and allele 2 have top-level selection boxes for the user to choose the

entire allele string in one stroke – when the Allele 1 top box is checked, all boxes on the right are automatically checked as well. Individual alleles can also be selected or de-selected. As each allele is checked, the resulting combination displays in the Final Allele Assignment text fields. Formatting of the fields is also variable.

When the demographic filter is applied the alleles are displayed with c , wd , I , or r notation to represent common, well document, intermediate and rare allele respectively.

The default configuration of the Assignment tab for new sessions analyzed using TSV 3.0 is based on the assignment configuration that is selected by the user during the session import.



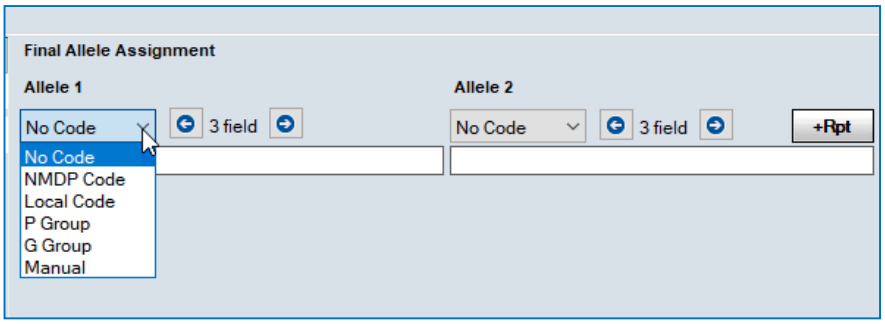
Final Assignment

User has a lot of latitude in determining the final genotype assignment. TypeStream is highly versatile in allowing last-minute changes is use of codes or even the number of fields to display if no code is selected. Final assignments can be saved down to the 1-field level.

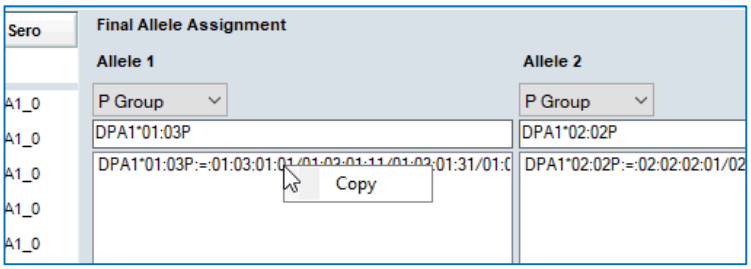
"Other Assignment" text field allows users to assign a different final assignment in free text.

Allele Codes

As defined earlier in this chapter, allele code will display based on the top genotype as selected by the software.



The software will allow the copy and paste of the code definition for NMDP, P, and G codes. Right-click on the definition, select copy, and code definition is copied to the clipboard. From there it can be pasted into any location that permits pasting.

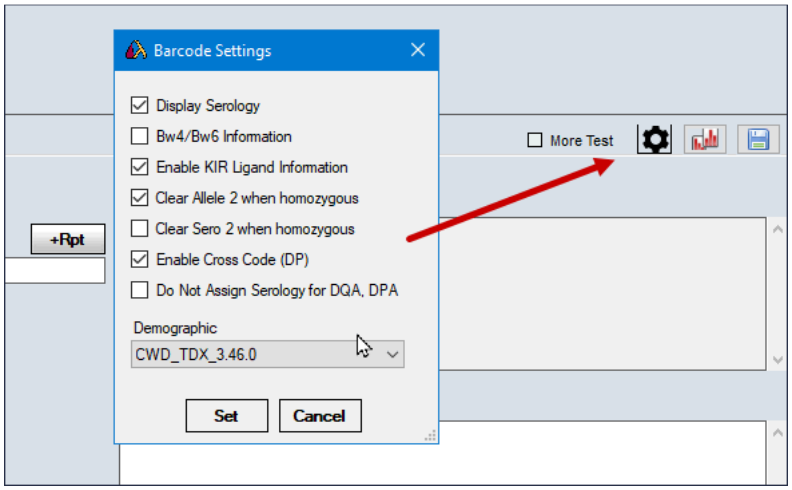


New in v3.0

Serology

The user may decide whether serology displays or not. There are two places to make this determination. To provide a global serology setting, from the file menu, navigate to Utilities → NGS Product Configuration. Selection of serology is on the lower half of the *Assignment Settings* tab. (See earlier section on product configuration.)

The second method is to click the small gear icon on the right side of the analysis panel. This will bring up a small configuration window where you can override global settings on a per-locus basis.

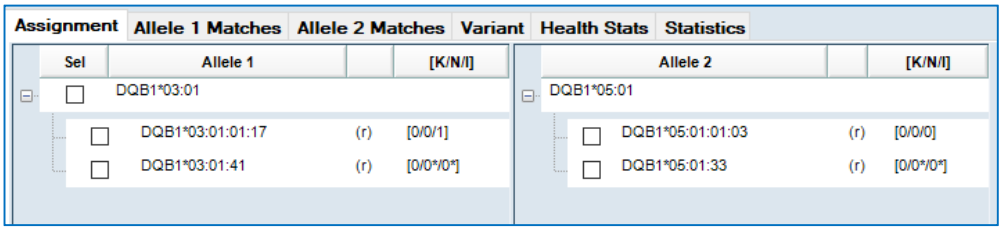


Note: Selection of a Demographic Group Filter such as CWD_TDX_#NOM# will causes CIWD alleles to be represented as follows in analysis screens where typing is displayed:

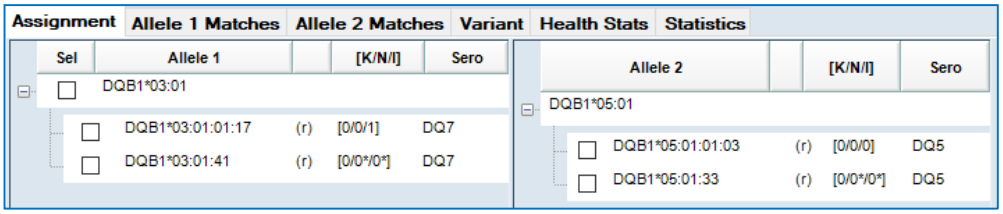
Common	– (c)
Well documented	– (wd)
Intermediate	– (i)
Rare	– (r)
Ambiguous	– (+)

The CWD_TDX_#NOM# filter is created based on the contents of the latest serology file when imported. If the most recently imported serological equivalent file had a CIWD column, the CIWD (CIWD_TDX_#NOM#) filter was automatically created at that time.

Bw4/Bw6, KIR/Ligand, and Demographics display can also be decided on a locus-by-locus basis. Opting to display sero inserts a column into the allele lists.



1 Sero not displayed



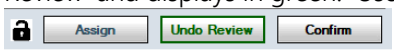
1 Sero displayed

Assign, Review, Confirm

On the Analysis Panel, the user may Assign, Review, and Confirm genotypes individually at the locus level. The same rules pertain here as they do with the bulk assign on the summary page with respect to the order of carrying out assign → review → confirm. See earlier in this chapter.

Additionally, on a locus level the genotype can be un-confirmed and un-reviewed if changes are deemed to be necessary.

- Assign – on clicking Assign, the final assignment displays in the Final Allele Assignment window and in the Final Assignment column on summary view.
- Review – on clicking Review, the Review button text changes to 'Undo Review' and displays in green. User comments become un-editable.



- Lock icon displays to the left of the buttons, signifying that assignments cannot be changed and user comments not added until either the lock icon or the Undo Review is clicked. At that time, button will go back to saying "Review."
- Confirm – this is a supervisor-only activity. On clicking Confirm, the Confirm button text changes to 'Undo Confirm' and displays in purple. The lock icon appears, and Undo Review becomes disabled.
- The Patient Assign checkbox is disabled if the patient is not assigned to the sample. If the sample is associated to a patient and the settings for automatic patient assignment is checked the Patient assign checkbox is set accordingly for each locus in each step of analysis. User can choose to uncheck an automatic checked patient assign checkbox.
- Lock icon here works the same as with Review.

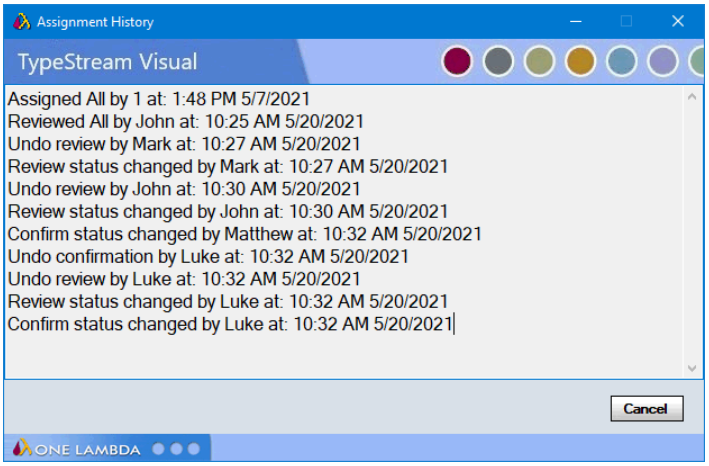
Patient Assign

When this box is checked prior to the Review/Confirm process, the saved genotyping, allele code, and/or serology will be saved to the patient associated with the analysis.

Patient must be assigned to the session prior to saving the results in order for them to appear on the patient information page.

Assignment History

All the changes to the assignments are logged and can be displayed by clicking "Assignment History" link under final assignments and sero.



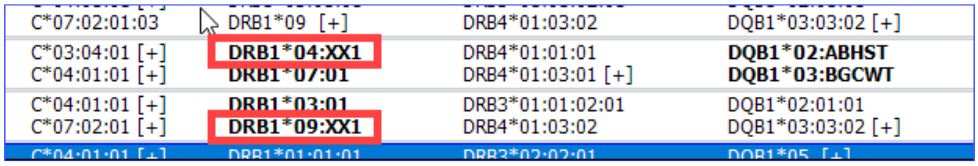
+Rpt

The +Rpt function allows you to look up and report unknown allele codes with the National Marrow Donor Program (NMDP).

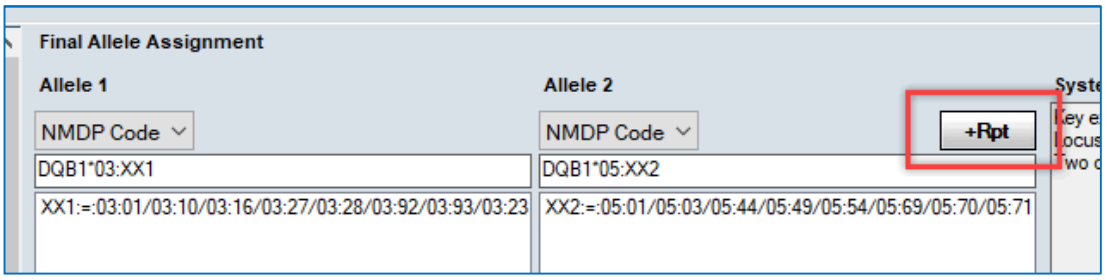
Unknown allele codes within Visual TypeStream analysis results are marked with XX followed by a sequential number. The numbers are reset to 1 for each sample and locus. For instance, DRB1*04:XX1 is an unknown allele code.

When you see unknown codes, you should first make certain you have imported the latest NMDP file. If you have the latest code file and are still seeing XX codes, you can store these unknowns for later submission to the NMDP. XX codes are stores in a ".txt" file named nmdp_code_report.txt, (by default stored in C:\OLI TSV\data\export). This location can be changed by modifying the path in Utilities->General Settings->Paths). Code information is appended to this text file as it is added; the newest additions are at the bottom.

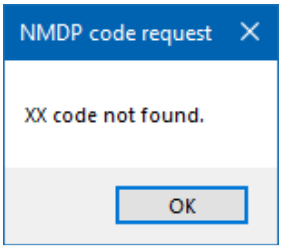
Unknown alleles appear like so in the Session Summary window:



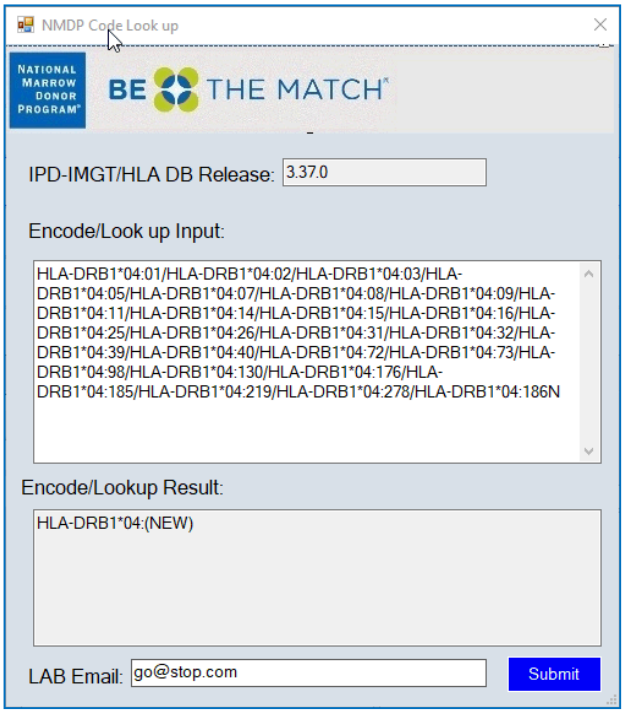
To send the unknown code information directly to NMDP, make a Final Assignment (1) of an allele that has incomplete information, then (2) click the +RPT button:



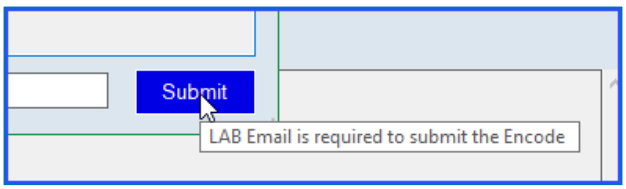
If an XX code is not found, you will receive the following message:



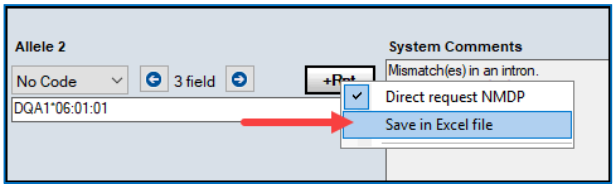
If an XX code is confirmed by the system, and you are connected to the Internet, TypeStream Visual will open the *Bioinformatics.NMDP.Org* webpage and allow you to look up the unknown allele:



To submit the unknown code to NMDP, you must type in your lab email address and click the Submit button. (Hovering your mouse over the Submit button will confirm this requirement).



To add the unknown code information to an Excel spreadsheet file, (by default stored in C:\OLI TSV\data\export) right-click on the +Rpt button and select Save in Excel file:



After the unknown code has been saved, TypeStream Visual displays a confirmation message that the text file has been saved (not shown).

When you are done, click the Close button, (on the right of the +Rpt button) to remove the buttons from the display.

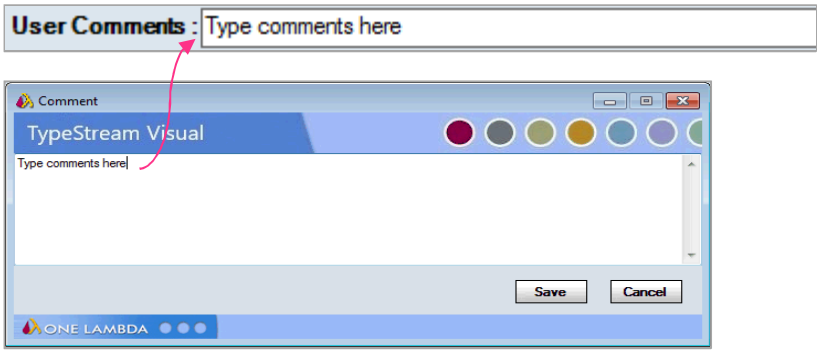
NOTE: The +Rpt button retains the last selection you made, (direct or Excel) so it can be used as a shortcut. Unless you want to change your selection, the next time you report XX code simply click +Rpt.

System Comments

This field is not editable by the user. System comments may include assignment information, saving and confirming by locus and by user. The system comments displayed in this panel should match those seen in the summary detail panel.

User Comments

Comments added by the user display here. Clicking in the user comment field brings up a comment text window. Comment may be saved or cancelled. Clicking "Cancel" will not remove comments entered on a different page.

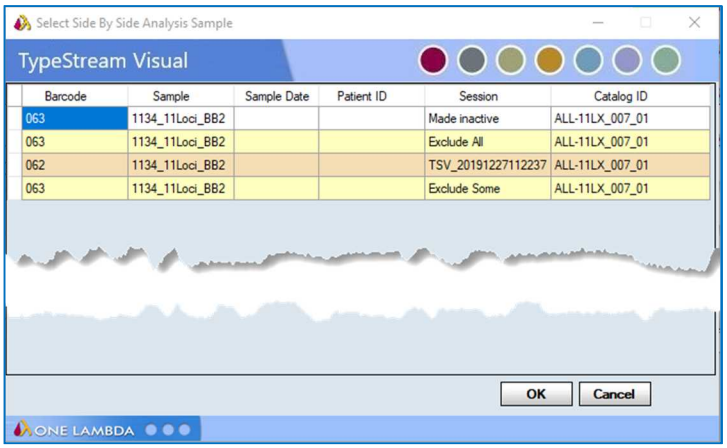


More Test

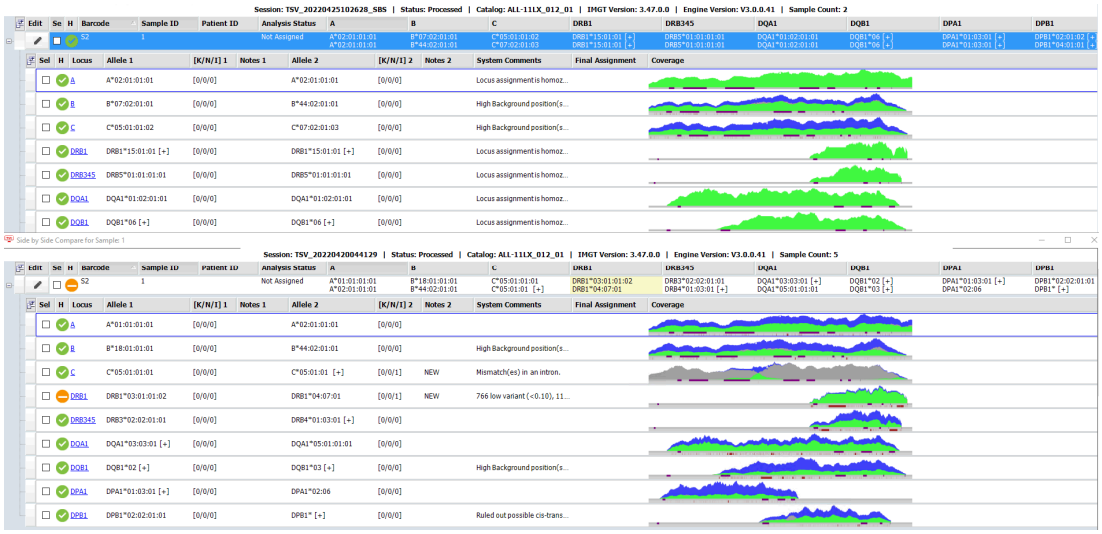
If "More Test" was selected on the session summary, it will display as checked here, too. If not check in session summary, More Test can still be check here on analysis page. More Test applies on a sample level, not a locus level, and when checked can be used as a search parameter in compiling a Clone Session or preparing reports.

Side-by-Side Analysis

For users who wish to compare current run results to previous results for the same sample, clicking the Side-by-Side Analysis icon brings up a grid with every session containing the same sample and have the same patient ID. User selects the session to which he would like to compare results and clicks OK.



The selected session opens on a half screen on the lower half of the current session, enabling direct sample-to-sample comparison of data.

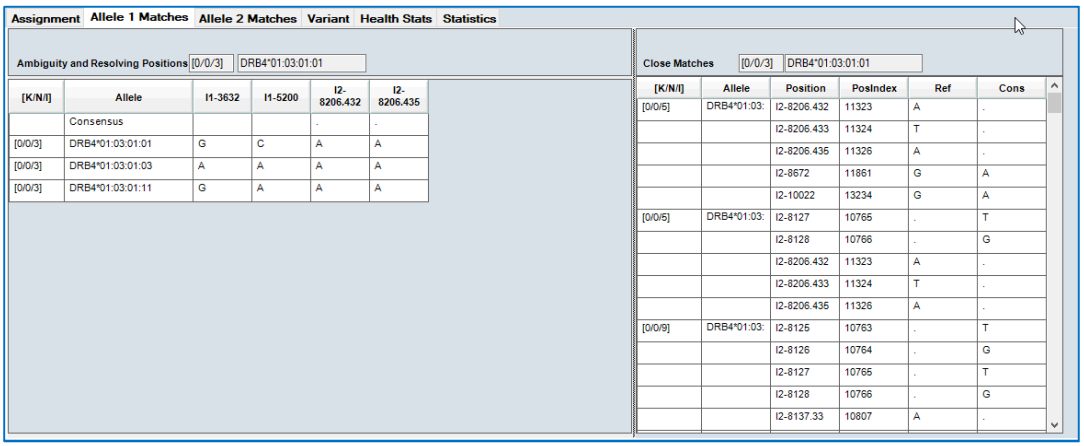


Windows may then be resized as required for a better look at the data of interest.

Save Locus Layout

On most of the tabs on the Analysis Panel, the boundaries between sections are movable. The user can maximize the space he uses most and save that layout. Text window will confirm that the layout has been saved. Every time a new locus or sample is opened, it will be formatted in the saved layout.

Allele 1 and 2 Matches tabs



[K/N/I]	Allele	I1-3632	I1-5200	I2-8206.432	I2-8206.435
	Consensus			.	.
[0/0/3]	DRB4*01:03:01:01	G	C	A	A
[0/0/3]	DRB4*01:03:01:03	A	A	A	A
[0/0/3]	DRB4*01:03:01:11	G	A	A	A

[K/N/I]	Allele	Position	PosIndex	Ref	Cons
[0/0/5]	DRB4*01:03:	I2-8206.432	11323	A	.
		I2-8206.433	11324	T	.
		I2-8206.435	11326	A	.
		I2-8672	11861	G	A
		I2-10022	13234	G	A
[0/0/5]	DRB4*01:03:	I2-8127	10765	.	T
		I2-8128	10766	.	G
		I2-8206.432	11323	A	.
		I2-8206.433	11324	T	.
		I2-8206.435	11326	A	.
[0/0/9]	DRB4*01:03:	I2-8125	10763	.	T
		I2-8126	10764	.	G
		I2-8127	10765	.	T
		I2-8128	10766	.	G
		I2-8137.33	10807	A	.

Resolving Positions

For alleles that contain a mismatch to the reference, TypeStream Visual identifies the location of the mismatch, the reference base, and the consensus base. Double-clicking the consensus cell for a position opens the Reads Viewer to that position.

[K/N/I]	Allele	UTR5-216	UTR5-114	I1-196	I3-1081	I6-2588	UTR3-3113	UTR3-3529	UTR3-3609	UTR3-3725
	Consensus	A		C	C	G	C	A	C	
[0/0/1]	B*40:01:02:01	A	T	C	C	G	C	A	T	A
[0/0/0*]	B*40:01:02:09	A	C	C	C	G	*	*	*	*
[0/0/1*]	B*40:01:02:02	G	T	C	C	G	*	*	*	*
[0/0/1*]	B*40:01:02:03	A	T	A	C	G	*	*	*	*
[0/0/1*]	B*40:01:02:04	A	T	C	C	G	C	A	T	G
[0/0/1*]	B*40:01:02:07	*	*	C	C	A	*	*	*	*
[0/0/1*]	B*40:01:02:08	*	T	C	T	G	*	*	*	*
[0/0/1*]	B*40:01:02:10	A	T	C	C	G	T	A	*	*
[0/0/1*]	B*40:01:02:11	A	T	C	C	G	C	G	*	*

The consensus base at each of the positions displays in the top row. The bases at the same positions are displayed for the three top ambiguous reference alleles. Notice that there is agreement between the positions and the K/N/I values – positions are correctly identified as intronic, and the presence of unknown bases is noted.

When a position cell is clicked, the reads viewer opens with the selected position highlighted and locked.

Close Match List

The Close Match list provides users with a list of perfect matches and close matches for the sample. Typing information is broken out by allele. For matches that contain a mismatch towards the reference, user may click the position, which will open the Reads Viewer to the position in question. For an ambiguous result, the software will identify the resolving position.

[0/1*/0*]	DRB4*01:06	E3-421	13559	T	C

The above can be read as "The DRB4*01:06 allele is a close match with a single mismatch in a non-key exon at position E3-421. The consensus base call at this position is a 'C' while the reference base at this position is a 'T'."

When a position cell is clicked, the reads viewer opens with the selected position highlighted and locked.

Variant tab

There are two parts to the Variant tab – the variant table and the bar chart which alternately displays base count and percentage at each position or allele balance.

Variant Table

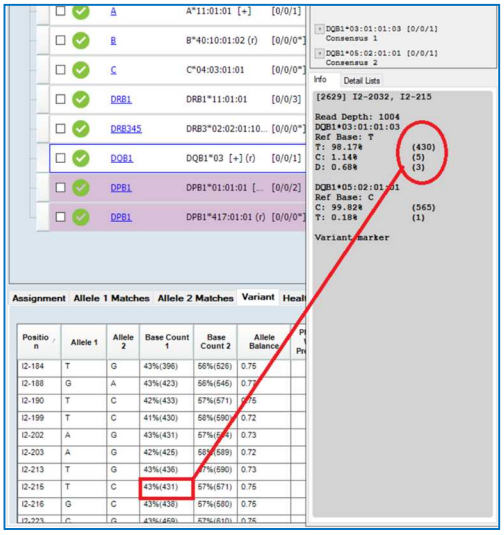
Position	Allele 1	Allele 2	Base Count 1	Base Count 2	Allele Balance	Phased With Previous	Bkgd
I4-74	A	G	49%(196)	51%(202)	0.97	☑	0%(0)
E5-900	G	A	48%(223)	52%(239)	0.93	☑	0%(0)
E5-916	G	A	48%(230)	52%(254)	0.90	☑	0%(1)
E5-985	G	A	49%(256)	51%(265)	0.96	☑	0%(1)
E5-1008	T	C	51%(250)	49%(246)	0.98	☑	0%(1)
I5-102	G	C	55%(237)	45%(194)	0.81	☑	0%(0)
I5-325	C	T	51%(217)	49%(212)	0.97	☑	0%(0)
I5-371	T	G	50%(215)	50%(218)	0.98	☑	0%(0)
I5-414	G	C	49%(214)	51%(221)	0.96	☑	0%(0)
E7-1046	G	C	54%(201)	46%(171)	0.85	☑	0%(0)
UTR3-579	A	G	50%(355)	50%(359)	0.98	☐	0%(0)
UTR3-682	T	C	53%(222)	47%(194)	0.87	☑	0%(0)
UTR3-796	C	T	53%(174)	47%(156)	0.89	☑	0%(0)
UTR3-853	A	G	50%(146)	50%(146)	1.00	☑	0%(0)

Variant tab displays a table of all the variants identified in the locus. A variant, also referred to a heterozygous position, is a position that has reads representing more than one base. The ratio to determine the variant positions is a user-defined Heath Metric parameter; the default is 0.2 or 20%. (This is not to be confused with the Analysis Parameter configuration item "Min. Hetero Allele Balance" which determines allele balance at a given base position to determine heterozygosity.)

Column	Description
Position	The cDNA or gDNA identification of the base position
Allele 1 / Allele 2	The bases at the variant position
Base Count 1 / 2	The Base count for allele 1 and allele 2 at each of the variant positions, showing in both hard count numbers and percentage of the total.
Allele Balance	Allele balance is calculated using the following formula: $AlleleBalance = \frac{(A1/A2)i_1 + (A1/A2)i_2 + \cdots (A1/A2)i_N}{N}$ where A1=the allele with the lower number of reads; A2=the allele with the higher number of reads, i=a heterozygous position; and N=the total number of heterozygous positions.

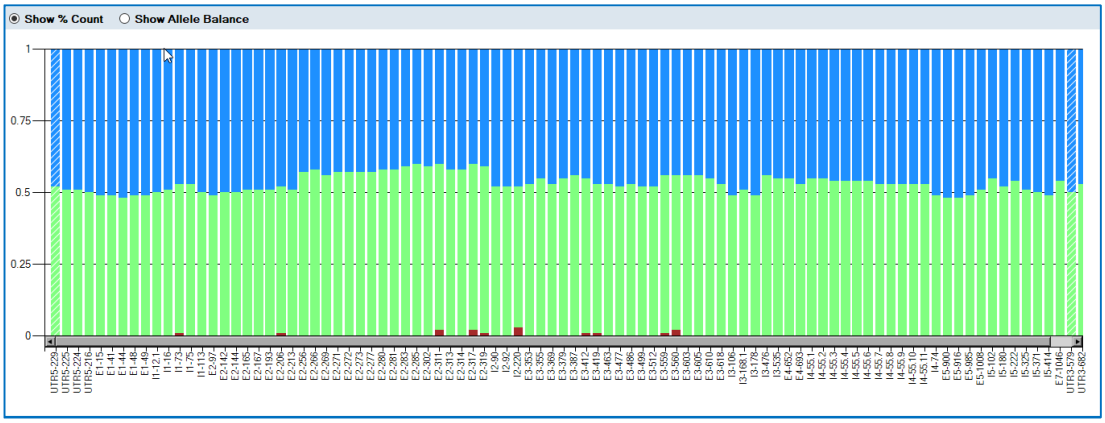
Phased with previous	Indicates if the phase was continued between current variant and the previous consecutive variant.
Bkgd	Background percentage

Note: The variant counts on this tab are based on the total for the locus, while the read coverage info on the Reads Viewer is split between allele 1 and 2. In the illustration below, the Variants tab for Base Count 1 shows the 'T' count as 431, adding the 430 from allele 1 to the 1 of allele 2. However, if a read is assigned to both allele 1 and allele 2, as with Base Count 2, the two sums may not match, as the read will be counted only once on the reads viewer and twice on the variant tab.



Each of the columns in the Variant Table is can be sorted, including Balance %, giving the user alternate ways to assess and present the analyzed data. Default sort order is by position. When a position cell is clicked, the reads viewer opens with the selected position highlighted and locked.

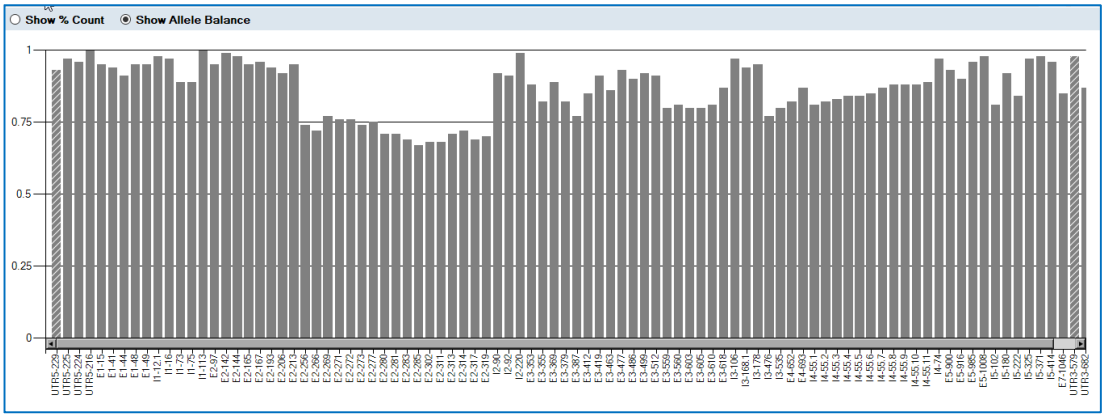
Show Percent Count



Selected by default, this chart shows the relative count of reads for Allele 1 and Allele 2 at each of the variant positions. These values will match the Base Count percentage values on the

Variant table. This table will change its sort, and therefore its profile, based on how the Variant Table is sorted.

Show Allele Balance



The Allele Balance graph depicts the relative balance between allele 1 and allele 2 representation within the raw data. At each variant position, a perfectly balanced allele would have a value of '1' and the bar would display to the top. Allele balance is calculated using the formula in the chart above. Length of the bar will match the corresponding allele balance value in the variant table. As with the Base Count graph, the Allele Balance graph will respond to the sorting options of the Variant Table and change its display accordingly.

Health Stats tab

Health Stats delivers results from Health Metrics configuration.

	Health Metric	Standard	Value	Pass/Fail	Comments	Include
✓	Break in Phase	0.00	1.00	Fail	Two or more variants cannot be phased.	☑
✓	Mismatch in Intron	0.00	1.00	Fail	Mismatch(es) in an intron.	☑
✓	Key Exon Coverage	100.00	100.00	Pass	Key exons not adequately covered.	☐
✓	Mismatch in Exon	0.00	0.00	Pass	Mismatch(es) in an exon.	☐
✓	Allele Balance	20.00	87.24	Pass	Alleles are not balanced.	☐
✓	Uniformity	1.00	0.27	Pass	Read depth is not uniform across the gene.	☐
✓	High Background in Exon	0.00	0.00	Pass	High Background position(s) present in an exon.	☐
✓	Homozygous Result	0.00	0.00	Pass	Locus assignment is homozygous.	☐
✓	Unexpected Linkage	0.00	0.00	Pass	Unexpected linkage detected between locus.	☐
✓	Null Allele Result	0.00	0.00	Pass	Locus assignment contains a null allele.	☐
✓	Splice Site Variant	0.00	0.00	Pass	Possible novel variant in splice site.	☐

This list will not display in the same order as on the configuration page. On this tab, the failed metrics display at the top of the grid, with the most severe (highest risk) metric listed first. The table shows the standard for the metrics and the actual value the locus along with Pass/Fail status. The text of the comment for failed metrics will display in system comments only if the 'Include' checkbox was checked in configuration.

Statistics tab

The statistics tab contains two tables – Mapped Read Metrics and Locus Coverage.

Mapped Read Metrics

The statistics for allele 1 and allele 2 are combined in the following table for accuracy. If using FASTPlex workflow, the forward and reversed read counts will be reduced by 20 bases, showing 130 instead of the 150 standard for MiSeq sessions.

Mapped Read Metrics

Mapped Read Metrics	Value
Reads for Typing	11078
Forward Read Count	5537
Averaged Forward Read Length	150
Reverse Read Count	5541
Averaged Reverse Read Length	150
Total Reads	13702

Statistic	Description
Reads for Typing	The total number of reads mapping to the alleles after read filtering has occurred
Forward Read Count	The total number of forward reads mapping the alleles
Averaged Forward Read Length	The average read length of the forward reads
Reverse Read Count	The total number of reverse reads mapping to the alleles
Average Reverse Read Count	The average read length of the reverse reads

Locus Coverage

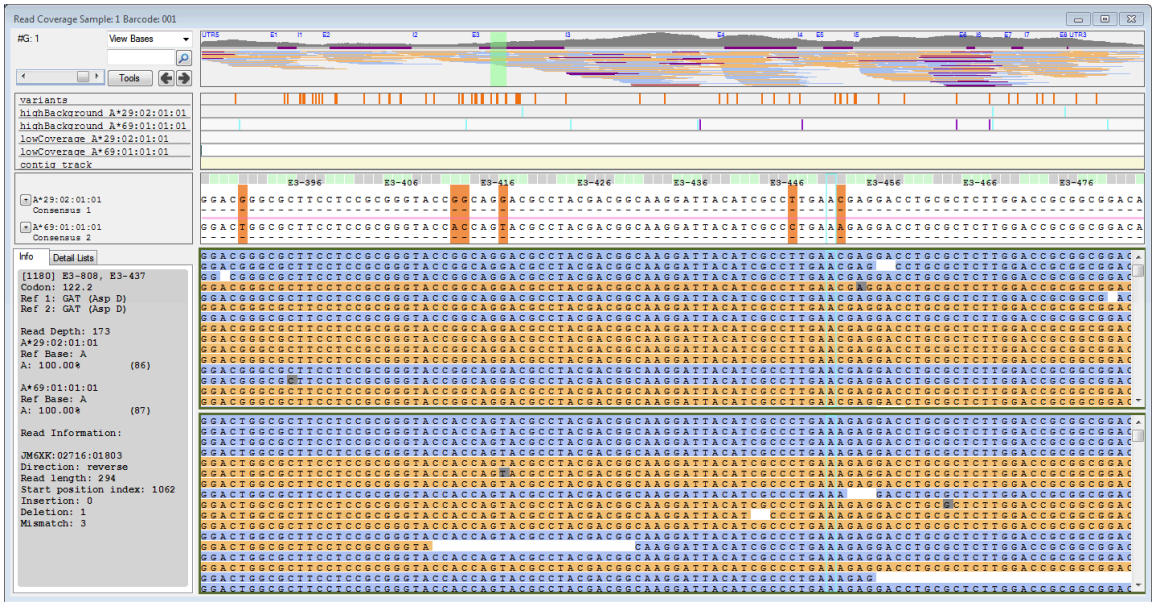
The locus-level statistics for the selected locus broken down by gene region.

Locus Coverage

Region	Base Covered (%)	Min Depth	Max Depth	Avg Depth
5'UTR	100%	145	458	311
Exon1	100%	428	463	445
Intron1	100%	302	453	363
Exon2	100%	291	489	388
Intron2	100%	214	369	310
Exon3	100%	217	432	355
Intron3	100%	366	562	461
Exon4	100%	408	583	511
Intron4	100%	337	460	381
Exon5	100%	451	555	514
Intron5	100%	365	521	451
Exon6	100%	399	468	429
Intron6	100%	377	467	430
Exon7	100%	346	372	357
3'UTR	100%	43	779	416
All	100%	0	779	413

Reads viewer

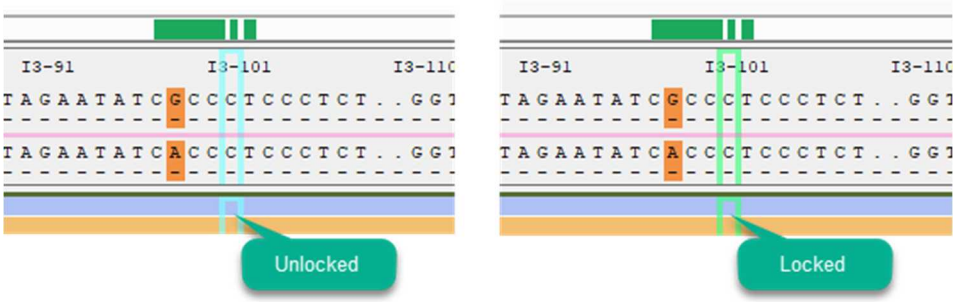
To access the Reads Viewer, click on the locus name link for any locus. The Sample Detail Interface displays in three main sections to the window.



	Window	Description
1	Sequence Coverage Viewer	The Sequence Coverage viewer allows the user to navigate around the regions of the gene that were sequenced. Included are the whole gene view histogram, annotation tracks and nucleotide sequence view.
2	Data panel	The data panel displays info about a base position and/or a specific read, and recaps some of the data tables from the analysis page.
3	Reads Tool	The reads tool allows the user to visualize individual sequence reads that cross user-specified positions.

Sequence Coverage Viewer

Sequence Coverage Viewer is further broken down into different sections: The whole gene viewer, the annotation tracks, and the nucleotide sequence viewer. On selecting any base position, the nucleotide viewer and reads viewer scroll to the selected position and outline it in a light blue. The green vertical bar on the whole gene viewer shows the area of the gene displayed in nucleotide and reads viewers. Move your cursor up and down the nucleotide viewer to select another position. Double-clicking on the base position in the nucleotide viewer will lock the indicator in place; the outlines of the locked position turn green. The position will remain locked until you click it again.



Whole Gene Viewer

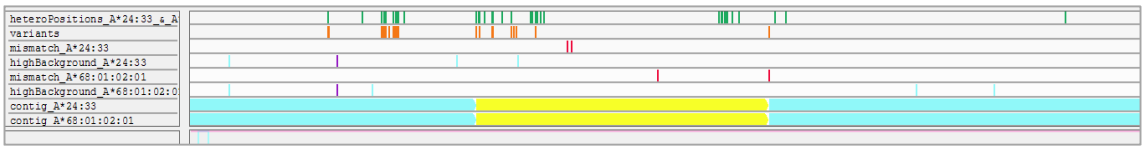
This histogram across the top of the screen echoes the locus histograms from the session and analysis screens. It provides a view of the entire gene being sequenced and allows for basic navigation through the sequence.

The location of exons are denoted by horizontal dark purple bars, while introns are denoted by light purple bars.

Below the exon/intron indicators, stacked horizontal lines signify reads spanning the region.

Annotation Tracks

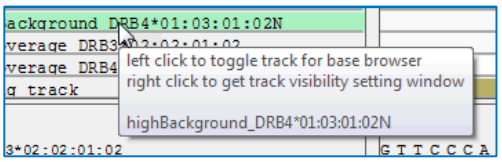
Annotation tracks display under the whole gene view and above the nucleotide viewer.
The tracks displayed will vary as needed depending on the locus and genotype. Selected tracks can be browsed using the browser mechanism or the right and left arrow keys on the keyboard.



Tracks will only display as they pertain to the locus selected. Below is a table of possible annotation tracks that may display.

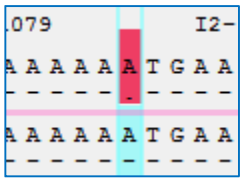
Track Name	Description	Flag Color
Variants	Heterozygous positions	Orange/brown
MismatchPos_[Allele 1]	Mismatch positions for allele 1	Red
MismatchPos_[Allele 2]	Mismatch positions for allele 2	Red
HighBackGround_[Allele 1]	High background positions and high background in homopolymer for allele 1	Purple or Light Blue if in homopolymer region
HighBackGround_[Allele 2]	High background positions and high background in homopolymer for allele 2	Purple or Light Blue if in homopolymer region
LowCoverage_[Allele 1]	Coverage has dropped below a preset minimum	Green
LowCoverage_[Allele 2]	Coverage has dropped below a preset minimum	Green
Hetero Positions_[*allele name+allele name*]	Will display when a comparison sequence is added to the sequence display. Both alleles for comparison are named.	Green
Excluded Regions	Displays the regions that have been excluded from analysis.	Pale Yellow

Hovering over the track names displays a tooltip describing actions that may be taken by right- or left-clicking.

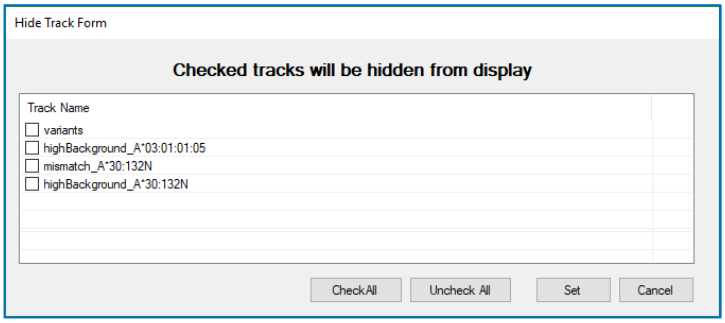


Left-clicking a track name will highlight the track name and make the flags on the track available for browsing via the browser arrows. If no tracks are selected, browser arrows will browse all flagged positions.

If more than one flag applies to a position, the software will split the position. Below, allele 1 displays the flag for mismatch while allele 2 displays the flag for high background in a homopolymer region.



Right-clicking on annotation track name will display the 'Hide Track Form.' User should check the tracks to be HIDDEN, then click 'Set.' Because there must be at least one track displaying, if all tracks are checked, the topmost track on the list will still display.

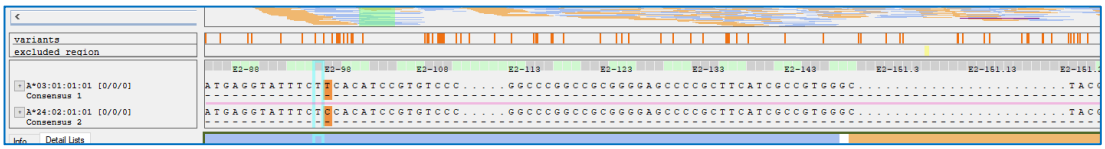


Nucleotide Sequence Viewer

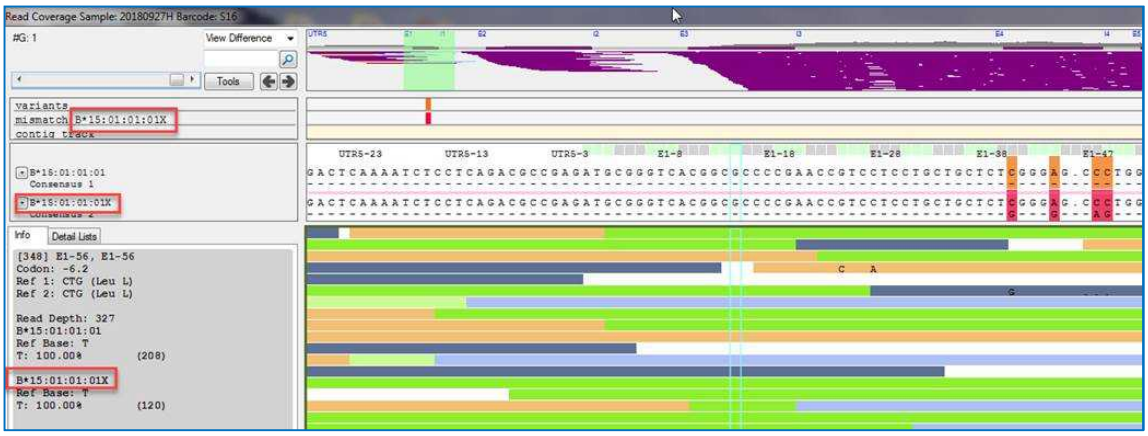
The consensus Sequence is displayed for each allele next to the sequence for the reference allele. Every matched position displays as a dash in the consensus sequence. Mismatched positions display the consensus base at the mismatch position. Codon position is displayed above the bases.

Nucleotides may be shaded in any of the colors orange, purple, light blue, red, or green to correspond to the annotation track flags (see previous entry). The shaded bases in the following illustration are variant positions.

Deletions are represented by single dots in place of the base. If the consensus has a deletion at the same base position, '-' will display to show agreement, just as if it were an actual base. In the illustration below, both reference alleles have deletion locations where the deletions are represented by dots '.'. The corresponding consensus sequences have deletions at the same locations, represented by dashes '-'.



At times the software may make a heterozygous call where the only variant identified is novel, and the typing call results in the same closest matching allele for both the Allele 1 and Allele 2 consensus. In this case, the software will report a heterozygous allele call and the read viewer will display the closest allele sequence with an 'X' appended to the allele name.



Navigating through the sequences

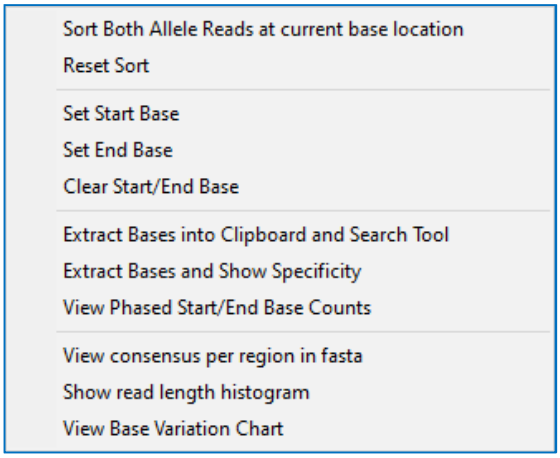
To browse bases of a certain type, e.g. high background bases, select the high background annotation track for one or both alleles. Use the arrows at the top of the page or the arrow on the keyboard to jump to the next (right) or previous (left) flagged position.

Add as many tracks as base types you would like to browse. Selecting no annotation tracks will browse all positions on all tracks.

To skip a portion of sequence, simply click a position upstream or downstream from the current position. Browsing will restart at the selected position without having to browse all flagged positions between.

Nucleotide Viewer Options

Right-click on the nucleotide viewer and the software displays a number of useful options for deeper sequence analysis.



Sort Both Allele Reads at current base location

Application will show sorted reads by base count at the marked position. This sort can then be reset to original configuration or logged.

Reset Sort

After viewing reads sorted by base position, "Reset Sort" will re-align to the original alignment. It is necessary to reset the sort prior to sorting alleles at another base location.

Set Start Base

TypeStream Visual allows the user to select multiple base positions by doing the following:

- Right-click in the sequence viewer on the first base you want to include.
- Select Set Start Base.
- Right-click on the last base you want to include.
- Select Set End Base.

When a start base is set, it will appear as a solid line through the nucleotide and reads, whereas the dynamic position indicator appears as an outline.

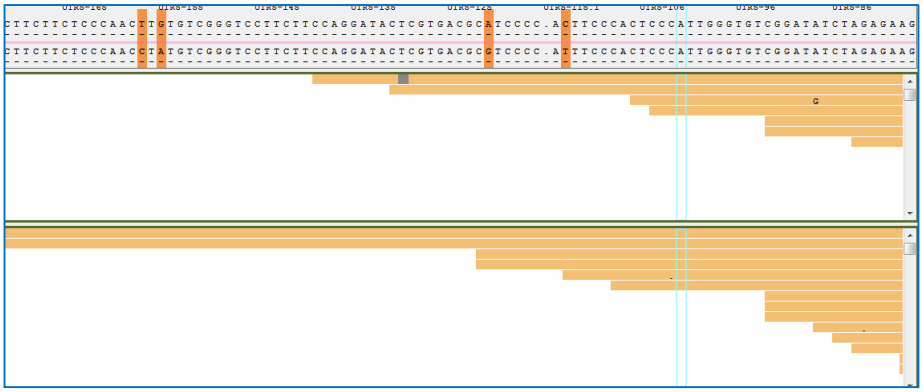
Other reasons to set a start base include:

- Extracting bases to clipboard
- Extracting bases to show specificity
- Getting phased based counts.

Set End Base

Most of the features using "Set Start Base" do not require the user to set an end base. The main reason to do so is to study reads that cross two specific positions of interest.

After setting an end base, the application filters out reads that do not cross both positions. This functionality is helpful when manually reviewing a break in phase or exploring mismatch positions. The reads are sorted by start position as illustrated below.



Clear Start/End Base

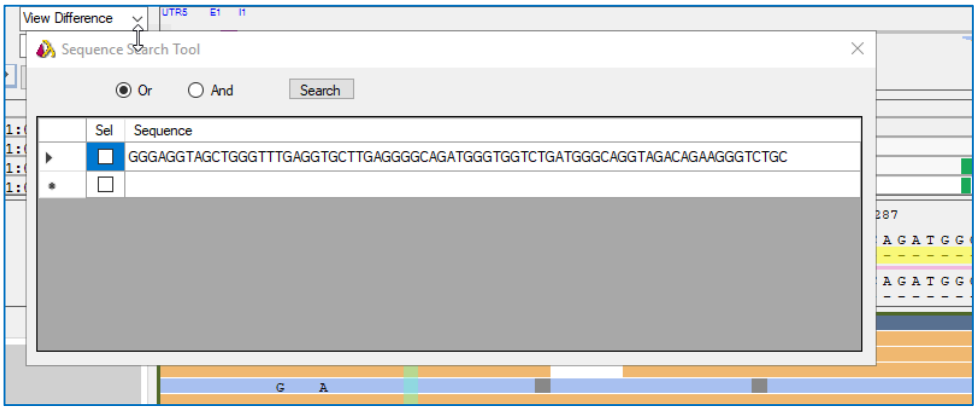
After viewing sorted reads as seen above, using "Clear Start/End Base" will clear the marked positions and return all reads to the original alignment.

Extract Bases onto Clipboard and Search Tool

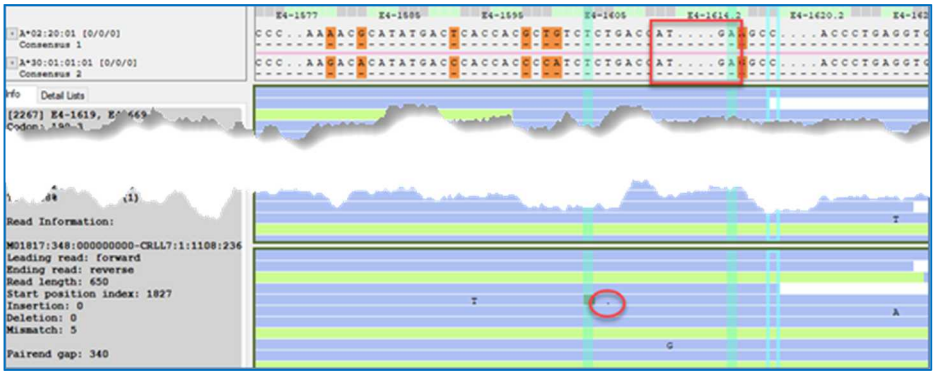
To extract bases to system clipboard, right-click on the start position and select 'Set Start Base.' Right-click on the desired end position (no need to set an end base) and select 'Extract Bases to Clipboard and Search Tool.' Software copies the base sequence from the set start position to the right-clicked final position and places it on your clipboard.

In addition, the application automatically opens the Search Tool and places the sequence on the tool for you. The user may then perform a search or manually add more sequences for a more complex search.

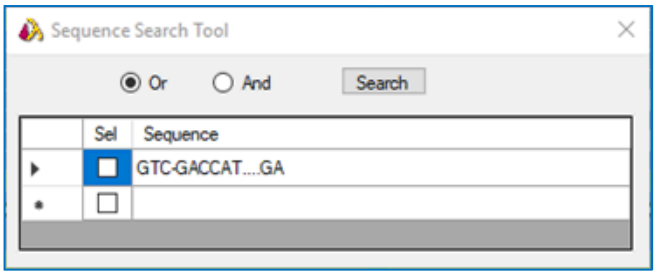
Please be aware that the extracted sequence is from the mapped read, not the original read.



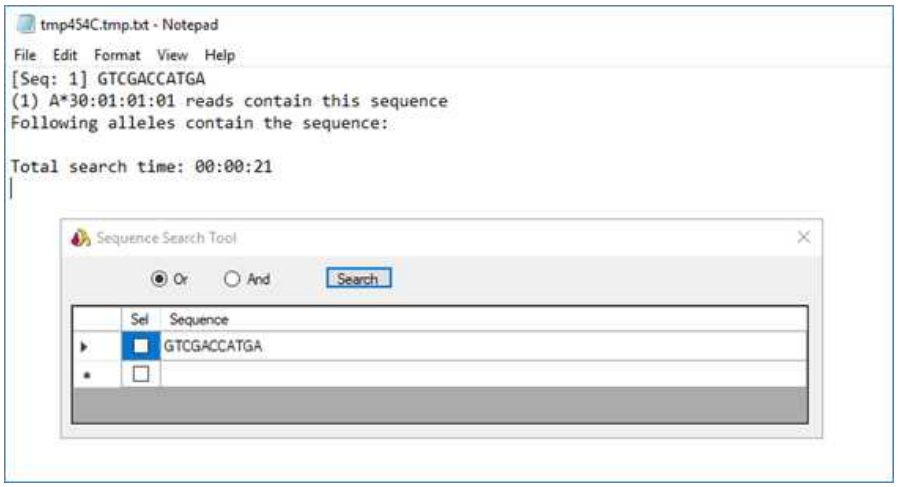
An exception to the that rule is illustrated below. The reference and consensus sequences have a 4-deletion sequence in Exon 4. The read of interest in allele 2 has an additional deletion that is not a part of the consensus or the reference.



When the extraction is from this specific read and encompasses both deletion locations, it appears on the Search Tool as a dash ("-") in the place of the single deletion.

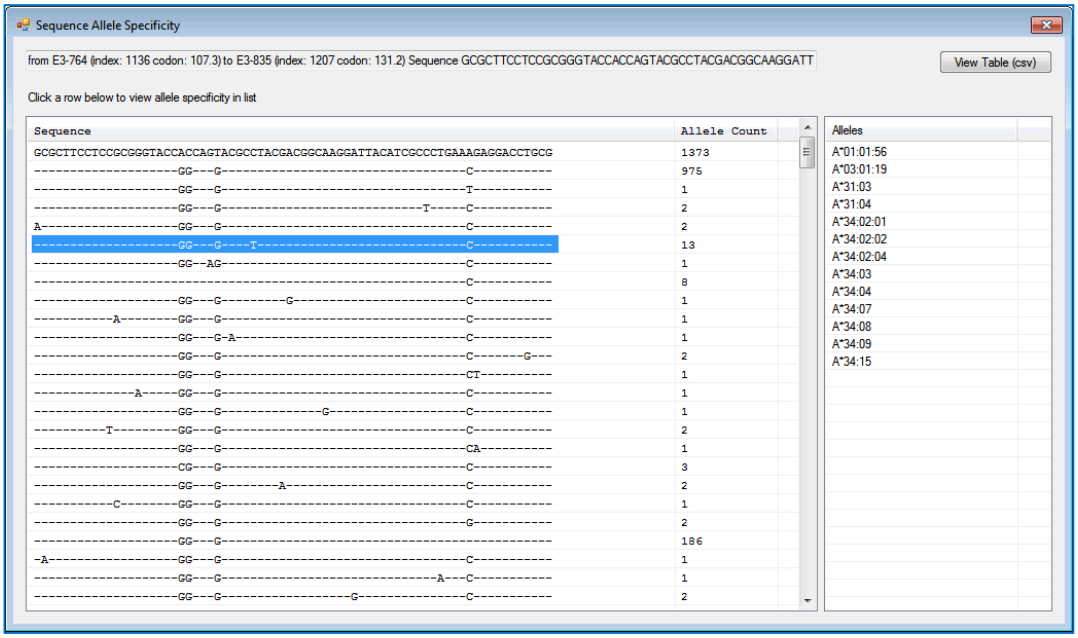


When Search is clicked, the software will remove all the deletions and results will be returned based on the original read.



Extract Bases and Show Specificity

Extract bases as described above and select "Extract Bases and Show Specificity." Table displays showing the unique sequences and the alleles that match it in the extracted region.



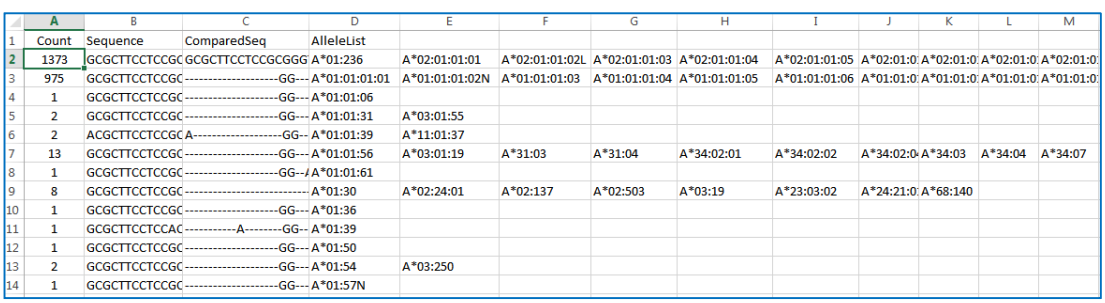
Data displays in three columns:

1. Sequence – the top entry is the extracted sequence. Subsequent entries show all the variant sequences related to the extracted sequence that can be found in the current library
2. Allele Count – displays the number of alleles in the current library that contain that exact sequence
3. Alleles – displays the specific alleles that contain the selected sequence.

In the example above, the selected sequence contains five mismatches from the original extracted sequence. We can see in column two that there are 13 alleles in the library that have that specific sequence. Column three lists each of the 13 alleles.

View Table (.csv)

Clicking the View Table button exports all the data in the Sequence Allele Specificity window to a .csv file which opens automatically in Microsoft Excel.



	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Count	Sequence	ComparedSeq	AlleleList									
2	1373	GCGCTTCCTCCGC	GCGCTTCCTCCGCGGG	A*01:236	A*02:01:01:01	A*02:01:01:02L	A*02:01:01:03	A*02:01:01:04	A*02:01:01:05	A*02:01:0	A*02:01:0	A*02:01:0	A*02:01:0
3	975	GCGCTTCCTCCGC	----------GG---	A*01:01:01:01	A*01:01:01:02N	A*01:01:01:03	A*01:01:01:04	A*01:01:01:05	A*01:01:01:06	A*01:01:0	A*01:01:0	A*01:01:0	A*01:01:0
4	1	GCGCTTCCTCCGC	----------GG---	A*01:01:06									
5	2	GCGCTTCCTCCGC	----------GG---	A*01:01:31	A*03:01:55								
6	2	ACGCTTCCTCCGC	A----------GG--	A*01:01:39	A*11:01:37								
7	13	GCGCTTCCTCCGC	----------GG---	A*01:01:56	A*03:01:19	A*31:03	A*31:04	A*34:02:01	A*34:02:02	A*34:02:0	A*34:03	A*34:04	A*34:07
8	1	GCGCTTCCTCCGC	----------GG--/	A*01:01:61									
9	8	GCGCTTCCTCCGC	----------	A*01:30	A*02:24:01	A*02:137	A*02:503	A*03:19	A*23:03:02	A*24:21:0	A*68:140		
10	1	GCGCTTCCTCCGC	----------GG---	A*01:36									
11	1	GCGCTTCCTCCAC	----------A--------GG--	A*01:39									
12	1	GCGCTTCCTCCGC	----------GG---	A*01:50									
13	2	GCGCTTCCTCCGC	----------GG---	A*01:54	A*03:250								
14	1	GCGCTTCCTCCGC	----------GG---	A*01:57N									

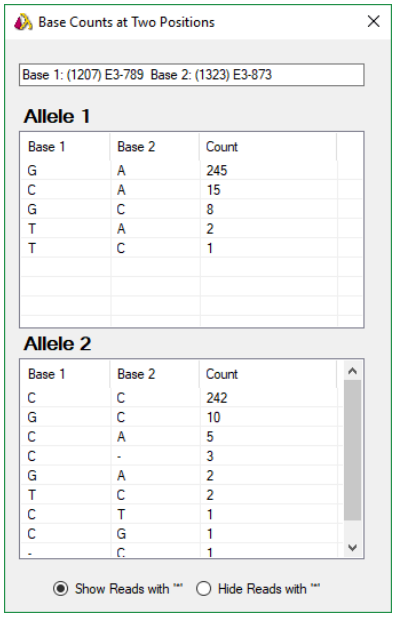
Again, be aware that the extracted sequence is from the mapped read, not the original read.

View Phased Start/End Base Counts

The 'View Phased Start/End Base Counts' tool can be used to confirm the phasing of variants. Some examples:

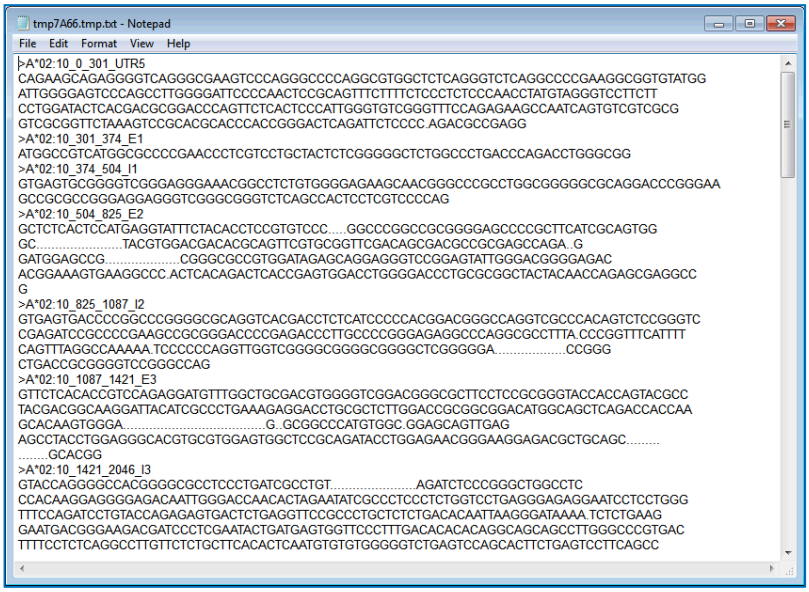
1. When System Comments reports that a cis-trans pair has been removed, user can add the removed pair and check the phase of the "flip" positions.
2. When a cis-trans is reported, user can check the phase counts to confirm removing one or the other allele.
3. For a novel position, user may want to check the phase with surrounding variants to confirm which allele it belongs with.

The tool displays both base positions, the base(s) present at the position for both alleles, and the count of reads that are in phase. Multiple phase count window can be opened simultaneously for comparison.



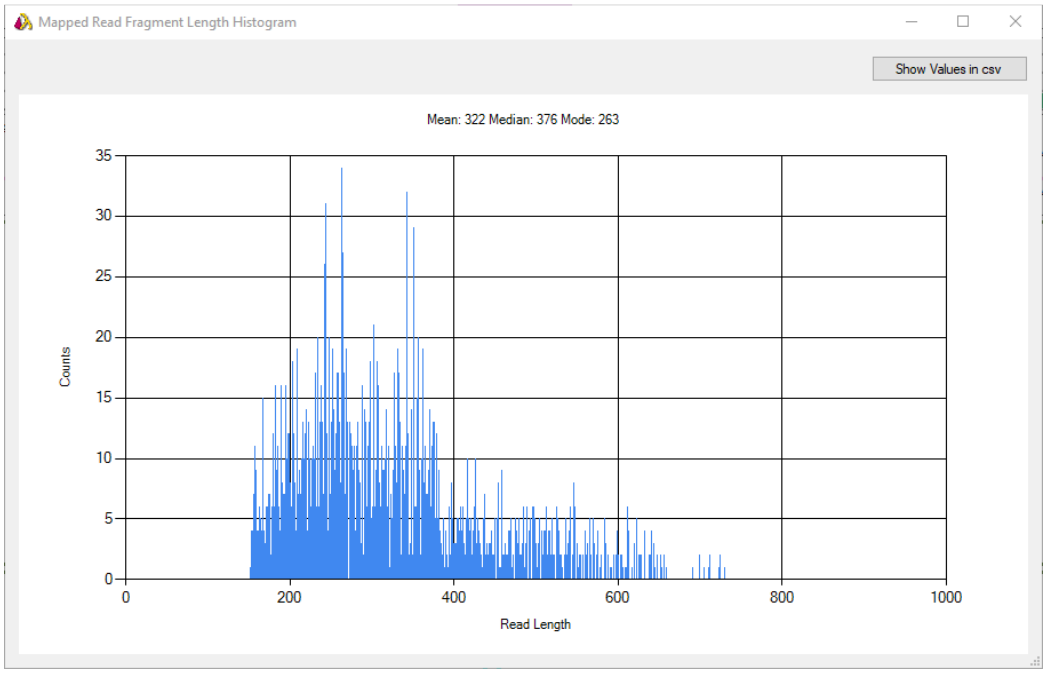
View consensus per region in fasta

Right-click on the sequence few and select "View consensus per region in fasta." Notepad window opens displaying mapped sequence broken out into regions. Allele name and region are clearly marked for each regional sequence.



Show Read Fragment Length Histogram

Right-click on the sequence viewer and select "Show read length histogram." A histogram representation of the lengths and their counts for all reads in the locus appears in a separate window displaying a histogram of mapped read fragments. Mean, median, and mode values are also displayed.



Show Values in csv

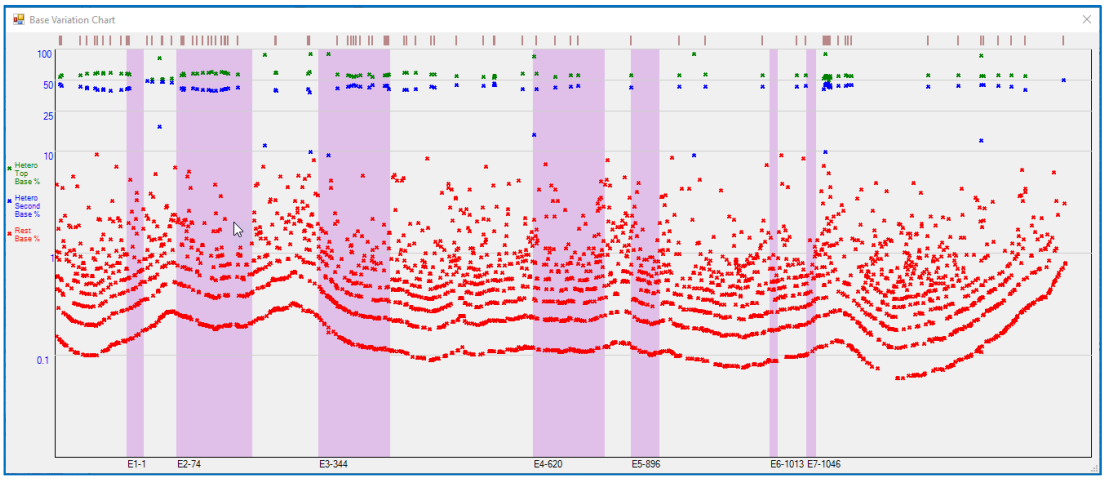
Clicking the button "Show Values in csv" opens a .csv file in Microsoft excel containing the read count values for each read length.

	A	B	C	D	E	F	G
1	Length	Count					
2	85	1					
3	86	6					
4	89	1					
5	92	2					
6	93	12					
7	96	4					
8	98	2					

View Base Variation Chart

This pop-out chart plots signal-to-noise at every position across an entire gene, giving a quick graphic representation of balance between allele 1 and allele 2, with additional representation of the remaining base possibilities.

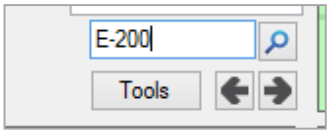
- Gene regions lie along the x-axis, with exons shaded in purple and introns remaining unshaded.
- The y-axis is a logarithmic scale which depicts the percentage representation of bases found in reads at that base position.
- Top hetero base percentage is a green '*'.
- Second hetero base percentage is a blue '*'.
- All remaining base percentages display with a red '*'.



Other Functions in Read Viewer UI

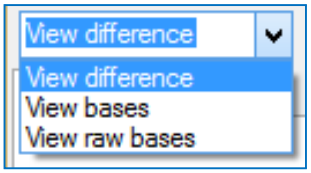
Position Search Tool

Enter position designation to go directly to a position. Can be done cDNA or gDNA format.



View Options

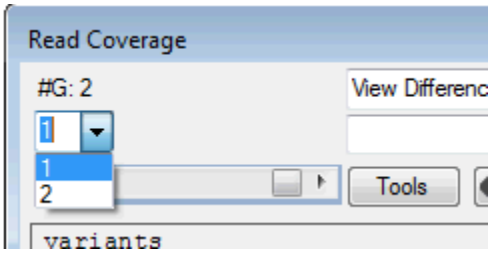
User may select how the reads appear on the reads viewers – view only the variant bases, view all bases, or view raw reads.



If you choose to view raw bases, the reads will not be mapped to the reference sequence, meaning that insertions or deletions have not been added into the sequence in order to force a concordance to a given reference allele. Therefore, a particular base in a particular read may not coincide with the base in the nucleotide viewer.

Genotype Selector

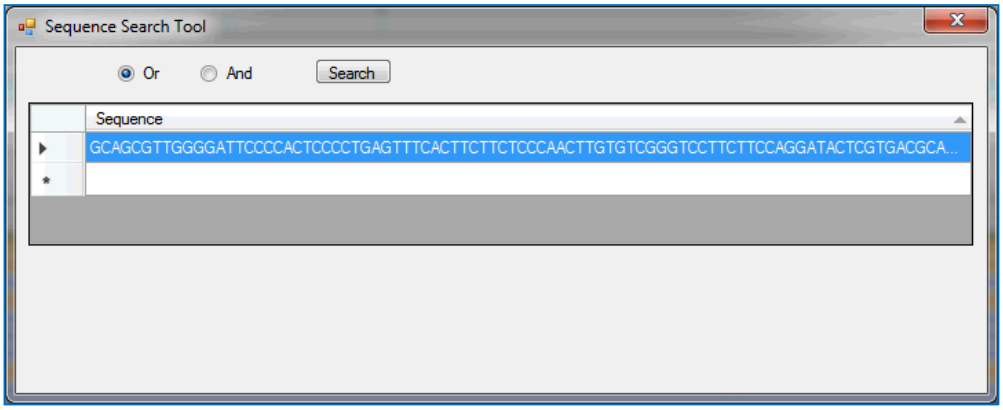
In the case of cis-trans ambiguities, a dropdown selector allows the user to select the particular genotype to display. The number in the corner (#G: 2) indicates how many total genotypes are in the locus.



Sequence Segment Search Tool

Clicking "Tool" button on Reads Coverage window displays tool for searching for specific segments of a sequence. User may input the sequence in one of two ways:

- Type in a sequence manually
- Right-click on a read, obtain its sequence, and paste it into the window.



Click on the second row in the grid to add another sequence to search. Add as many sequences as needed. Search can be in either of two modes:

- OR – application will locate reads and alleles containing **any** of the sequences
- AND – application will locate reads and alleles containing **all** of the sequences

Results for each search are delivered in a new Notepad window and lists the following:

- Sequence(s)
- Unmapped reads containing the sequence(s)
- Alleles containing the sequence(s)
- Total search time

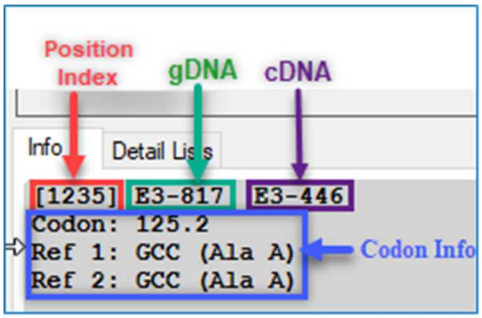
Details panes for base position and/or read information

This panel displays read details or position details for the location over which the mouse is hovering.

Info Tab

The Info tab displays data for reads or for base positions, depending where the mouse is hovering.

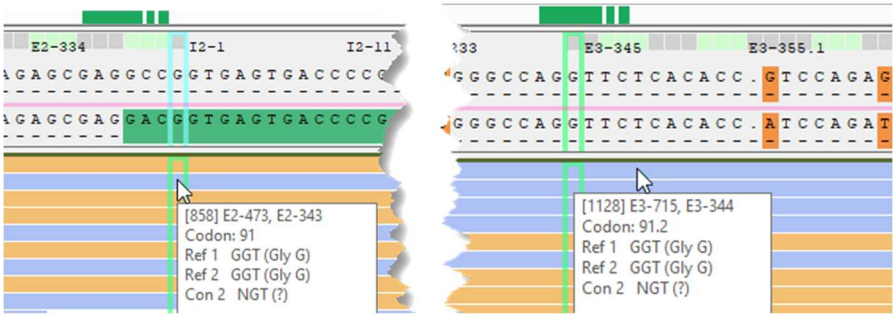
The three numbers at the top of the panel represent the position index, gDNA base number, and cDNA base number.

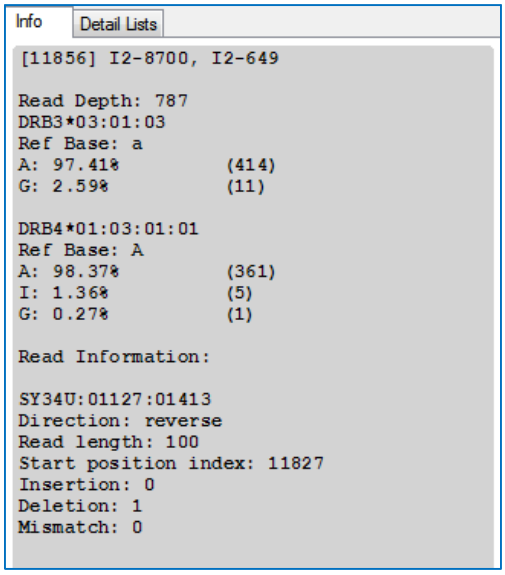


- Position Index – The overall reference for base positions from the first upstream position in 5′ UTR to the last downstream position in 3′ UTR.
- gDNA – "Genomic DNA" – The position count is continuous, starting with exon 1 (E1) through the remainder of the gene, including 3′ UTR; the 5′ UTR begins with "-1", at the junction of 5′ UTR and E1, and continues upstream with negative numbering.
- cDNA – "Complementary DNA" – This notation mirrors IMGT in which all introns begin with position "1" and each exon continues numbering from the previous exon.

Codon numbers display for all exon positions. A whole number, e.g. '125', means that this is the first position in the codon triad. '125.2' means the second position, and '125.3' means the third position.

For splice site codons, the software displays the whole codon, allowing the amino acid at the splice site to be displayed. The illustration below shows how the last base of Exon 2 and the first two bases of Exon 3 are combined in the info panel to display the full codon and full amino acid sequence.





The Info Tab also displays the **read depth** for the combined allele 1 and allele 2 reads. Per allele read count is also broken down by read count per base. Because many reads are assigned to both allele 1 and allele 2, the count per allele may not add up to the total read depth.

The reference, or expected base, is displayed along with all other base represented at that position, with percentages representation.

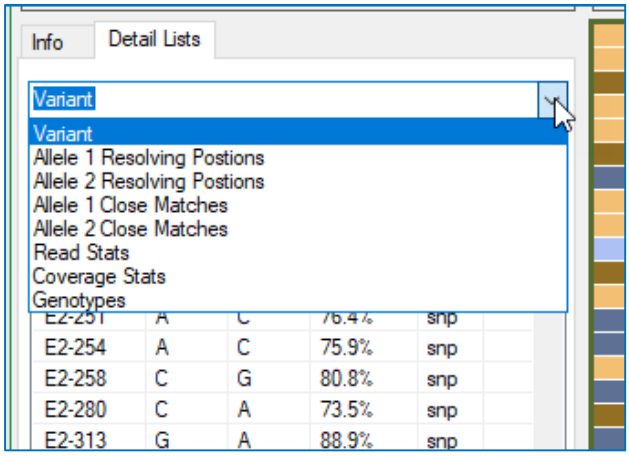
If the mouse cursor is hovering over the reads view panel, Read Information will also display. This includes system-assigned read name, direction, length, start position, and number of insertions, deletions and mismatches positions for the read.

Hover Info

While Positions tab is selected, info data is still visible as a pop-up when hovering over a read. Hover over a base in the sequence viewer displays base data.

Detail Lists Tab

The details tab displays variant, close matches, resolving positions, and statistics and reflects the data displayed on the Analysis page.



Variant

A subset of the information available on the Variant tab of the Analysis Panel, the Variant list displays position location, base 1, base 2, balance %, and also displays the Type of variant. In most cases the variant will be a single nucleotide polymorphism (snp) but may also indicate if the variant is a deletion (del). In the variants list, the exons are shaded in purple for easy identification, while introns remain unshaded. Any variant with a minimum hetero allele balance below 10%, or other configured minimum, is shaded in red.

DRB1*04:08:01 [0/0/0*]
Consensus 2

Info | Detail Lists | Novel Bases

Variant

Position	Base 1	Base 2	Count 1	Count 2	Bkgd	Balance	Type	Phased
E2-5387	T	C	82% (325)	17% (68)	00% (1)	0.209	snp	false
E2-5389	C	G	83% (327)	17% (65)	00% (1)	0.199	snp	
E2-5390	T	G	83% (328)	17% (65)	00% (0)	0.198	snp	
E2-5391	C	T	84% (328)	16% (64)	00% (0)	0.195	snp	
E2-5394	C	A	84% (340)	16% (65)	00% (1)	0.191	snp	
E2-5395	G	A	84% (350)	16% (65)	00% (0)	0.186	snp	
E2-5396	T	C	84% (354)	15% (65)	00% (1)	0.184	snp	
E2-5397	C	A	85% (354)	15% (64)	00% (0)	0.181	snp	
E2-5416	T	C	85% (396)	14% (67)	00% (1)	0.169	snp	
E2-5436	A	T	87% (417)	13% (64)	00% (1)	0.153	snp	
E2-5453	C	T	88% (416)	12% (59)	00% (0)	0.142	snp	
E2-5456	A	C	88% (414)	12% (56)	00% (0)	0.135	snp	
E2-5461	G	A	89% (427)	11% (55)	00% (0)	0.129	snp	
E2-5468	A	T	89% (450)	11% (54)	01% (3)	0.120	snp	
E2-5499	T	A	92% (501)	07% (39)	00% (2)	0.078	snp	
E2-5571	A	G	92% (510)	08% (42)	00% (0)	0.082	snp	
E2-5577	G	C	93% (521)	07% (40)	00% (2)	0.077	snp	
E2-5579	C	G	93% (527)	07% (41)	00% (0)	0.078	snp	

C T G G A C

Allele 1 (and 2) Resolving Positions

This information will match the resolving position information from Analysis Panel and reflects the differences in consensus and reference base.

Info | Detail Lists

Allele 2 Resolving Postions

Allele	K/N/I	Con.	Ref.	Location
DPB1*04:01:01:01	[0/0/0]		C	I1-931
			G	I1-1074
DPB1*04:01:01:29	[0/0/0]		T	I1-931
			G	I1-1074
DPB1*04:01:01:30	[0/0/0]		C	I1-931
			A	I1-1074

Allele 1 (and 2) Close Matches

Lists the Closely Matches alleles, their mismatch counts, consensus and reference bases, and location of the resolving position.

Info | Detail Lists

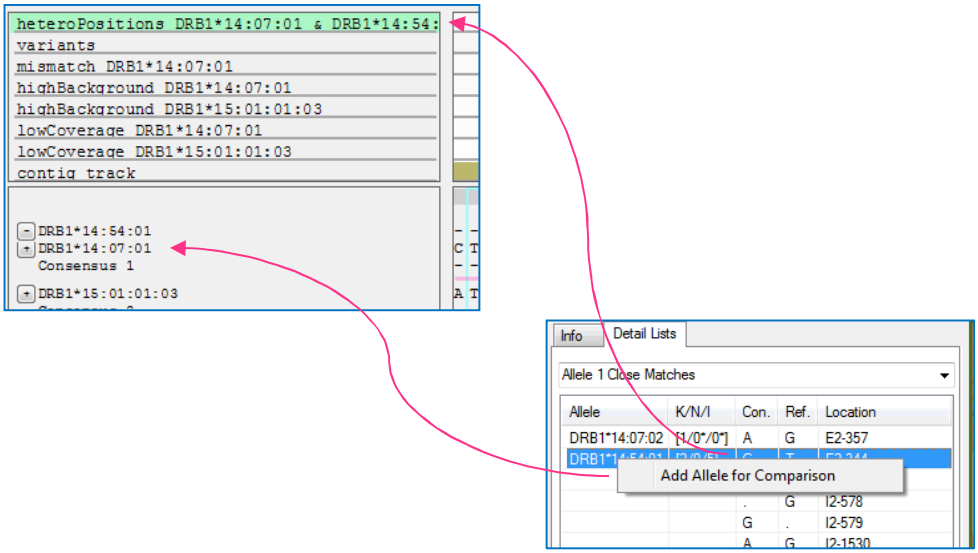
Allele 1 Close Matches

Allele	K/N/I	Con.	Ref.	Location
DPB1*03:01:01:11	[0/0/1]	C	A	I1-4522
DPB1*03:01:01:04	[0/0/1]	C	G	I2-2447
DPB1*50:01	[0/0/1]	A	G	I1-4467
DPB1*03:01:01:07	[0/0/1]	T	C	I2-3453
DPB1*03:01:01:10	[0/0/2]	A	G	I1-4467
		T	G	I2-1170
DPB1*03:01:10	[0/1/0]	C	T	E3-507
DPB1*03:01:11	[0/1/0]	C	T	E3-478
DPB1*03:01:12	[0/1/0]	G	A	E3-564
DPB1*669:01	[0/1/0]	G	A	E3-637
DPB1*675:01	[0/1/0]	G	T	E3-442
DPB1*676:01	[0/1/0]	G	A	E3-470

Clicking on any of the base positions on the Resolving Positions or Close Matches tab will scroll the reads view, whole gene view and nucleotide view to the selected position.

Add directly to allele comparator

In either of the close match or resolving positions list, right-clicking on the ambiguous allele names allows the user to add that allele directly to the comparator. See section below, "Setting Comparison Sequences" for more detail.



Read Stats

This chart expands on Mapped Read Metrics from Analysis Panel to display additional metrics on read depth and reads identified for locus.

Info | Detail Lists

Read Stats

Key	Value
avg_forward_read_length	309
avg_reverse_read_length	282
avg_read_length	297
max_read_depth	559
min_read_depth	0
forward_read_count	3237
reads_for_typing	6161
reads_identified_for_locus	8955

Coverage Stats

Coverage Stats echoes those from the Statistic tab of the Analysis Panel.

Info | Detail Lists

Coverage Stats

Region	Base Covered (%)	Min Depth	Max Depth	Avg Depth	Avg Balance
UTR5	0%	0	0	0	0
E-1	0%	0	0	0	0
I-1	87%	12	76	48	0.7428572
E-2	100%	67	103	85	0.6938776
I-2	100%	42	559	327	0.8795812
E-3	100%	314	404	357	0.8716577
I-3	100%	386	495	444	0.95671
E-4	100%	286	387	343	0
I-4	100%	130	331	268	0.7837838
E-5	100%	117	126	120	0
UTR3	100%	96	113	104	0
All	99%	0	559	314	0.8938547

Genotypes List

On reads view, Details Lists, one option is Genotypes. All permutations of allele pairings based on top types plus ambiguities display on this list.

Info | Detail Lists

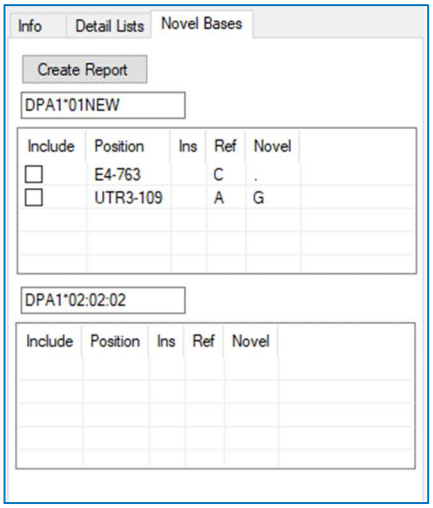
Genotypes

All Genotypes

A*03:01:01:01 & A*24:02:01:01
A*03:01:01:01 & A*24:163N
A*03:01:01:02N & A*24:02:01:01
A*03:01:01:02N & A*24:163N
A*03:20 & A*24:02:01:01
A*03:20 & A*24:163N

Novel Bases Tab

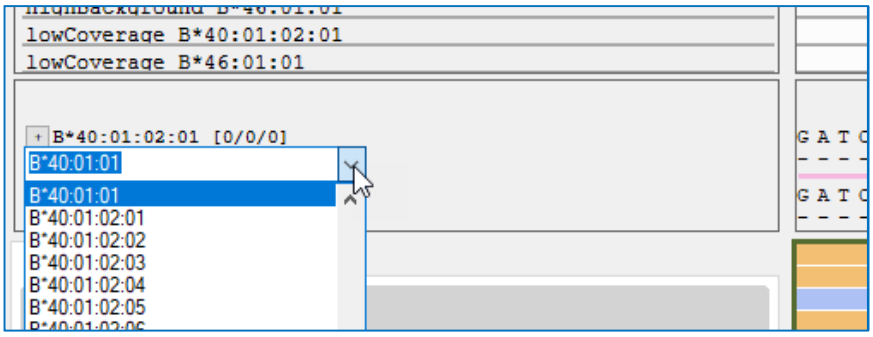
For any allele determined to have a new sequence combination – identified by "NEW" on the Summary Page – the novel bases are listed on the 'Novel Bases' tab. User may select one, several, or all positions to include in a ,fasta report.



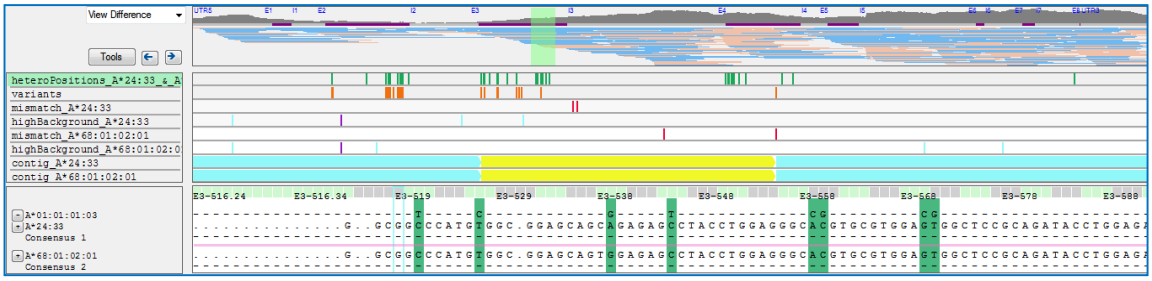
On clicking "Create Report" a navigation window opens where the report can be named and saved to selected location.

Setting Comparison Sequences.

This functionality allows the addition of one or more sequences for comparison study.
To select an allele, click the ⊞ next to the allele for which you want to do a comparison and select the allele from the dropdown list.

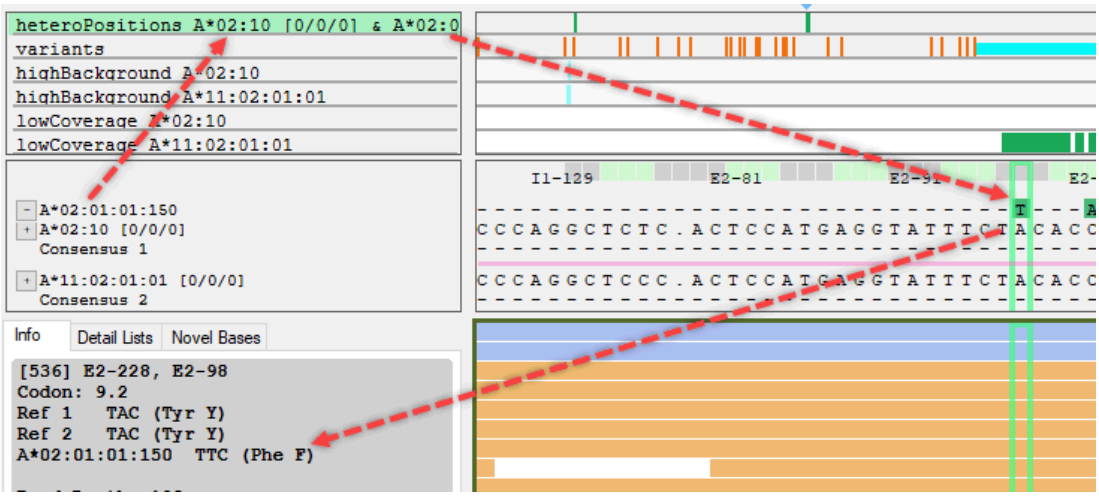


Selected allele name displays above for allele 1 or below for allele 2. Annotation track is added for the comparison sequence. Annotation track flags are shaded green, as are the heterozygous positions on the nucleotide viewer.



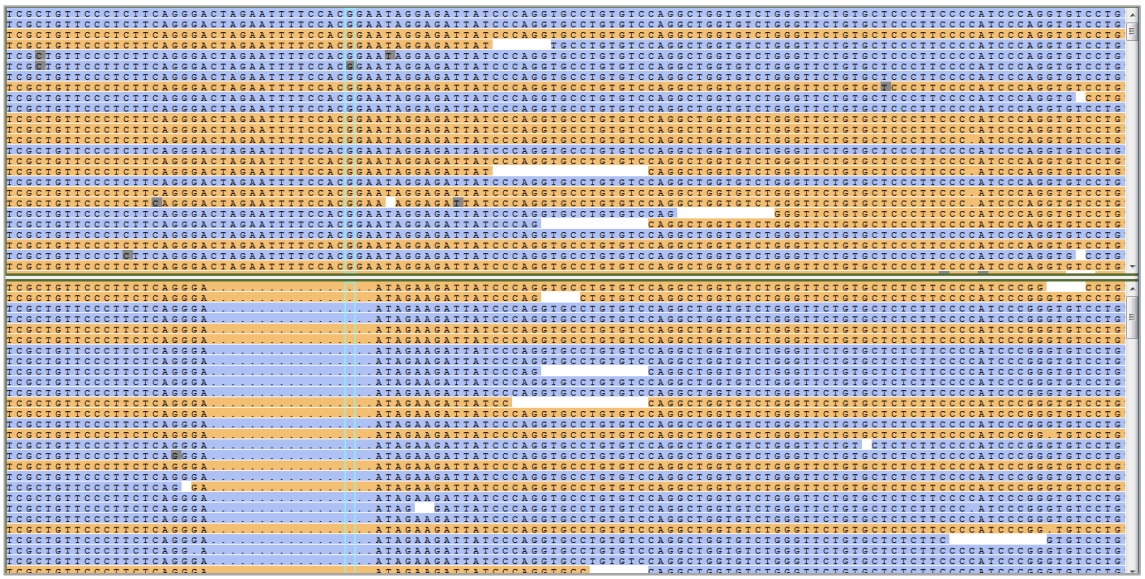
User may add multiple comparison alleles for each of Allele 1 and Allele 2.

In selecting one of these green-shaded heterozygous bases, the info panel displays the difference in the amino acid and codon sequence between the original reference and the comparison.



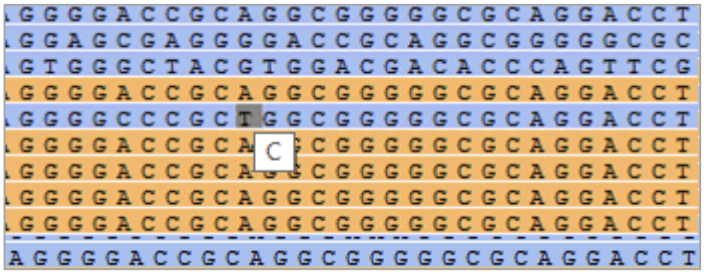
Reads viewer in detail

The reads subview allows users to visualize individual sequence reads. Reads display only for the selected position and are separated by allele. Each of the allele panels scrolls separately.



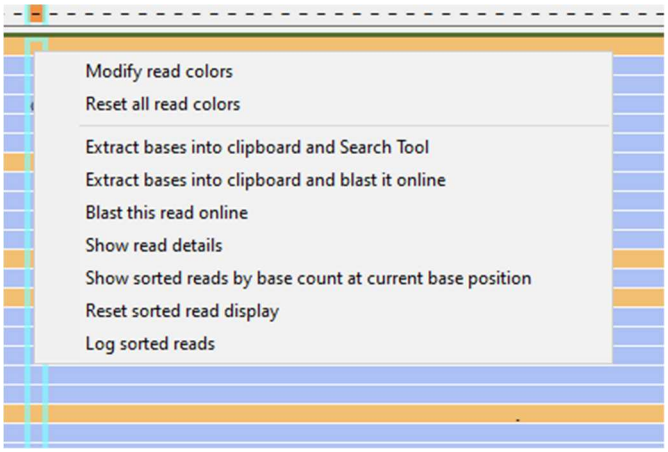
Insertion Base

The location of insertion bases is displayed with a light gray shading over the previous base. Hovering over the gray shading displays the insertion.



Reads Viewer Options

Right-clicking on the reads viewer offers the user additional functionality from that in the Nucleotide Viewer.



Modify read colors

Read colors have been set for both Ion S5 and Illumina samples. Beginning in TypeStream Visual 2.0, the user is able to set reads, insertions and deletion to a shade of their own choosing.

Default Read Colors for Ion S5 files

Reads from Ion S5 sequencers display with the following default coloring for reads.

- Dark brown = cross allele 1 & 2 forward reads
- Light brown = single forward reads
- Light blue = single reverse reads
- Dark blue = cross allele 1 & 2 reverse reads

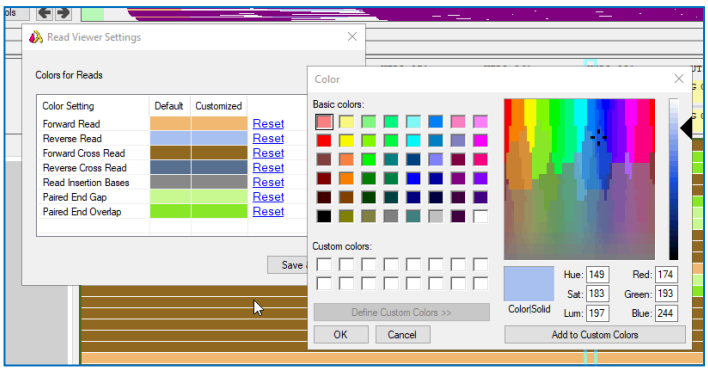
Default Read Colors for MiSeq files

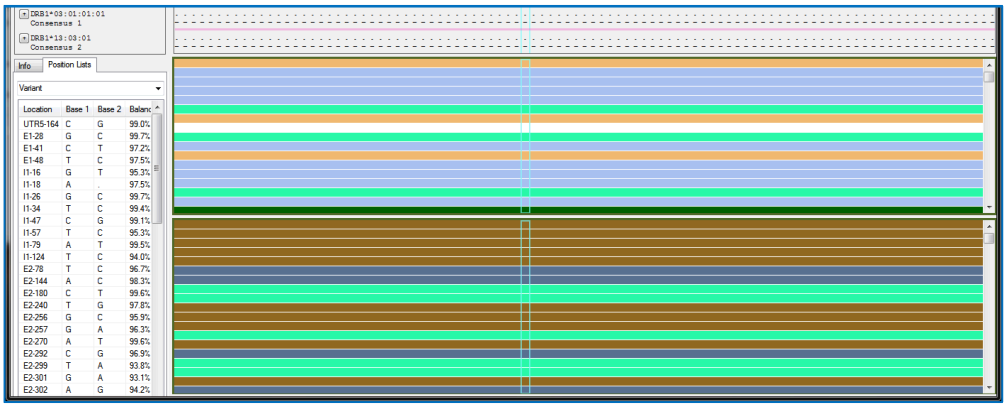
MiSeq paired-end reads display with additional default coloring for reads.

- Dark green = overlapping region in paired-end reads
- Light green = gap between paired-end reads
- Dark brown = cross allele 1 & 2 forward reads
- Light brown = single forward reads
- Light blue = single reverse reads
- Dark blue = cross allele 1 & 2 reverse reads

New Read Colors Available

Right-click within the reads view and select 'Modify Read Colors.' Click on the color bar under 'Customized' for the read type you want to change. Select standard colors or customize your own.





Reset all read colors

If you then feel you've made a terrible mistake, right-click on reads and select 'Reset all read colors." They will return to defaults.

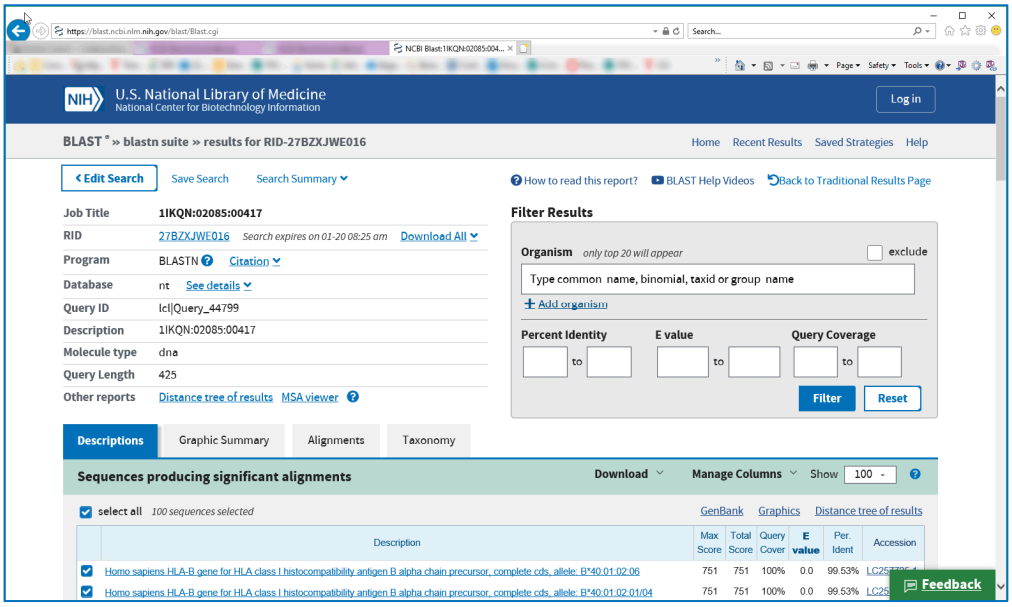
Extract base into clipboard and Search Tool

Like the functionality of the same name in the Nucleotide Sequence Viewer, a specified sequence will be put on the clipboard and into the search tool. You must use the nucleotide

viewer to set the start base and to reset the start/end bases. After the start base has been chosen, you may click the last position from within the reads viewer.

Extract bases into clipboard and blast it online

After setting start base, find last base and select this option. The application with open a browser window that takes the user to NCBI (National Center for Biotechnology Information) website and opens a job request. Web page displays the job request number and is available for any deeper dive into the sequence data.

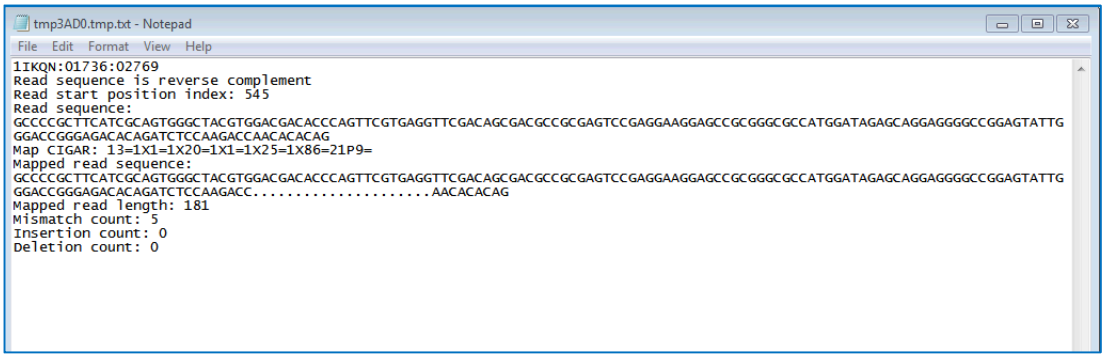


Blast this read online

This is similar to the previous functional option, but all the user need do is to point the cursor at a particular read he wants to view, then right-click and select this option. The application will take you to the NCBI web page as before.

Show Read Details

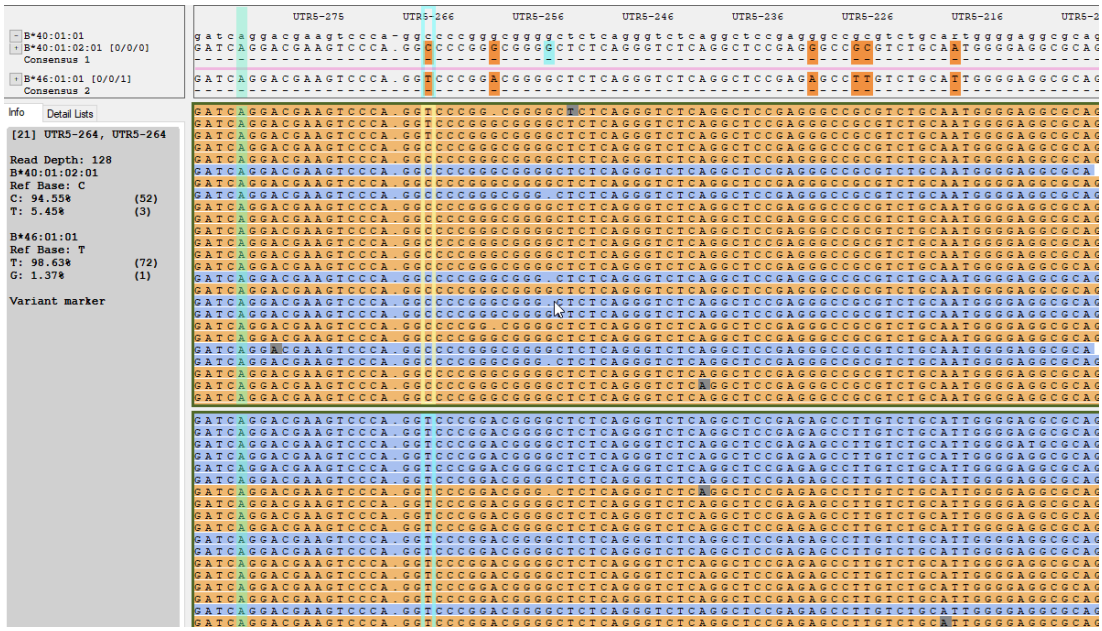
This options opens a window in notepad with details, including software-generated read name, start and stop positions, sequence, mismatch, insertion and deletion counts.



The read sequence shows the complete sequence as it emerged from the sequencer. The mapped read sequence has had insertions and deletions added in order to match the selected reference allele.

Show sorted reads by base count at current base position

To use this option, set the view option to 'bases' so that all bases can be seen. At the position of interest, right-click and select this option. The example below was sorted at position index 21 and is highlighted. In allele 1 it can be seen that the reads containing the 'T' base are listed first, followed by read with 'C' base. Allele 2 will have the reads sorted in the same order.



Reset sorted read display

When user is finished, this option will set the reads into the original alignment.

Log sorted reads

If the user would like a log of the reads sorted by base count at the position of interest, select this option prior to resetting. The application will open a text file in Notepad with a complete log of the reads sorted at that position.

tmpC3A1.tmp.txt - Notepad

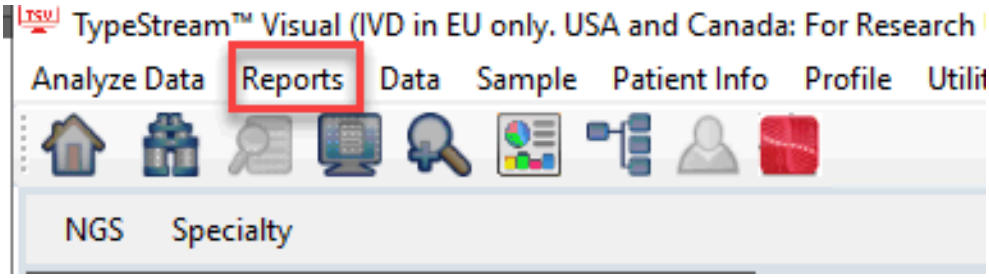
File Edit Format View Help

```
[55] C:\OLI TSV\data\Daniel\NGS\Daniel\049_36e680d1-aa16-4abb-825e-5338750ec884\mappedReads.bam
                                                                                    21
1IKQN:02157:02462  GATCAGGACGAAGTCCCA.GGTCCCGG-
CGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCACTCCCATTGGGTGTCGGGTGTCTAGAGAA
GCCAATCAGTGTCGCCGGGGTCCCAGTTCT...AAAGTCCCACGCAC
                                                                                    1
1IKQN:03104:00469
GATCAGGACGAAGTCCCA.GGTCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGTGTCGCCGGGGTCCCAGTTCT...AAAGTCCC-ACGCAC
1IKQN:03355:02225
GATCAGGACGAAGTCCCA.GGTCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGTGTCGCCGGGGTCCCAGTTCT...AAAGTCCCCCCGCAC
1IKQN:00295:00788
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGCGTCGCCGTGGTCCCAGTTCT...AAA
1IKQN:02108:02762
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCC
1IKQN:02141:02917  GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCA
1IKQN:02158:00405
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGAC
1IKQN:02174:01533  GATCAGGACGAAGTCCCA.GGCCCCGGGCGGG-
CTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCC
1IKQN:02240:01317
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGCGTCGCCGTGGTCCCAGTTCT...AAAGTCCCCACGCACCCACCCGGACTCAGAATCTCCTCAGACGCCGAGATGCGGGTCACGGCACCCCGAACCGTCCTCCTGCTGCTCTCGGCGG.CCCTGGCCCTGACCGAGACCTGGGCCG
GTGAGTGCGGG.TCGGCAGGGAAATGGCCTC
1IKQN:02272:01044
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGCGTCGCCGTGGTCCCAGTTCT...AAAGTCCCCACGCACCCACCCGGACTCAGAATCTCCTCAGACGCCGAGATGCGGGTCACGGCACCCCGAACCGTCCTCCTGCTGCTCTCGGCCG.CCCTGGCCCTGACCGAGACCTGGGCCG
GTGAGTGCGGG.TCGGCAGGGAA-TGG
1IKQN:02270:02880
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCA
1IKQN:02413:01832  GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCC
1IKQN:02451:01573
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGCGTCGCCGTGGTCCCAGTTCT...AAAGTCCCCACGCACCCACCCGGACTCAGAATCTCCTCAGACGCCGAGATGCGGGTCACGGCACCCCGAACCGTCCTCCTGCTGCTCTCGGCGG.CCCTGGCCCTGACCGAGACCTGGGCCG
GTGAGTGCGGG.TCGGCAGGGAAATGGCCTCTGTGGGGAG
1IKQN:02085:00417
GATCAGGACGAAGTCCCA.GGCCCCGGGCGGGGCTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCAC
TCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGCGTCGCCGTGGTCCCAGTTCT...AAAGTCCCCACGCACCCACCCGGACTCAGAATCTCCTCAGACGCCGAGATGCGGGTCACGGCACCCCGAACCGTCCTCCTGCTGCTCTCGGCGG.CCCTGGCCCTGACCGAGACCTGGGCCG
GTGAGTGCGGG.TCGGCAGGGAAATGGCCTCTGTGGGGAG
1IKQN:02646:00869  GATCAGGACGAAGTCCCA.GGCCCCGGGCGGG-
CTCTCAGGGTCTCAGGCTCCGAGGGCCGCGTCTGCAATGGGGAGGCGCAGCGTTGGGGATTCCCCACTCCCAC...GAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGACGCGTCCCC.ATTTCCCACTCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAA
TCAGCGTCGCCGTGGTCCCAGTTCT...AAAGTCCCCACGCACCCACCCGGACTCAGAATCTCCTCAGACGCCGAGATGCGGGTCACGG
1IKQN:02699:03116
```

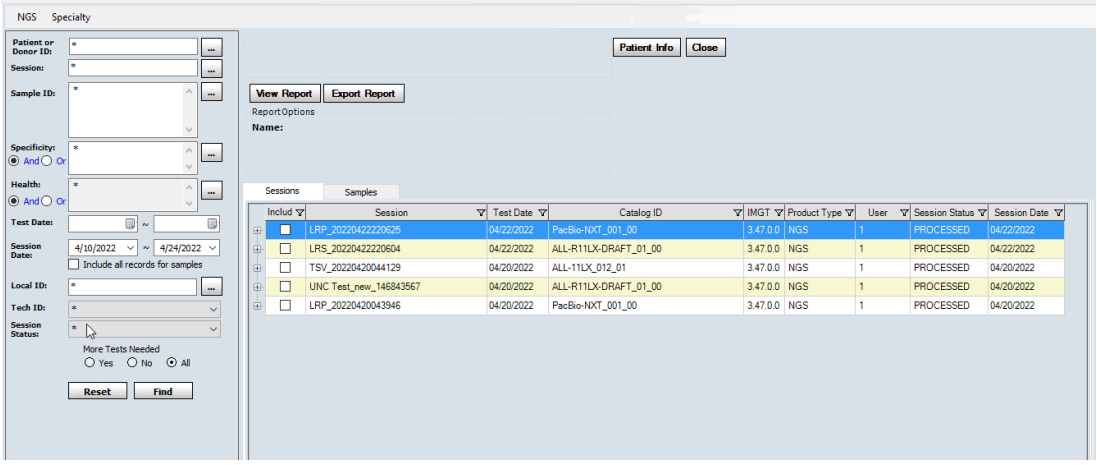
7

Reports

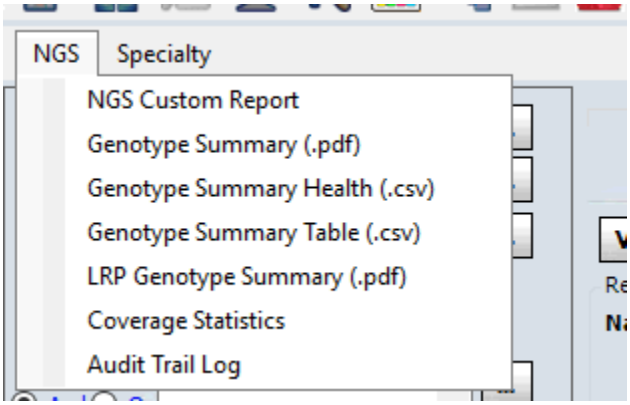
From any page, click 'Reports' on the menu bar or click the Reports icon on the toolbar.



Reports main page displays. All samples available in the database display on the grid.

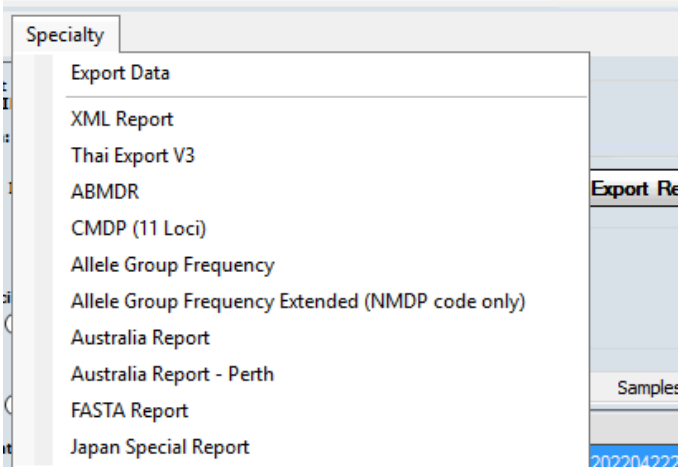


There are two categories of reports.



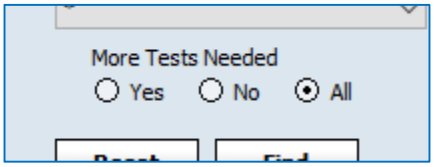
Note: LRP Genotype Summary (.pdf) report is available only in the RUO mode.

Basic reports for all Ion S5, MiSeq, LRP or LRS data. If Audit Log has been enabled in General Settings, a report of the Audit Trail Log can be created.



In addition to configurable Export Data option, specialty reports are available for specific data retrieval.

For any report, the user has the option of flagging samples for which More Tests are needed. There are three options for inclusion.



They will impact the grid in the following way:

> "Yes" – all samples from selected sessions that were marked "More Test" during analysis will be displayed in the grid.
> "No" – all samples from selected sessions that were marked "More Test" during analysis will NOT be displayed in the grid.
> "All" – all samples from selected session will be displayed in the grid irrespective of being marked for more testing.

User then selects sessions/samples for inclusion in the reports in the usual way.

Basic Reports

Genotype Summary .pdf

To create a PDF report, click NGS and select Genotype Summary (.pdf).

1. Select the sessions you want to include in the report.

Includ	Session	Test Date	Catalog ID	IMGT	Product Type	User	Session Status	Session Date
	TSV_S5_10.164.84.167_432	01/03/2019	ALL-11LX_002_03	3.33.0.1	NGS	1		01/03/2019
	TSV_20190108133605	01/08/2019	ALL-11LX_002_03	3.33.0.1	NGS	1	PROCESSED	01/08/2019
	TSV_20190108133726	01/08/2019	ALL-11LX_002_03	3.33.0.1	NGS	1	PROCESSED	01/08/2019
	TSV_20190108133758	01/08/2019	ALL-11LX_002_03	3.33.0.1	NGS	1	PROCESSED	01/08/2019

2. Click View Report

The pdf is created. The report displays the following:

- Sample ID, barcode, session name
- Sample ID, Patient ID, and Local ID on each page.
- TypeStream Visual version, IMGT library version, catalog used
- Analysis and confirmation date and user
- Path to raw file
- Final Assignment Table
- Final Allele Code
- Genotyping (including ambiguities)
- Statistics per barcode and locus
- Analysis parameters with configuration name
- System and user comments
- Lab information details in the footer that includes the regulatory mode

Clicking "Export Report" from the reports page will bypass the preview stage and directly open a navigation page where you may name and save your report, either in the file path set in General Settings or in a separate location of your choosing.

If "1 Sample Per Report" is selected, the text entered will serve as a prefix to sample names to complete a full file name. Example: I have selected two sessions, sample names "TER123" with barcode 18 and "9132" with barcode 24. On the navigation page I enter the text "FP"; the two files created will be "FP_TER123_18" and "FP_9132_24."

Genotype Summary Table .csv

To create a Genotype Summary .csv report, click NGS and select Genotype Summary Table (.csv).

- Select sessions from session grid.
- Click Export Report

CSV Report is created. You will be asked to enter a report name and then save. You have the

option to browse to a different folder to save the report.

- Final assignment displays with the number of fields selected, as well as in full nomenclature.
- Session name, Sample ID barcode, Locus
- K/N/I values per allele
- Name and date for analysis and confirmation
- Number of ambiguities
- Possible allele assignment and g/l string
- Final assignment definition
- User comments display for every locus
- Notes 1 and Notes 2 columns

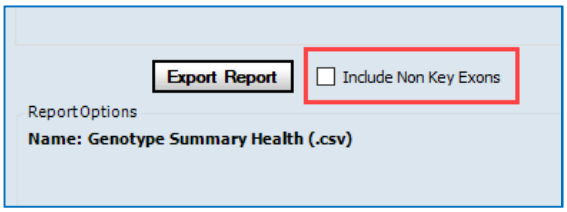
Genotype Summary Health .csv

The Genotype Summary Health report (.csv) is a compilation of the health statistics from the Coverage Stats and Health Stats tabs on the analysis page.

Session Name	Sample ID	Barcode	Locus	Uniformity	Allele Balance	Key Exon Coverage	Exon Mismatches	Unexpected Linkage	Mismatch in Intron	Homozygous Result	Break in Phase	Null Allele Result	High Backgrou nd in Exon	Ambig Count Allele1
TSV_20200313153923	eenie	49	A	Pass	Pass	Fail	Pass	Pass	Pass	Pass	Fail	Pass	Pass	1
TSV_20200313153923	eenie	49	B	Pass	Pass	Pass	Pass	Pass	Fail	Pass	Pass	Pass	Fail	2
TSV_20200313153923	eenie	49	C	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	1

High ckgrou d in Exon	Ambiguity Count Allele1	High Background Count Allele1	High BackGround Non Homopolymer Count Allele1	Ambiguity Count Allele2	High Background Count Allele2	High BackGround Non Homopolymer Count Allele2	Exon 2 Min Depth	Exon 2 Max Depth	Exon 3 Min Depth	Exon 3 Max Depth	Exon 4 Min Depth	Exon 4 Min Depth
Pass	1	4	4	1	6	4	44	133	81	172	193	330
Fail	2	7	7	1	8	6	60	124	89	207	226	325
Pass	1	8	6	1	8	7	80	163	90	211	310	418

User may include Non-Key Exons by checking the checkbox prior to exporting the report.



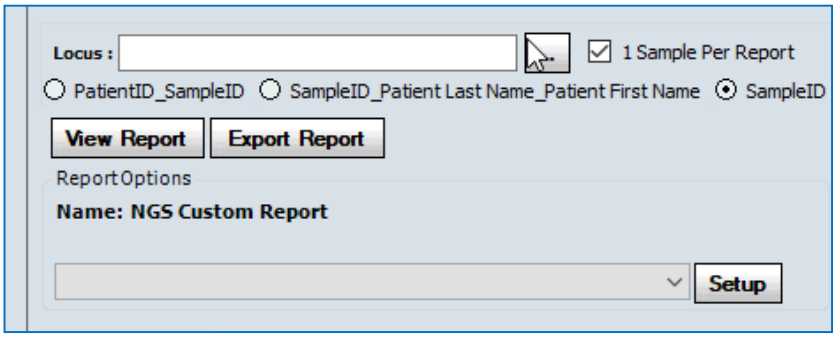
When this is selected, report will include Min and Max Depth columns for all exons.

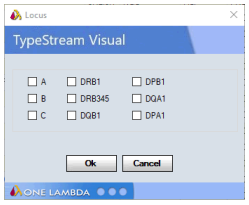
ol	Exon 1 Min Depth	Exon 1 Max Depth	Exon 2 Min Depth	Exon 2 Max Depth	Exon 3 Min Depth	Exon 3 Max Depth	Exon 4 Min Depth	Exon 4 Max Depth	Exon 5 Min Depth	Exon 5 Max Depth	Exon 6 Min Depth	Exon 6 Max Depth	Exon 7 Min Depth	Exon 7 Max Depth	Exon 8 Min Depth	Exon 8 Max Depth
4	163	189	44	133	81	172	193	330	218	269	369	393	356	385	347	347
6	122	143	60	124	89	207	226	325	181	244	267	306	242	289		
7	157	192	80	163	90	211	310	418	343	369	387	416	378	405	504	514
3	0	0	543	700	911	1789	0	137	0	0	0	0				
5	0	0	128	168	529	687	0	53	0	0	0	0				

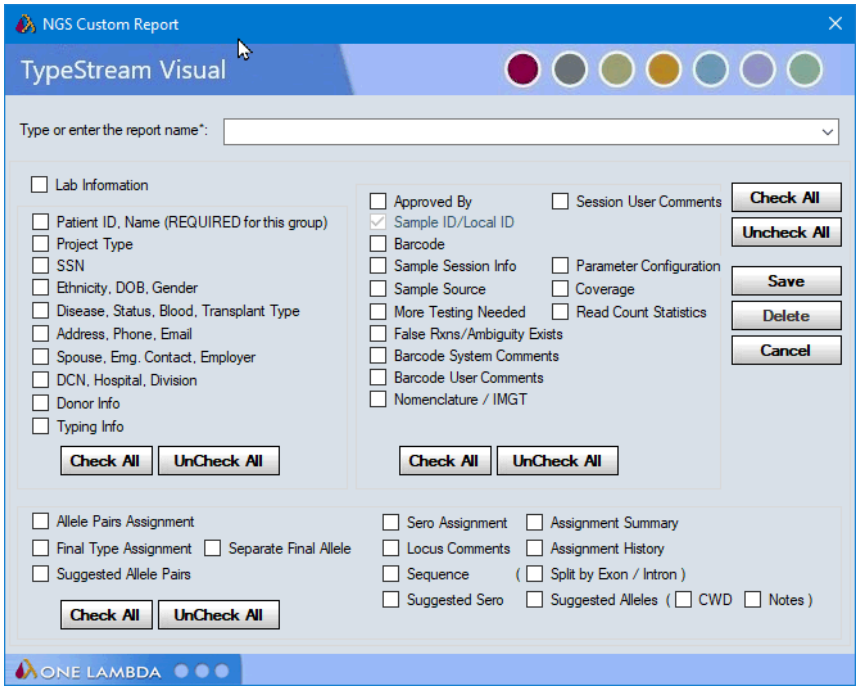
NGS Custom Report

User may create a customized report to suit the needs of the lab. TypeStream Visual can keep numerous uniquely-named report templates ready for use at any time. Data for inclusion may be selected individually or by groups Genotyping, Session Information, and Patient Information.

Multiple options display at the top of NGS Custom Report page.



Item	Description
Locus:	User may select which loci to include in the report. Click ellipsis to display selection. Selected loci display in the 'Locus:" text field. Leaving the field blank will include all loci. 
1 Sample Per Report	When selected, all samples will receive an individual report, independently paginated and numbered.
o PatientID_SampleID o SampleID_Patient_Last Name_Patient First Name o SampleID	1. Default selection is "Sample ID- when report exported, the text entered will serve as a prefix to sample names to complete a full file name. 2. SampleID_Patient_Last Name_Patient First Name - when report exported, the text entered will serve as a prefix to sample name_Patient Last Name_Patient First name to complete a full file name (if Patient is associated with sample) 2. PatientID_SampleID - when report exported, the text entered will serve as a prefix to PatientID_Sample name to complete a full file name (if Patient is associated with sample)
View Report	This button allows the user to view the report prior to exporting it.
Export Report	This button will immediately create and export the report. The user must give the report a name before it is saved.
Setup	This button allows the full customization of the report through templates (see section below). Multiple templates may be saved.



There are additional options for the NGS Custom Report:

- Parameter Configuration – shows the parameters used in the analysis and the configuration name
- Coverage – will include the coverage histogram
- Read Count Statistics – Displays the Mapped Reads, Total Reads and %Mappability at the locus level
- Separate Final Allele – if checked, the final assigned is reported in two columns with a larger font size of 12pt.
- Sequence – will display the genetic sequence in the report
- Split by Exon/Intron – when Sequence is selected, it will appear as a single sequence unless this option is selected, which divide the sequence into specific regions.
- Suggested Alleles– Displays the possible / computer suggested alleles in a table format.
- CWD – if the sample is saved in a demographic filter, the suggested alleles table displays the demographic configuration name and if each of the allele is either a c(common), wd (well documented) or as r(rare). If a session was analyzed using a CIWD filter each of the allele is either a c(common), wd (well documented) , i(intermediate) or r(rare).
- Notes – Adds Notes 1 and Notes 2 columns to the suggested alleles table.
- Lab information details in the footer that includes the regulatory mode

New in v3.0

There are a few additional options and behaviors for the NGS Custom Report:

- Security Masking – When reports are displayed or printed, for security, digits of SSN are masked with X and only the last four digits of SSN are visible.

In the Setup screen, there are new and renamed options:

- Session User Comments – if data was entered into the Session Summary Comments for a session, it will be included in the report.
- Barcode System Comments – Was named "system comments" in prior versions of TypeStream. Renamed to distinguish it from Session User Comments.
- Barcode User Comments – Same as "user comments" option in prior versions of TypeStream.
- Coverage – formerly named "Typing Histogram" in prior versions of TypeStream.
- Assignment History – adds a history of assignments made by lab personnel to the report. When the checkbox is set, the report outputs a table containing Assignment History ordered by locus and assignment actions done.

Assignment History output in the NGS Custom Report

Assignment History:

Locus	Assignment History
A	Assigned by 1 at: 11:18 AM 3/2/2022 Review status changed by 1 at: 11:18 AM 3/2/2022
B	Assigned by 1 at: 11:18 AM 3/2/2022
C	Assigned by 1 at: 11:18 AM 3/2/2022 Review status changed by 1 at: 11:18 AM 3/2/2022 Confirm status changed by 1 at: 11:19 AM 3/2/2022
DRB1	Review status changed by 1 at: 11:20 AM 3/2/2022 Confirm status changed by 1 at: 11:20 AM 3/2/2022
DRB345	Assigned by 1 at: 11:20 AM 3/2/2022 Assigned by 1 at: 11:20 AM 3/2/2022
DQA1	
DQB1	
DPA1	
DPB1	

Locus	RefName	Length	Sequence
A	A*03:01:01:01	3914	UTR5: 0-300 CAGGAGCAGAGGGGTCAGGGCGAAG TATGGATTGGGGAGTCCCAGCCTTG GGTCCTTCATCCTGGATACTCACGA

New in v3.0

G group (or P Group) definitions are now displayed in the NGS custom report similarly to how they are displayed on the Final Allele Assignment area. Earlier versions of the software did not show the definitions, which should be in the same format for G Group, P Group, and NMDP.

Approved By: **Date:**

Final Assignment:

Locus	Allele Assignment	Final Assignment	Sero	Reviewed By	Confirmed By	User Comments
A	A*02:01:01:01 A*02:05:01:01	A*02:01P A*02:05P A*02:01P=:02:01:01:01 A*02:05P=:02:05:01:01	A2 A2	1, 10/11/2021		
B	B*15:17:01:03 B*58:01:01:01	B*15:17:01G B*58:01:01G B*15:17:01G=:15:17:01:03 B*58:01:01G=:58:01:01:01	B63 B58	1, 10/11/2021		
C						

Session Summary content

If "1 Sample Per Report" is selected, the text entered will serve as a prefix to sample names to complete a full file name. Example: I have selected two sessions, sample names "TER123" with barcode 18 and "9132" with barcode 24. On the navigation page I enter the text "FP"; the two files created will be "FP_TER123_18" and "FP_9132_24."

Final typing information will display in a grid format like that of the Genotype Summary Report (.pdf).

Final Assignment:

Locus	Allele Assignment	Final Assignment	Sero	Saved By	Confirmed By	User Comments
A	A*02:10 A*11:02:01	A*02:10 A*11:02:01	A210 A11	Daniel, 03/17/2020	TJ, 03/17/2020	
B	B*40:01:02:01 B*46:01:01/B*40:01:02:04 B*46:01:01	B*40:01:02:01/40:01:02:04 B*46:01:01	B60 B46	Daniel, 03/17/2020	TJ, 03/17/2020	
C	C*07:02:01:15 C*08:01:01:01	C*07:02:01:15 C*08:01:01:01	Cw7 Cw8	Daniel, 03/17/2020	TJ, 03/17/2020	
DRB1	DRB1*08:03:02:01 DRB1*09:01:02:01/DRB1*08:03:02:02 DRB1*09:01:02:01	DRB1*08:03:02 DRB1*09:01:02	DR8 DR9	Daniel, 03/17/2020	TJ, 03/17/2020	
DRB345	DRB4*01:03:02 DRB4*01:03:02	DRB4*01:03:02 DRB4*01:03:02	DR53 DR53	Daniel, 03/17/2020	TJ, 03/17/2020	
DQB1	DQB1*03:03:02:02 DQB1*06:01:01:01/DQB1*03:398 DQB1*06:01:01:01	DQB1*03:03:02/03:398 DQB1*06:01:01	DQ9 DQ6	Daniel, 03/17/2020	TJ, 03/17/2020	
DPB1	DPB1*135:01 DPB1*834:01	DPB1*135:01 DPB1*834:01	DPw- DPw-	Daniel, 03/17/2020		Two or more variants cannot be phased. Mismatch(es) in an intron. Two or more variants cannot be phased. Mismatch(es) in an intron.

LRP Genotype Summary .pdf

When this option is selected from the dropdown, only LRP sessions will display on the screen for selection.

See section 'Genotype Summary.pdf' above for the description of the complete functionality for this report.

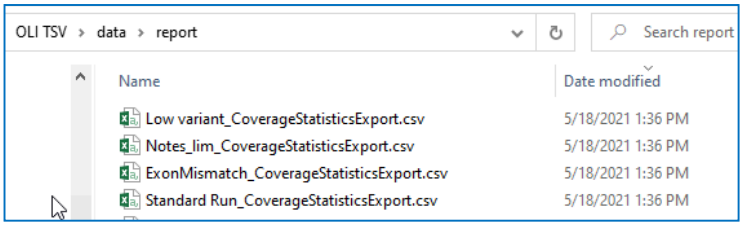
Coverage Statistics Report

Mapped Read Metrics and Locus Coverage as displayed on the Statistics tab of the Analysis Panel can be output into a .csv report. Select eligible sessions from the grid on the reports main page after selecting 'Coverage Statistics' from the NGS dropdown and click Export Report. Report will be created and saved in the location saved in General Settings. Default path is C:\OLI TSV\data\report. Generating the report will take a few moments; TSV will confirm that the report was saved.

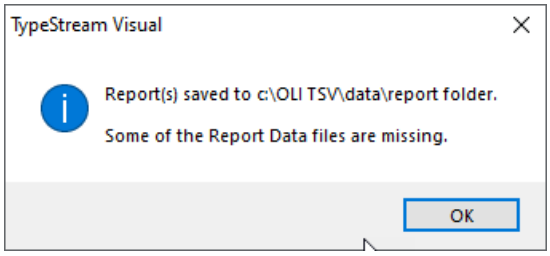
	A	B	C	D	E	F	G	H	I	R	S	T	U	V
1	Barcode	Sample	Locus	Metric	All	UTR5	E-1	I-1	E-2	I-6	E-7	I-7	E-8	UTR3
2	60	Sc	A	average_allele_balance	0.74	0.432	0.558	0.74	0.	0.6 NA	NA	0.921	NA	0.572
3	60	Sc	A	min_coverage	0	77	52	43	28	271	308	298	273	276	0
4	60	Sc	A	average_coverage	132	102	67	48	49	285	319	312	295	277	171
5	60	Sc	A	detected_variants	127	4	2	9	4	2	0	0	8	0	2
6	60	Sc	A	max_coverage	335	134	80	63	6	296	335	323	323	278	285
7	60	Sc	A	bases_covered	99%	100%	100%	100%	100	.%	100%	100%	100%	100%	99%
8	60	Sc	B	average_allele_balance	0.785	0.816	0.609	0.687	0.88		0.532	0.532	NA	NA	0.985
9	60	Sc	B	min_coverage	0	64	59	49		120	108	118	NA	NA	0
10	60	Sc	B	average_coverage	102	87	66	53		126	112	131	NA	NA	125
11	60	Sc	B	detected_variants	89	15	4	5		0	1	1	NA	NA	11
12	60	Sc	B	max_coverage	220	108	71	60		131	123	140	NA	NA	220
13	60	Sc	B	bases_covered	96%	100%	100%	100%	100	0%	100%	100%	NA	NA	96%
14	60	Sc	C	average_allele_balance	0.89	0.917	0.859	0.833	0.86		0.841	0.735	0.913	NA	0.897

ExonMismatch_CoverageStatistics

If multiple files are selected, a separate file will be created for each session. The naming convention used is [SessionName]_CoverageStatisticsExport.csv.



If the selected session's NGS output folder is not in the right location, the below message will appear.



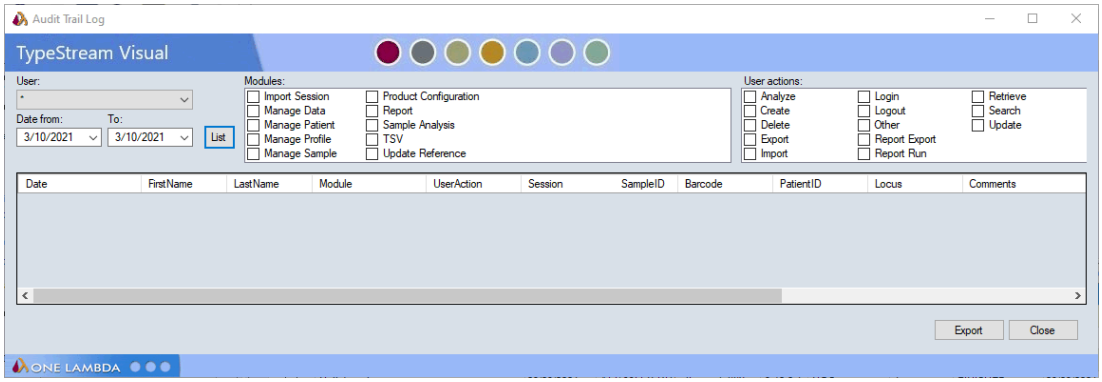
Audit Trail Log

You can view and print a report of user activity for the current database. This data is only available if you have done the following:

- Set up and connected to an audit trail database using the TSV database utility
- Enabled Audit Logging from TSV General Settings

Once you have completed the above, to view audit log data, take the following steps:

1. Access the Reports window in one of two ways:
   - From the home page, click Reports icon.
   - From the main menu options, select Reports.
2. Select NGS > Audit Trail Log. The Audit Trail Log dialog box displays.



3. Use the drop-down arrow to select the User for whom you want to see database actions.
4. Select the date range and options you want the report to include.
5. Click List to see the report. If you want to export the audit trail report to Excel, click Export.

Specialty Reports

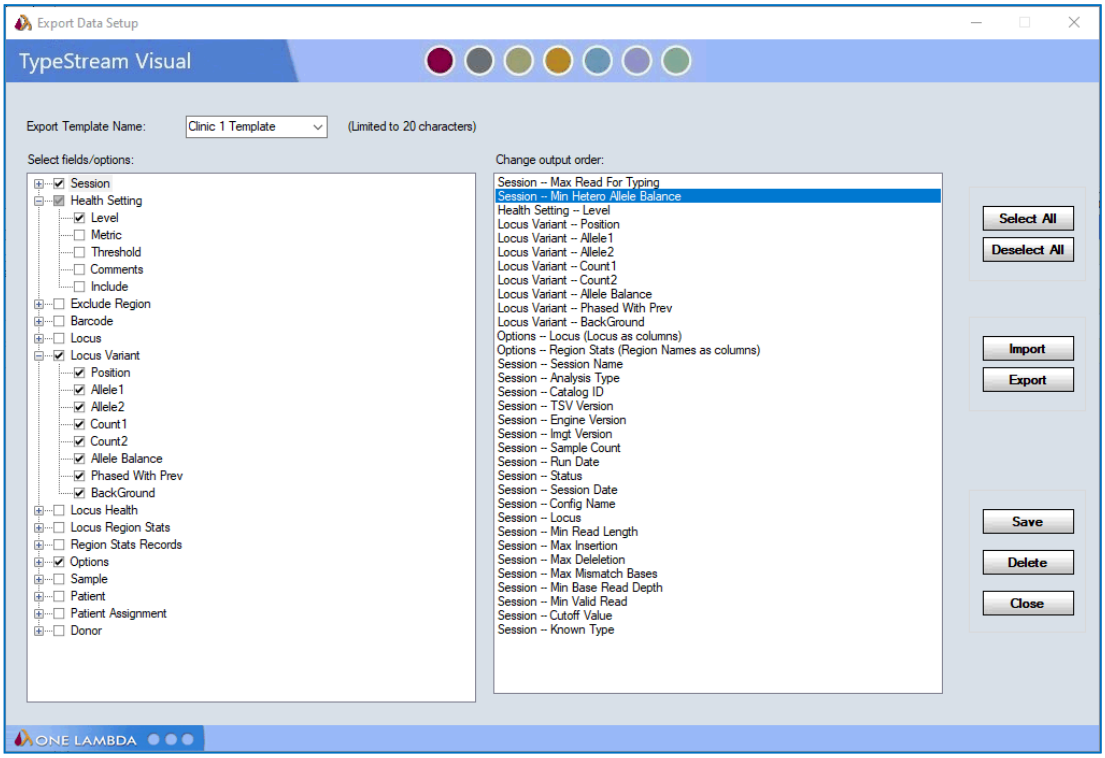
Export Data

The user has the ability to export data in a variety of combinations to suit a particular need, and to save the template in repository for future use.

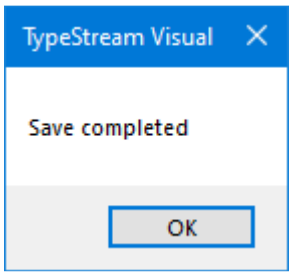
In the Export Data Setup window user may create a template name of up to 20 characters, then select the data desired. The output order can be changed to user's preference by using a simple drag-and-drop.

Once created, the template can be modified by adding or removing any of the output options. The template can also be exported for use on other systems.

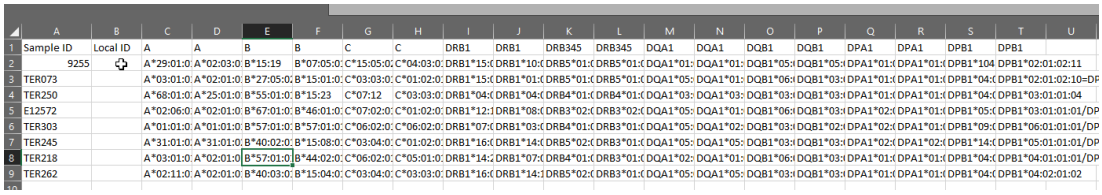
Additionally, the user can import template from other systems. Any saved or imported template can be deleted using the Delete button.



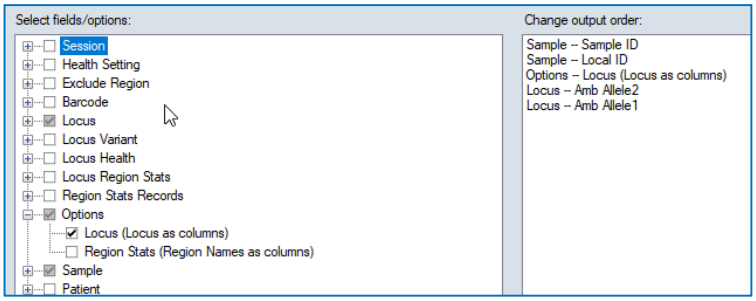
When satisfied with the template setup, click Save. The software will then acknowledge the save. The default save location is C:\OLI TSV\data\export



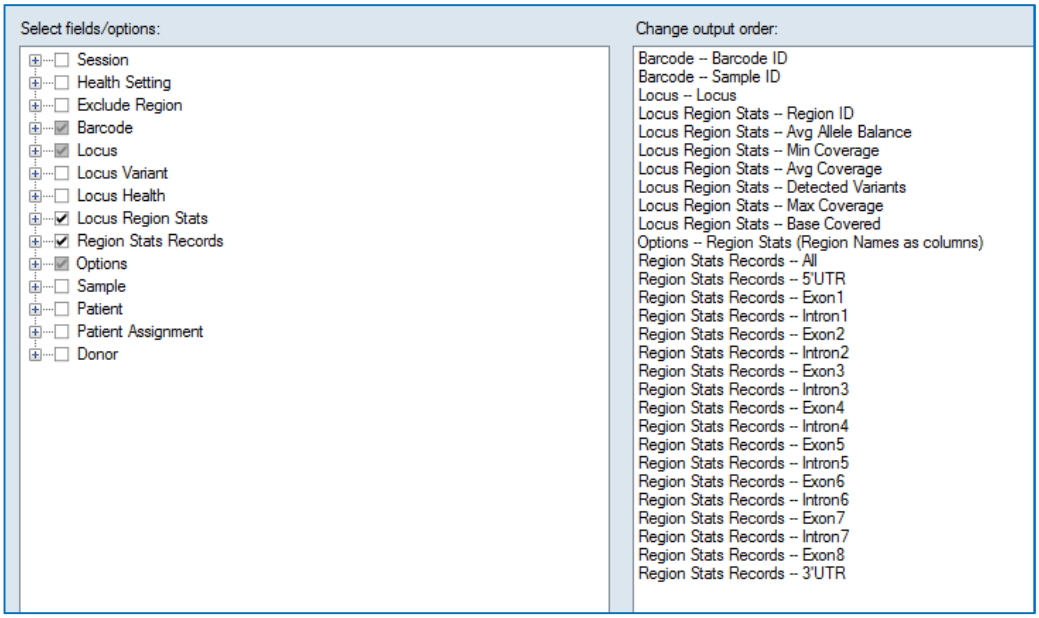
The option to display "Locus as columns" can be used to generate a quick export report as below –



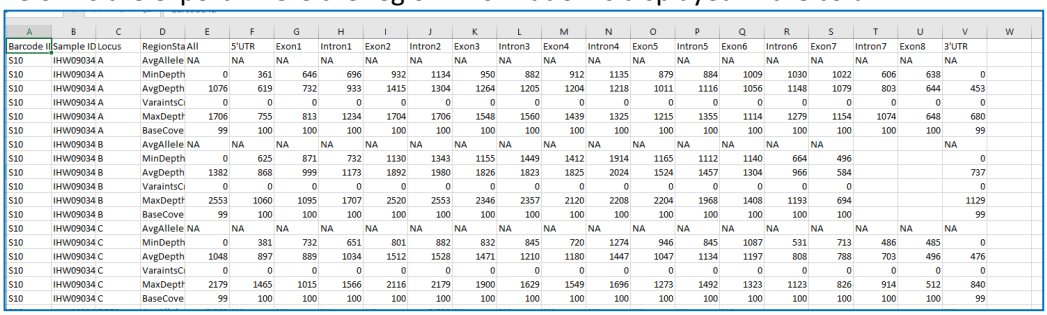
	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U
1	Sample ID	Local ID	A	A	B	B	C	C	DRB1	DRB1	DRB345	DRB345	DQA1	DQA1	DQB1	DQB1	DPA1	DPA1	DPB1	DPB1	
2	9255		A*29:01:0	A*02:03:0	B*15:19	B*07:05:0	C*15:05:0	C*04:03:0	DRB1*15:	DRB1*10:	DRB5*01:	DRB5*01:	DQA1*01:	DQA1*01:	DQB1*05:	DQB1*05:	DPA1*01:	DPA1*01:	DPB1*104	DPB1*02:01:02:11	
3	TER073		A*03:01:0	A*02:01:0	B*27:05:0	B*15:01:0	C*03:03:0	C*01:02:0	DRB1*15:	DRB1*01:	DRB5*01:	DRB5*01:	DQA1*05:	DQA1*01:	DQB1*06:	DQB1*03:	DPA1*01:	DPA1*01:	DPB1*04:	DPB1*02:01:02:10=DF	
4	TER250		A*68:01:0	A*25:01:0	B*55:01:0	B*15:23	C*07:12	C*03:03:0	DRB1*04:	DRB1*04:	DRB4*01:	DRB4*01:	DQA1*03:	DQA1*03:	DQB1*03:	DQB1*03:	DPA1*01:	DPA1*01:	DPB1*04:	DPB1*03:01:01:04	
5	E12572		A*02:06:0	A*02:01:0	B*67:01:0	B*46:01:0	C*07:02:0	C*01:02:0	DRB1*12:	DRB1*08:	DRB3*02:	DRB3*02:	DQA1*05:	DQA1*01:	DQB1*06:	DQB1*03:	DPA1*02:	DPA1*01:	DPB1*05:	DPB1*03:01:01:01/DP	
6	TER303		A*01:01:0	A*01:01:0	B*57:01:0	B*57:01:0	C*06:02:0	C*06:02:0	DRB1*07:	DRB1*03:	DRB4*01:	DRB3*01:	DQA1*05:	DQA1*02:	DQB1*03:	DQB1*02:	DPA1*02:	DPA1*01:	DPB1*09:	DPB1*06:01:01:01/DP	
7	TER245		A*31:01:0	A*31:01:0	B*40:02:0	B*15:08:0	C*03:04:0	C*01:02:0	DRB1*16:	DRB1*14:	DRB5*02:	DRB3*01:	DQA1*05:	DQA1*05:	DQB1*03:	DQB1*03:	DPA1*02:	DPA1*02:	DPB1*14:	DPB1*05:01:01:01/DP	
8	TER218		A*03:01:0	A*02:01:0	B*57:01:0	B*44:02:0	C*06:02:0	C*05:01:0	DRB1*14:	DRB1*07:	DRB4*01:	DRB3*01:	DQA1*02:	DQA1*01:	DQB1*06:	DQB1*03:	DPA1*01:	DPA1*01:	DPB1*04:	DPB1*04:01:01:01/DP	
9	TER262		A*02:11:0	A*02:01:0	B*40:03:0	B*15:04:0	C*03:04:0	C*03:03:0	DRB1*16:	DRB1*14:	DRB5*02:	DRB3*01:	DQA1*05:	DQA1*05:	DQB1*03:	DQB1*03:	DPA1*01:	DPA1*01:	DPB1*04:	DPB1*04:02:01:02	



Region Stats option allows user to configure the export that displays the Region Names as columns.



Below is the export where the region information is displayed in the column.

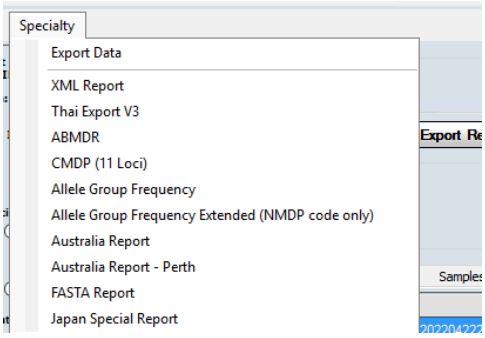


Barcode II	Sample ID	Locus	RegionSta	All	5'UTR	Exon1	Intron1	Exon2	Intron2	Exon3	Intron3	Exon4	Intron4	Exon5	Intron5	Exon6	Intron6	Exon7	Intron7	Exon8	3'UTR
S10	IHW09034	A	AvgAllele	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
S10	IHW09034	A	MinDepth	0	361	646	696	932	1134	950	882	912	1135	879	884	1009	1030	1022	606	638	0
S10	IHW09034	A	AvgDepth	1076	619	732	933	1415	1304	1264	1205	1204	1218	1011	1116	1056	1148	1079	803	644	453
S10	IHW09034	A	VaraintsCi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S10	IHW09034	A	MaxDepth	1706	755	813	1234	1704	1706	1548	1560	1439	1325	1215	1355	1114	1279	1154	1074	648	680
S10	IHW09034	A	BaseCove	99	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	99
S10	IHW09034	B	AvgAllele	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA			NA
S10	IHW09034	B	MinDepth	0	625	871	732	1130	1343	1155	1449	1412	1914	1165	1112	1140	664	496			0
S10	IHW09034	B	AvgDepth	1382	868	999	1173	1892	1980	1826	1823	1825	2024	1524	1457	1304	966	584			737
S10	IHW09034	B	VaraintsCi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			0
S10	IHW09034	B	MaxDepth	2553	1060	1095	1707	2520	2553	2346	2357	2120	2208	2204	1968	1408	1193	694			1129
S10	IHW09034	B	BaseCove	99	100	100	100	100	100	100	100	100	100	100	100	100	100	100			99
S10	IHW09034	C	AvgAllele	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
S10	IHW09034	C	MinDepth	0	381	732	651	801	882	832	845	720	1274	946	845	1087	531	713	486	485	0
S10	IHW09034	C	AvgDepth	1048	897	889	1034	1512	1528	1471	1210	1180	1447	1047	1134	1197	808	788	703	496	476
S10	IHW09034	C	VaraintsCi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S10	IHW09034	C	MaxDepth	2179	1465	1015	1566	2116	2179	1900	1629	1549	1696	1273	1492	1323	1123	826	914	512	840
S10	IHW09034	C	BaseCove	99	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	99

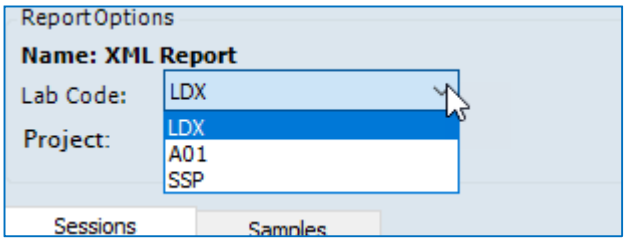
Note: for this option the region stats records field must be selected.

Genotype Summary XML Report

To create an XML report, click Specialty and select XML Report.



Select the desired Lab Code from the dropdown.



Select sessions to include as explained above.

Click Export Report

The XML report is created. You will be asked to enter a report name and then save. You have the option to browse to a different folder to save the report.

Please note that session must be **saved** with a final assigned type before the XML Report (.xml) can be run.

The illustration below shows the first part of the .xml file displayed in Notepad ++. Schemas are clearly displayed along with Project Name, sample name and barcode, name and version number of TypeStream Visual application, IMGT library version used, and additional data as needed.

Please note the following:

1. Reporting center ID will display as three digits. If actual lab code is longer, it will be truncated. If the actual lab code is short, the remainder will be filled in by trailing '0's.
2. If collected method is not included in the original session information, 'BUCCAL SWAB' will be inserted by default.
3. The allele-version field will be truncated to 3 fields to represent the IMGT version of the HLA Library file
4. If there is no final assignment assigned to a locus of a sample, the typing section for that locus is skipped
5. Haploid type represents the preliminary computer assignment. In case of cis-trans ambiguity both the genotypes are reported.
6. All the phase breaks are recorded in case of the cis-trans ambiguity results

```
- <allele-assignment date="2021-04-29" allele-version="3.43.0" allele-db="IMGT/HLA">
      <haploid type="09:01:01/463:01:01" method="DNA" locus="HLA-DPB1"/>
      <haploid type="105:01:01/899:01" method="DNA" locus="HLA-DPB1"/>
      <glstring>HLA-DPB1*09:01:01/463:01:01+HLA-DPB1*105:01:01/899:01</glstring>
  </allele-assignment>
- <typing-method>
    - <sbt-ngs locus="HLA-DPB1" test-id-source="1" test-id="NGS">
        <raw-reads quality-trimmed="true" adapter-trimmed="true" pooled="true" paired="true" format="gz.fastq" uri="D:\tsv data files\fas
          HL\TER389_S1_L001_R1_001.fastq.gz"/>
      </sbt-ngs>
  </typing-method>
- <consensus-sequence date="2021-04-29">
    - <reference-database name="IMGT/HLA" availability="public">
        <reference-sequence name="HLA-DPB1*105:01:01:01" id="Ref9" strand="+" end="11616" start="0"/>
        <reference-sequence name="HLA-DPB1*09:01:01" id="Ref10" strand="+" end="11616" start="0"/>
      </reference-database>
    - <consensus-sequence-block end="1509" start="207" continuity="true" phase-set="1" reference-sequence-id="Ref10">
        <sequence>CAGTGTCCATTGGTTCTTTTCTCAGACTCTGTCCAATCCCAGGGTCACAGAAGACTACTTGGGTTCATGGTCTCTAATATTTCAAACA
      </consensus-sequence-block>
    - <consensus-sequence-block end="1509" start="192" continuity="true" phase-set="2" reference-sequence-id="Ref9">
        <sequence>GACTCATACAAAGCTCAGTGTCCATTGGTTCTTTTCTCAGACTCTGTCCAATCCCAGGGTCACAGAAGACTACTTGGGTTCATGGTC
      </consensus-sequence-block>
    - <consensus-sequence-block end="2115" start="1513" continuity="true" phase-set="3" reference-sequence-id="Ref10">
        <sequence>TTGTCCTTGCAATAGTTTGCTGTGAATGATGGTTTCCAGCTTCCTCCATGTCCCTACAAAGGACATGAACTCATCCTTTTTTATGGCT
      </consensus-sequence-block>
    - <consensus-sequence-block end="2115" start="1513" continuity="true" phase-set="4" reference-sequence-id="Ref9">
        <sequence>CTGTCCTTGCAATAGTTTGCTGTGAATGATGGTTTCCAGCTTCCTCCATGTCCCTACAAAGGACATGAACTCATCCTTTTTTATGGCT
      </consensus-sequence-block>
    - <consensus-sequence-block end="5021" start="2115" continuity="true" phase-set="5" reference-sequence-id="Ref10">
        <sequence>GAAGGTACTGACATCATGTCACCTCCTCATCTTTCAGGGTAGCAAGGTTGGAATCTCCTGAATACAGCCCCTCAAGCCCTAAAACCT
      </consensus-sequence-block>
    - <consensus-sequence-block end="5022" start="2115" continuity="true" phase-set="6" reference-sequence-id="Ref9">
        <sequence>AAAGGTACTGACATCATGTCACCTCCTCATCTTTCAGGGTAGCAAGGTTGGAATCTCCTGAATACAGCCCCTCAAGCCCTAAAACCT
      </consensus-sequence-block>
    - <consensus-sequence-block end="6544" start="5022" continuity="true" phase-set="7" reference-sequence-id="Ref10">
        <sequence>GTGCACCAGTTACGGCAGGAATGCTACGCGTTTAATGGGACACAGCGCTTCCTGGAGAGATACATCTACAACCGGGAGGAGTTCGT
      </consensus-sequence-block>
    - <consensus-sequence-block end="6544" start="5022" continuity="true" phase-set="8" reference-sequence-id="Ref9">
        <sequence>CTTTTCCAGGGACGGCAGGAATGCTACGCGTTTAATGGGACACAGCGCTTCCTGGAGAGATACATCTACAACCGGGAGGAGTTCGT
      </consensus-sequence-block>
    - <consensus-sequence-block end="10615" start="6582" continuity="true" phase-set="9" reference-sequence-id="Ref10">
        <sequence>GTAATGCAATTGGCAAAAACTGTTACTAAGACTTTGTAGAGGCACAAATCAGTGACACGGCAGCATCTTCTTTCACAGTAATCAACT
      </consensus-sequence-block>
    - <consensus-sequence-block end="10687" start="6582" continuity="true" phase-set="10" reference-sequence-id="Ref9">
        <sequence>ATAACGCAATTGGCAAAAACTGTTACTAAGACTTTGTAGAGGCACCAATCAGTGACATGGCAGCATTTTCTTTCACAGTAATCAACT
      </consensus-sequence-block>
  </consensus-sequence>
/typing>
```

CMDP (11 Loci) Specialty Report

To create a CMDP (Chinese Marrow Donor Program) specialty report, from the reports page select Specialty and select "CMDP (11 loci)." Select session(s) to include as explained above.

Click Export Report. Report is created in Microsoft Excel format. You will be asked to enter a

report name and then save. You have the option to browse to a different folder to save the report.

CMDP Specialty report contains the following per locus/sample:

- Sample name
- Assigned allele code
- Possible allele pairs
- Code definition
- Assigned serology
- Assigned allele pairs
- User who approved and confirmed the locus and date
- Resolution
- Locus and sample user comments

Note that "Resolution" column is blank by default. User may manually fill in the resolution value and save.

Australia Specialty Report

To create Australia Specialty Report, select Specialty and Select Australia Report. Select session(s) to include as explained above. Click Export Report.

- A separate .csv report will be generated for each session, irrespective of the number selected.
- Each report title will follow the naming convention "TSVExport_[session name]_[date].csv"
- Final genotype and final allele code will be displayed without locus designation or "*" and will display the selected fields only. For DRB345, display shall be "3*xx.xx," "4*xx.xx," and "5*xx.xx" respectively.
- It is recommended to open this report in a text reader, such as Notepad or Notepad++.
- If you want to make adjustments and rerun the report, be aware that the it will overwrite the first copy, if rerun on the same date. To keep both copies, rename the first before running the second.
- Australia Specialty report contains the following per locus/sample:

Session Name	Sample ID
Patient ID	Barcode
Locus	Analysis date and user
Locus User comments	Allele Code Assignment for each allele
Final assignment for each allele	Confirmation date and user
Overall user comments	

Australia Report - Perth

To create Australia Report-Perth, select Specialty and Select Australia Report-Perth. Select session(s) to include as explained above. Click Export Report.

- A separate .csv report will be generated for each session, irrespective of the number selected.
- Each report title will follow the naming convention "AustraliReportPerth_TSVExport_[session name]_[date].csv"
- Display Allele 1 first digit for Allele_B1 column and Allele 2 first digit for Allele_B2 column.
- Display Allele 1 possible allele pairs for Allele_S1 and Allele 2 possible allele pairs for Allele_S2.

Related to the Australia Report, in the Perth report each row represents a genotype for a sample. If the sample has two genotypes, each row has a genotype row. If either Consensus_1 or Consensus_2 contains "N" value for a base that is not covered, the "N" is replaced with a space.

barcode	sampleid name	Locus	Library Date	file	Allele_B1	Allele_B2	Allele_S1	Mismatch_key_exons_allele1	Mismatch_non_key_exons_allele1	Mismatch_introns_allele1	Allele_S2
S5	Sample13	A	3.37.0.1	THX1138	2	11	02:06:01:01 or 02:06:01:03	0	0	0	11:01:01
S5	Sample13	B	3.37.0.1	THX1138	13	27	13:01:01:01 or 13:01:01:02	0	0	0	27:03 or 2
S5	Sample13	C	3.37.0.1	THX1138	4	12	04:03:01:01 or 04:107 or 0	0	0	0*	12:02:02
S5	Sample13	DRB	3.37.0.1	THX1138	11	3	11:01:35 or 11:31 or 12:01	0	0	0	03:06 or 0
S5	Sample13	DRB3	3.37.0.1	THX1138	3		03:01:03:01 or 03:01:03:02	0	0	0	
S5	Sample13	DRB5	3.37.0.1	THX1138	1		1:02	0	0	0	
S5	Sample13	DQB	3.37.0.1	THX1138	3	5	03:01:01:12 or 03:01:08 or	0	0	0	05:01:03 o
S5	Sample13	DPA	3.37.0.1	THX1138	2	2	02:01:01:01 or 02:01:01:06	0	0	1	02:02:02:0
S5	Sample13	DPB	3.37.0.1	THX1138	5	107	05:01:01:01 or 05:01:01:02	0	0	0	107:01
S5	Sample13	DPB	3.37.0.1	THX1138	1034	112	1034:01 or 107:01 or 117:0	0	0	1	112:01 o
S5	Sample13	DPB	3.37.0.1	THX1138	206	206	206:01 or 438:01 or 519:01	0	0	0*	206:01

Mismatch_introns_allele1	Allele_S2	Mismatch_key_exons_allele2	Mismatch_non_key_exons_allele2	Mismatch_introns_allele2	NMDP1	NMDP2	G1	G2	Consensus_1	Consensus_2
0	11:01:01:01 or 11:01:01:04	0	0	0	02:XX1	11:XX2				CAG
0	27:03 or 27:04:01 or 27:05:	0	0	0*	13:XX1	27:XX2				
0*	12:02:02:01 or 12:02:02:03	0	0	0*	04:XX1	12:XX2			TTATTTTGCTG	TTATTTTGCTGGATGTA
0	03:06 or 03:07:01 or 03:10	0	0	0*	03:XX1/08:X	11:CWA/12:XX2/13:AVU/11:EH				
0					3:01					
0					1:02					
0	05:01:03 or 05:01:05 or 05:	0	0	0	03:XX1	05:XX2				
1	02:02:02:01 or 02:02:02:02	0	0	0	02:01:01/02	02:02:02/02:14				
0	107:01 or 117:01 or 13:01:0	0	0	0	206:01:00	206:01/438:01/519:01/609:01/9				
1	112:01 or 333:01 or 563:01	0	0	0	206:01:00	206:01/438:01/519:01/609:01/9				
0*	206:01 or 438:01 or 519:01	0	0	0*	206:01:00	206:01/438:01/519:01/609:01/9				

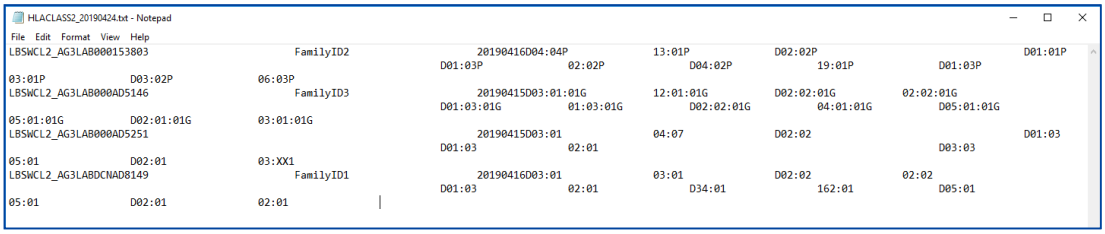
Thai Export V3 Specialty Report

Thai specialty report exports data for a single sample or multiple samples into a text file. Each sample occupies a single row in the file. The first 'field' indicates a standard descriptor with merged metadata following.

HLACLASS1_20190424.txt - Notepad

File Edit Format View Help

```
LBSWCL1_AG3LAB000153803     FamilyID2     20190416D29:02P     31:01P     D15:01P     44:03P
D03:03P     16:01P
LBSWCL1_AG3LAB000AD5146     FamilyID3     20190415D30:02:01G     68:01:02G     D18:01:01G     35:03:01G
D04:01:01G     05:01:01G
LBSWCL1_AG3LAB000AD5251     20190415D02:01     30:02     D07:02     08:01
D07:02     07:18
LBSWCL1_AG3LABDCNAD8149     FamilyID1     20190416D02:01     23:01     D15:17     44:03
D04:01     05:01
```



```
HLACLASS2_20190424.txt - Notepad
File  Edit  Format  View  Help
LBSWCL2_AG3LAB000153803                    FamilyID2                20190416D04:04P          13:01P          D02:02P                                  D01:01P
                                                                D01:03P          02:02P          D04:02P          19:01P          D01:03P
03:01P          D03:02P          06:03P
LBSWCL2_AG3LAB000AD5146                    FamilyID3                20190415D03:01:01G       12:01:01G       D02:02:01G       02:02:01G
                                                                D01:03:01G       01:03:01G       D02:02:01G       04:01:01G       D05:01:01G
05:01:01G       D02:01:01G       03:01:01G
LBSWCL2_AG3LAB000AD5251                                            20190415D03:01           04:07           D02:02                                   D01:03
                                                                D01:03           02:01                                            D03:03
05:01           D02:01           03:XX1
LBSWCL2_AG3LABDCNAD8149                    FamilyID1                20190416D03:01           03:01           D02:02           02:02
                                                                D01:03           02:01           D34:01           162:01          D05:01
05:01           D02:01           02:01
```

In the example above, find the following:

"LBSWCL1-AG3" for class I and "LBSWCL2-AG3" for class II
First three letters of lab code or displays '000' if none
First three letters of DCN as displayed in sample management window or displays '000' if none
Sample ID
Family ID
Analysis date – "20190416" in example.
Allele code for all Class I or Class II alleles with constant "D" as separator for each locus.

NOTE: File name is auto-generated by the software. Care must be taken not to over-write a file saved on the same day.

ABMDR Specialty Report

To create an ABMDR specialty report, from the reports page select Specialty and select "ABMDR." Select session(s) to include as explained above.

Click Export Report. Report is created in .xml format. You will be asked to enter a report name and then save. You have the option to browse to a different folder to save the report.

To be included in this report, samples must be saved with final allele code.

```xml
<hml version="0.2"><project name="LAB"> <reporting-center code="labcode"/>
<sample center-code="090" id="sampleid">
<hla-typing>
<interpretation date="20190109">
 <haploid locus="A" method="D" type="03:01:01:01"/>
 <haploid locus="A" method="D" type="03:01:01:01"/>
 <haploid locus="BPR" method="D" type="53:01P"/>
 <haploid locus="BPR" method="D" type="53:01P"/>
 <haploid locus="C" method="D" type="04:01:01:11/04:01:01:14"/>
 <haploid locus="C" method="D" type="04:01:01:11/04:01:01:14"/>
 <haploid locus="DPA1" method="D" type="01:03:01G"/>
 <haploid locus="DPA1" method="D" type="02:01:01G"/>
 <haploid locus="DPB1" method="D" type="01:01:01:01/01:01:01:02/01:01:01:03"/>
 <haploid locus="DPB1" method="D" type="02:01:02:08"/>
 <haploid locus="DQA1" method="D" type="01:02:01:03"/>
 <haploid locus="DQA1" method="D" type="01:03:01:02"/>
 <haploid locus="DQB1" method="D" type="03:BGCWT"/>
 <haploid locus="DQB1" method="D" type="12:XX"/>
 <haploid locus="DRB1" method="D" type="11:01:02"/>
 <haploid locus="DRB1" method="D" type="13:01:01:01"/>
 <haploid locus="DRB3" method="D" type="01:01:02:02"/>
 <haploid locus="DRB3" method="D" type="02:02:01:02"/>
</interpretation>
</hla-typing></sample>
</project> </hml>
```

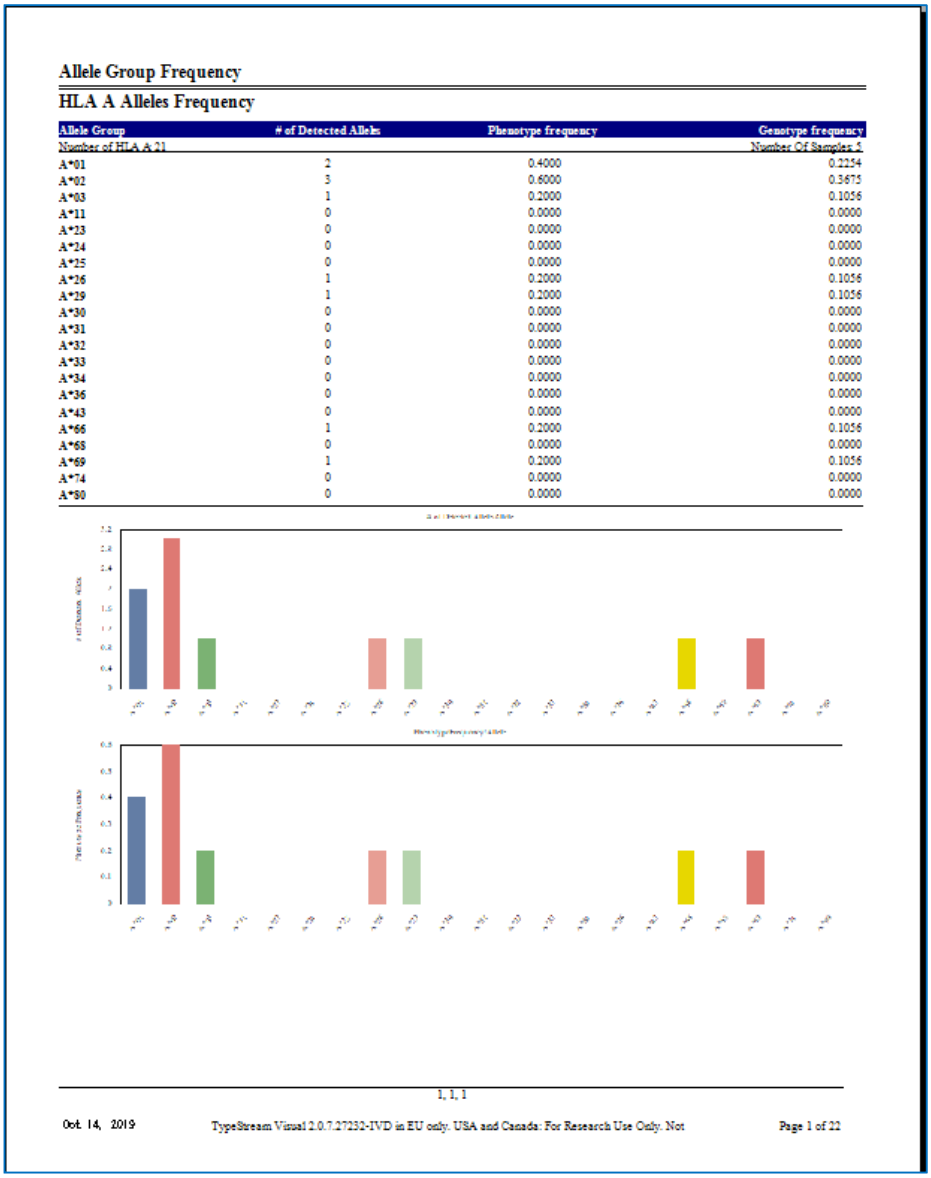
The example above contains the following:

"LAB" – hard-coded project name

Sample Center-code – hard-coded to “090”
Sample ID as existed or entered when session was created.
The date the sample was analyzed (“interpretation”).
Locus order - A, B, C, DPA1, DPB1, DQA1, DQB1, DRB1, DRB345
Allele code assignments.
For alleles whose code is represented by “XX1” (e.g.), software shall include only “XX” in this report and leave off the numeral.
B locus display as “BPR”

Allele Group Frequency Report

This option generates a .pdf report representing the frequency of each of the loci at the two-field level. Graphical display represents the number of detected alleles, Phenotype Frequency, and Genotype Frequency.



Allele Group Frequency

HLA A Alleles Frequency

Allele Group	# of Detected Alleles	Phenotype frequency	Genotype frequency
Number of HLA A 21			Number Of Samples 5
A*01	2	0.4000	0.2254
A*02	3	0.6000	0.3675
A*03	1	0.2000	0.1056
A*11	0	0.0000	0.0000
A*23	0	0.0000	0.0000
A*24	0	0.0000	0.0000
A*25	0	0.0000	0.0000
A*26	1	0.2000	0.1056
A*29	1	0.2000	0.1056
A*30	0	0.0000	0.0000
A*31	0	0.0000	0.0000
A*32	0	0.0000	0.0000
A*33	0	0.0000	0.0000
A*34	0	0.0000	0.0000
A*36	0	0.0000	0.0000
A*43	0	0.0000	0.0000
A*66	1	0.2000	0.1056
A*68	0	0.0000	0.0000
A*69	1	0.2000	0.1056
A*74	0	0.0000	0.0000
A*80	0	0.0000	0.0000

1, 1, 1

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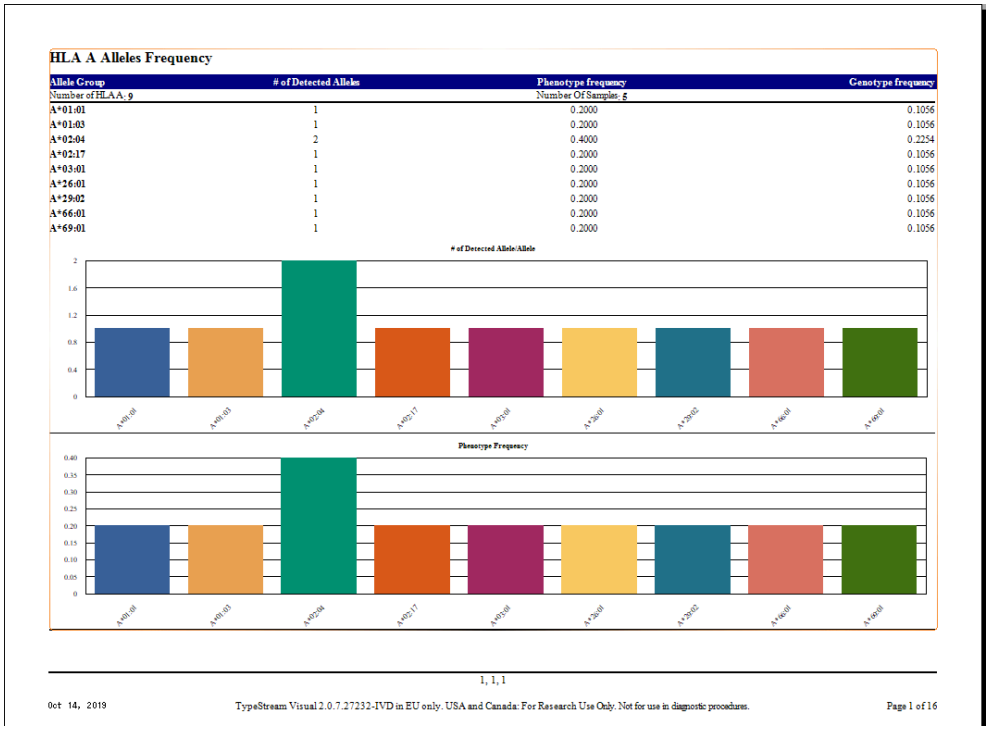
Allows the user can select the number of field options to customize if the report output should

be at 1 field, 2 field, 3 field or 4 field resolution for the suggested alleles.

Allele Group Frequency Extended (NMDP code only)

This option generates a .pdf report which extends the functionality of the Allele Group Frequency Report to NMDP code distribution only. Graphical display represents the number of detected alleles, Phenotype Frequency, and Genotype Frequency.



HLA A Alleles Frequency

Allele Group	# of Detected Alleles	Phenotype frequency	Genotype frequency
Number of HLA: 9		Number Of Samples: 5	
A*01:01	1	0.2000	0.1056
A*01:03	1	0.2000	0.1056
A*02:04	2	0.4000	0.2254
A*02:17	1	0.2000	0.1056
A*03:01	1	0.2000	0.1056
A*26:01	1	0.2000	0.1056
A*29:02	1	0.2000	0.1056
A*66:01	1	0.2000	0.1056
A*69:01	1	0.2000	0.1056

FASTA Report

FASTA report will generate sequences for all samples from a session in .fasta format.

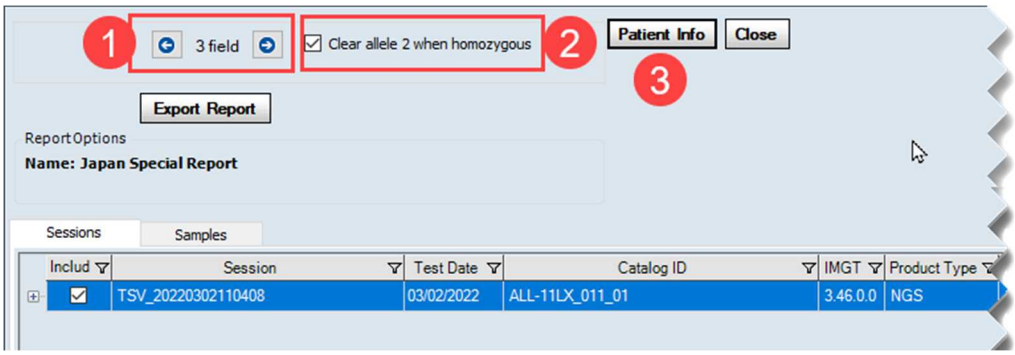
```
>009|TER069|A|001|consensus 1|A*26:01:01:01|total base 3851
CAGGAGCAGAGGGGTCAGGGCGAAGTCCCAGGGCCCCAGGCGTGGCTCTCAGGGTCTCAGGCCCCGAAGGCGGTATATGG
ATTGGGGAGTCCCAGCCTTGGGGATTCCCCAACTCCGCAGTTTCTTTTCTCCCTCTCCCAACCTATGTAGGGTCCTTCTT
CCTGGATACTCACGACGCGGACCCAGTTCTCACTCCCATTGGGTGTCGGGTTTCCAGAGAAGCCAATCAGTGTCGTCGCG
GTCGCGGTTCTAAAGTCCGCACGCACCCACCGGGACTCAGATTCTCCCC.AGACGCCGAGGATGGCCGTCATGGCGCCCC
GAACCCTCGTCCTGCTACTCTCGGGGGCCCTGGCCCTGACCCAGACCTGGGCGGG.TGAGTGCGGGGTCGGGAGGGAAAC
GGCCTCTGTGGGGAGAAGCAAGGGGCCCGCCCGGCGGGGGCGCAGGACCCGGGAAGCCGCGCCTGGAGGAGGGTCGGGCG
GGTCTCAGCCACTCCTCGCCCCCAGG.CTCCC.ACTCCATGAGGTATTTCTACACCTCCGTGTCCC.....GGCCCGGCC
GCGGGGAGCC....CCGCTTCATCGCCGTGGGC.......................TACGTGGAC....GACACG.CAGT
```

New in v3.0

Japan Export Report

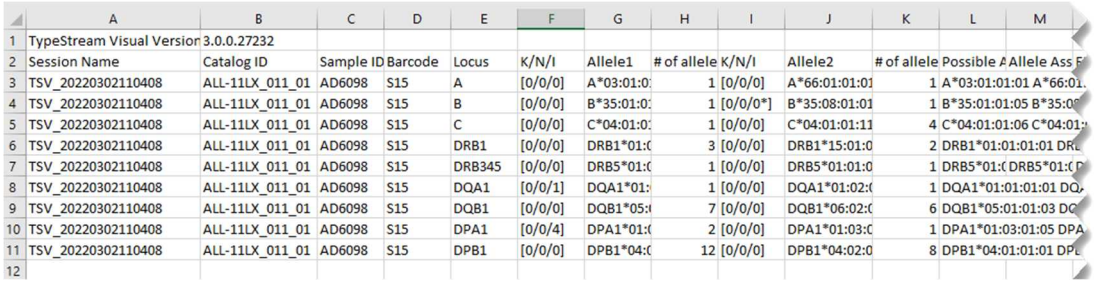
The Japan Export report will generate and export a Genotype Summary report for Veritas.

The figure below shows how to invoke the report. You can select up to 4 fields of resolution for the Allele Code Assignment field output using the arrow controls **(1)** and choose whether to clear allele 2 when homozygous **(2).** The **Patient Info button (3)** allows you to view patient and test information:



Press the **Export button** to generate the export file. A file browse window opens. When you give the output file a name and click OK, a .csv report file is generated, and this message appears:

The .csv file will contain patient and session information:



	A	B	C	D	E	F	G	H	I	J	K	L	M
1	TypeStream Visual Version	3.0.0.27232											
2	Session Name	Catalog ID	Sample ID	Barcode	Locus	K/N/I	Allele1	# of allele	K/N/I	Allele2	# of allele	Possible A	Allele Ass F
3	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	A	[0/0/0]	A*03:01:0	1	[0/0/0]	A*66:01:01:01	1	A*03:01:01:01	A*66:01.
4	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	B	[0/0/0]	B*35:01:0	1	[0/0/0*]	B*35:08:01:01	1	B*35:01:01:05	B*35:0
5	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	C	[0/0/0]	C*04:01:0	1	[0/0/0]	C*04:01:01:11	4	C*04:01:01:06	C*04:01:
6	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	DRB1	[0/0/0]	DRB1*01:(	3	[0/0/0]	DRB1*15:01:0	2	DRB1*01:01:01:01	DRL
7	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	DRB345	[0/0/0]	DRB5*01:(	1	[0/0/0]	DRB5*01:01:0	1	DRB5*01:(	DRB5*01:(D
8	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	DQA1	[0/0/1]	DQA1*01:	1	[0/0/0]	DQA1*01:02:(	1	DQA1*01:01:01:01	DQ
9	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	DQB1	[0/0/0]	DQB1*05:(	7	[0/0/0]	DQB1*06:02:(	6	DQB1*05:01:01:03	DQ
10	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	DPA1	[0/0/4]	DPA1*01:(	2	[0/0/0]	DPA1*01:03:(	1	DPA1*01:03:01:05	DPA
11	TSV_20220302110408	ALL-11LX_011_01	AD6098	S15	DPB1	[0/0/0]	DPB1*04:(	12	[0/0/0]	DPB1*04:02:0	8	DPB1*04:01:01:01	DPL
12													

Following fields are exported in the below order:

- Session name, Catalog ID, Sample ID, barcode
- Locus
- K/N/I, Allele1, # of allele 1 alleles
- K/N/I, Allele2, # of allele 2 alleles
- Possible allele assignment
- Allele Assignment (glstring)
- Final assignment
- Possible Allele Code Assignment – Computed based on the allele pairs that are selected by the user
- Possible Allele Code Def – obtained from the final allele assignment allele code definition
- Allele Code Assignment – value is <blank> for samples analyzed using TSV 2.0 or higher
- Allele Code Def - value is <blank> for samples analyzed using TSV 2.0 or higher
- Allele Code Assignment – displays the Final Allele assignment
- Allele Code Def – displays the Final Allele assignment allele code definition

- Possible Sero Assignment, Sero Assignment
- ReviewedBy, ReviewedDate,ConfirmedBy,ConfirmedDT

8

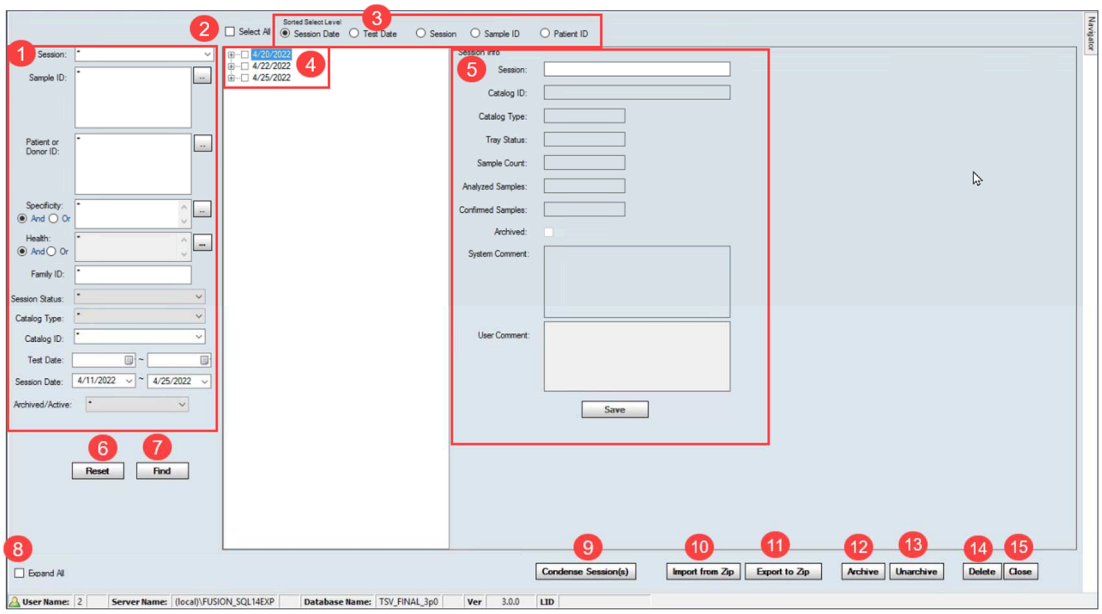
Data Management

To manage your data at the session level, use the Data option from the TypeStream Visual main menu. When you select the Data main menu, the Manage Data window is displayed. From this window the user may manage session files, delete or archive sessions.

Manage Data Window

It is possible to search for specific sessions based on multiple criteria:

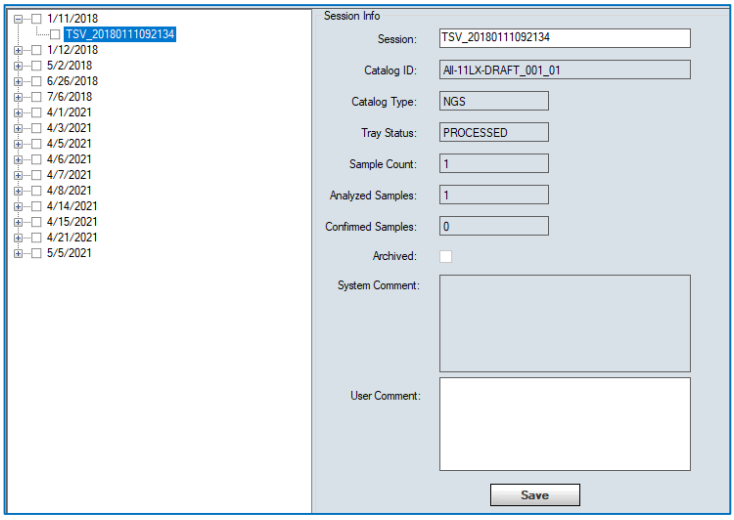
- Session name
- Sample ID
- Patient/Donor ID
- Family ID
- Session Status
- Catalog Type
- Catalog ID
- Test Date
- Session Date
- Archival status



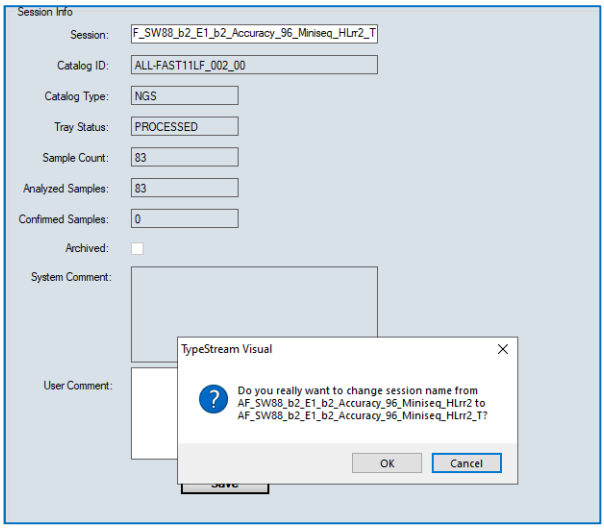
These criteria may be used alone or in combination with others.

	Item	Description
1	Search criteria panel	From this panel user may select a single criterion or a combination of criteria upon which to perform a search.
2	Select All	Will select all sessions in directory tree
3	Sorted Select Level	Sessions will be sorted per the selected radio button option. Session date (shown above) is the default.
4	Sessions panel	Search results are returned here in a tree-structured hierarchy.
5	Session Info	When a specific session is selected in the tree, details of that session display here.
6	Reset	This button resets all search criteria
7	Find	This button executes the search based on the selected criteria
8	Expand All	Expands all the nodes in the hierarchical tree
9	Condense Session(s)	Allows the user to condense the size of files to save drive space
10	Import from Zip	Will import a zipped session file to the database
11	Export to Zip	Will export selected file(s) into a zip file which can be saved to any location.
12	Archive	This will archive any session selected
13	Unarchive	This will make active any archived session.
14	Delete	Will delete the selected session or sample
15	Close	Closes the data management window

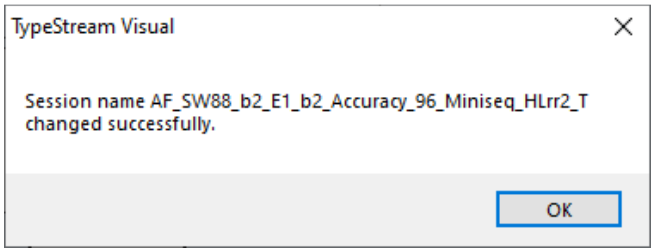
Select a date and expand the tree structure to display sessions for that date. Select a session and the right-hand panel displays information pertaining to the session.



The session name field is editable field that allows the user to update the name of the session. The user can choose to cancel the rename operation by clicking on Cancel button in the message box.

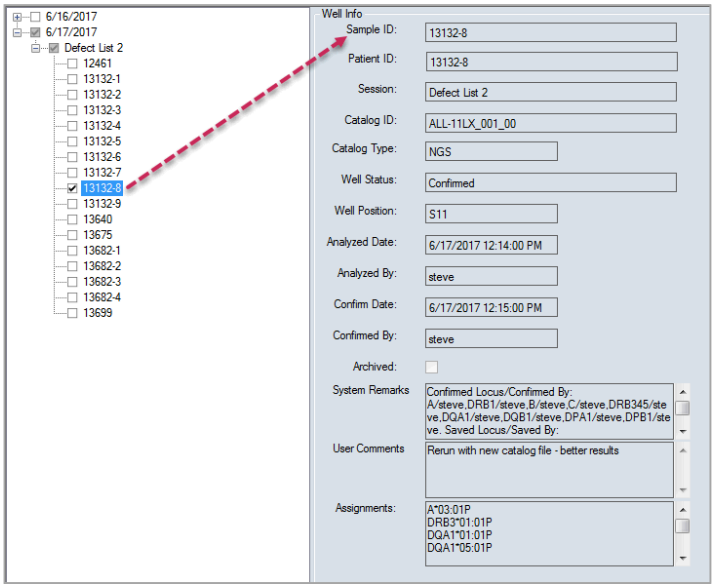


Upon confirmation, the below message appears

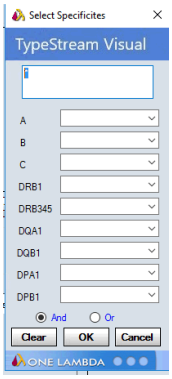


Note:	Updating the session name , does not change the name of the folder in the session folder (default folder is C:\OLI TSV\data\session)

Expand the tree structure to display samples for that session. Select a session and the right-hand panel displays information pertaining to the sample.

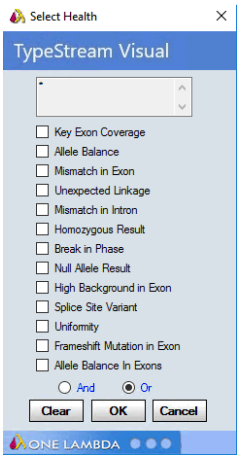


Search by Specificity



Allows users to enter one or more alleles into the search field by separating them by commas. Samples that have the alleles assigned in the computer suggested or in the final assignment are displayed.

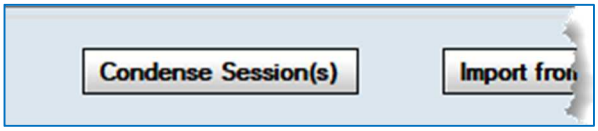
Search by Health



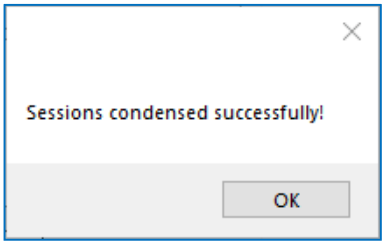
Allows users to search samples by the health metrics.

Condense Session(s)

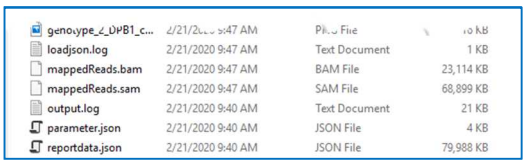
A new feature to help conserve space on your drives, Condense Session allows the user to condense a single or multiple selected sessions.

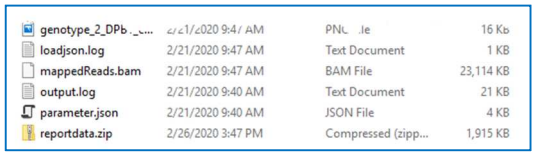


To use, select a session from the Data Management window and click the Condense Session(s) button. After a moment, a message will display that the session condensed successfully.



During the condensing process, the software takes the two most data-heavy files for each barcode (mappedReads.sam and reportdata.json) and creates a .zip file. In a current example, TypeStream Visual condensed a total 148,887 KB down to a 1,915 KB zip file.



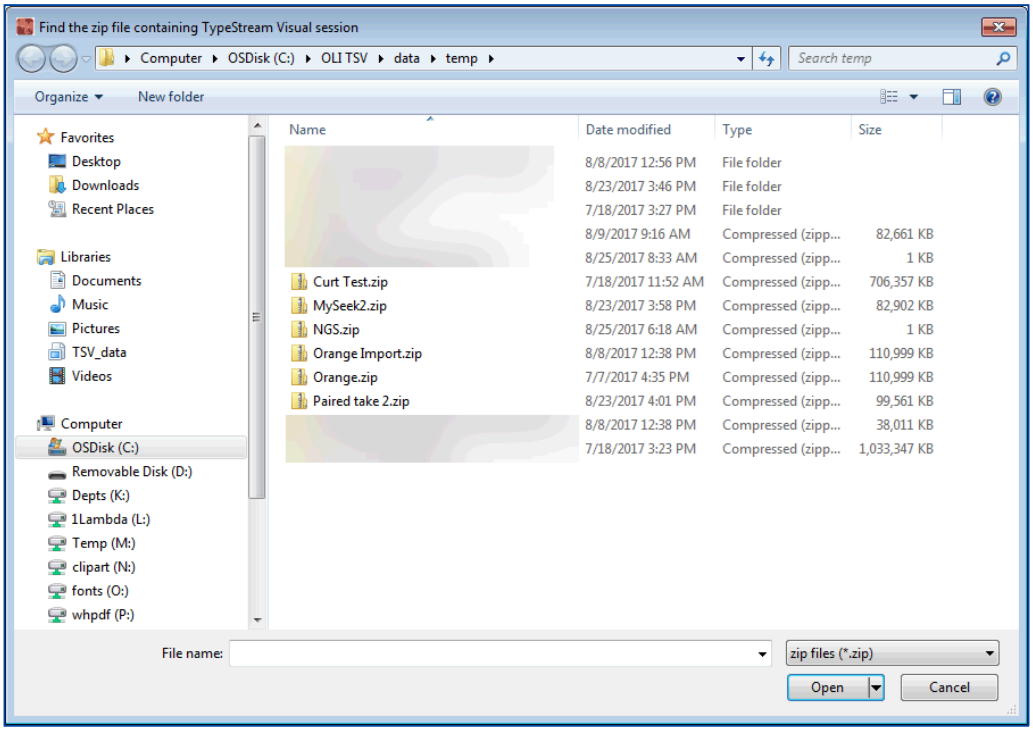


If the user navigates to the read viewer of a condensed session, the software unzips and restores the reportdata.json and mappedReads.sam files and the .zip file is deleted.

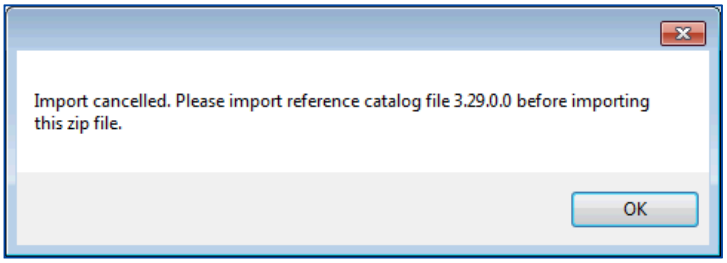
Note – User must have WinZip installed on their computer for this feature to work.

Import Session

On clicking 'Import from Zip' button, software will open a navigation window to the default folder C:\OLI TSV\data\temp. (If exported files have been saved to a different location, user may navigate to that location. This path can be set by navigating to Utilities → General Settings → Paths and changing the path for 'Temp'.) Select a session (only one session at a time may be imported) and click Open.

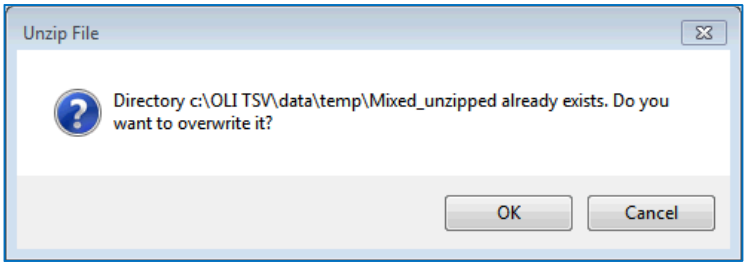


Database must contain the library used for the original analysis. If it is not in the database, the software will display a message like the following:



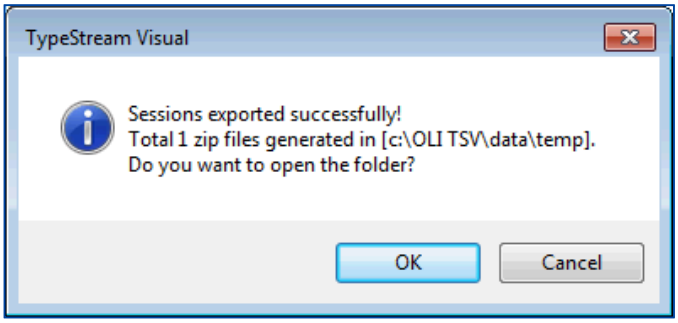
If this happens, simply import the correct library file and perform the import again.

On occasion, you may need to import a session that has the same session name as one previously imported, though it may not be in your active database. In this case you will get a message saying that the unzipped file already exists. What really exists, however is a placeholder in the temp folder and not an actual file. Therefore, you may click 'OK' on the message below without overwriting an analyzed file.



Export Session

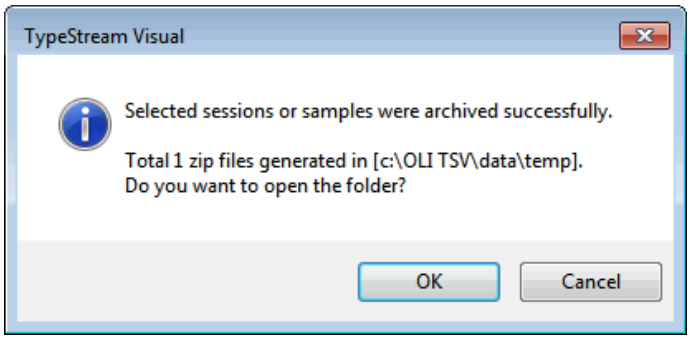
To export a session, select desired session(s) by clicking 'Export to Zip' button. The zipped file is stored by default to C:\OLI TSV\data\temp. When completed, the software will offer to open the folder location.



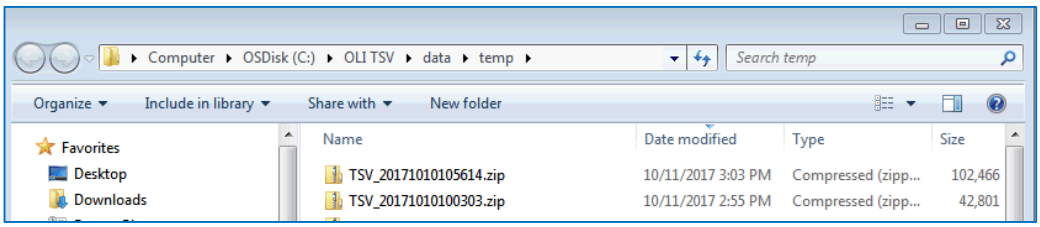
Archive and Unarchive Sessions

The user has the option of archiving an entire session or a subset of samples within the session. Select a session by check the checkbox next to the session name. Click 'Archive' and the software will create a zipped file of the session.

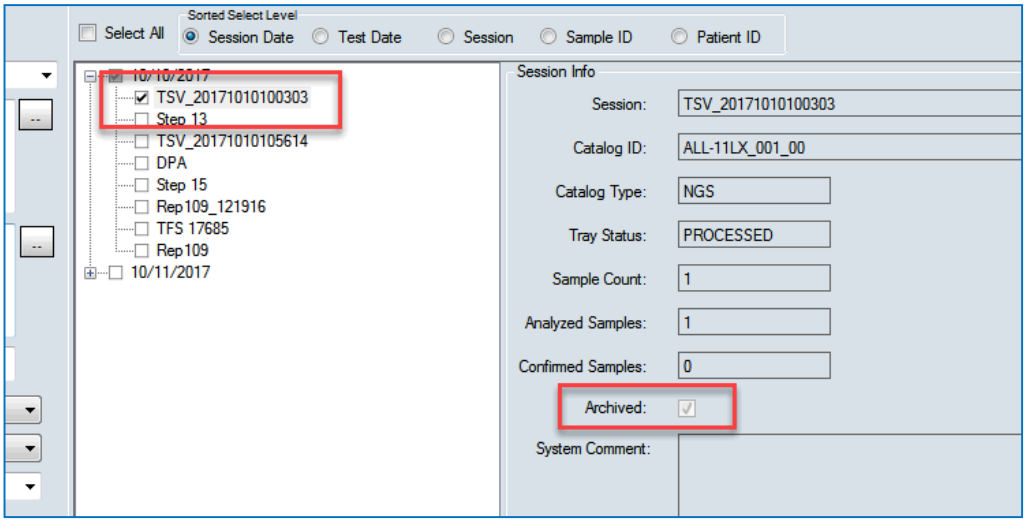
When finished, you will receive a confirmation that the archive was successful and an offer to open the folder to view the file.



On clicking OK, folder opens to display zipped file.

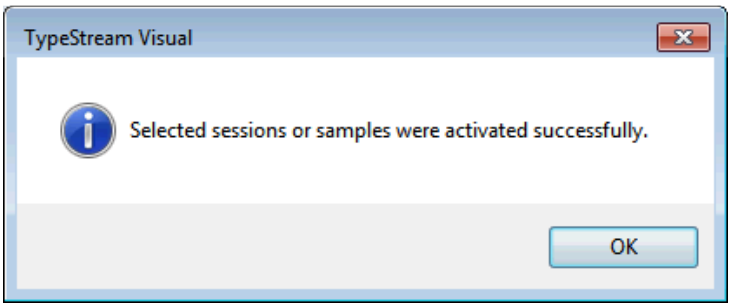


Although zipped files will no longer display in the Navigator and cannot be viewed, they will still display in the Data Management window. When an archived session is selected, it displays as any other session, but the 'Archived' check box will be checked and grayed out.



If at a future point the user wants to view or reanalyze an archived session, the unarchive process is the just the reverse of the archive process.

Check the archived session and click 'Unarchive.' When process is complete a message of successful activation will be displayed.



Delete Session

Any session in the active database may be deleted using the Delete function in Data Management. Select session(s) and click Delete. A confirmation message will confirm that these sessions are to be deleted.

When naming sessions, please be aware of the following: Although local databases do not cross-reference session names, all session folders are stored in the same location – C:\OLI TSV\data\session\NGS by default, though this can be modified by navigating to Utilities → General Settings → Paths. If there are duplicate session names coming from different databases, samples from both sessions will be stored in the same folder.

Therefore, when a 'Delete Session' is about to be executed, the software looks first into the session folder and only deletes the samples associated with session in the active database, leaving the rest and also leaving the session folder.

Example: DB-Alpha and DB-Beta both have a session named 'Test4'.

- On DB-Alpha, 'Test4' contains samples 'RakB', 'Toks', 'Ahm', and 'Est'.
- On DB-Beta, 'Test4' contains samples 'AnLiu', 'Zelm', 'Est', and 'RobS'.
- User is working on DB-Beta and requests to delete 'Test4.'

- Software will look at the samples in the folder and delete ‘AnLiu’, ‘Zelm’, ‘Est’, and ‘RobS’.
- Note that because there was also a duplicate sample name, ‘Est’, it was deleted and will not be available for use by DB-Alpha.
- Similarly, if all sample names were the same for both databases, the software would delete all samples and the session folder.

Sample Management

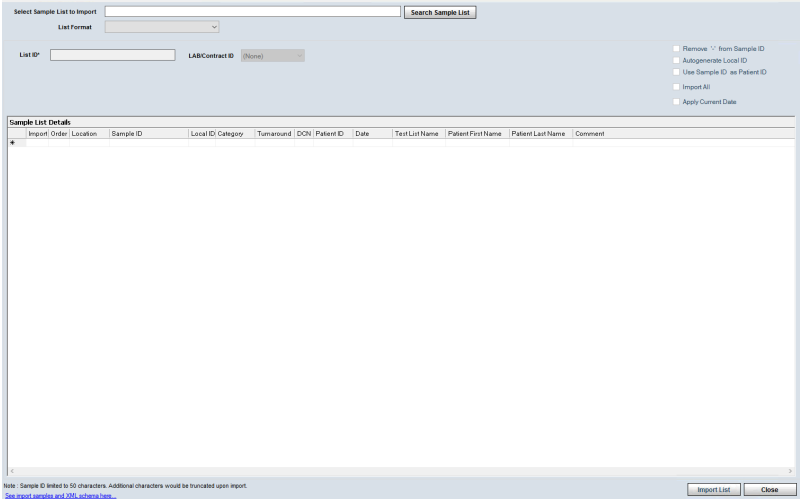
In TypeStream Visual, sample lists are an easy way to input a large list of sample IDs and other sample information into the database for use in analysis sessions. Sample lists may be in .xlm, .csv or .txt file format. From the Sample List Import menu, you can import sample lists or edit sample lists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

> **NOTE:** Please verify all data you import as HLA TypeStream performs minimal data validation upon import.

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.

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.
5. Click to clear the check boxes of any samples you do not want to import.
6. Click Import List to import the selected sample lists.
7. Click Close to return to the Main Menu.

Three list formats are accepted in TypeStream Visual:

1. Sample List (.csv)

	A	B	C	D	E
1	local	sample	patient	Date	
2	B201651	B201651	20743		
3					
4					

Sample list with patient first name and last name

A	B	C	D	E	F	G
local	sample	patient	Date	patient first name	patient last name	
101	Sample1	KM	24-Aug-03	John	Smith	
101	Sample2	AM	11-Jul-08	Mark	Smith	
102	SM1	SM2	1-Aug-79	SM2	SM2	
1002	SM1	SM1	1-Aug-79	SM1	SM2	

Sample list with patient first name, last name and comments

A	B	C	D	E	F	G	H
local	sample	patient	Date	patient first name	patient last name	Comments	
Sample1101	Sample1	p1	27-Sep-10	mike	Sample1LN	comments1	
Sample2101	Sample2	s1	29-Sep-10	luke	CheetiNEW	comments1	
Sample3101	Sample3	38557	29-Sep-10	mark	sam	comments1	
Sample4101	Sample4	38559	1-Oct-10	pfirstname	plastname_1	comments1	
101	2010-11261_Quin	35720	30-Sep-10	pfirstname	plastname	comments1	
101	2010-11262_Ramc	29817	30-Sep-10	29817	29817	comments1	

2. Sample List with Packlist (.csv)

	A	B	C	D	E
1	100	Loc SampleID Cat TurnA DCN asda	1QC	1/1/1980	
2	101	Loc1 SampleID1 Cat1 TurnA1 DCN1 asdsa	38450	27-Sep-10	
3	101	Loc2 SampleID2 Cat2 TurnA2 DCN2 sds	27614	29-Sep-10	
4					
5					

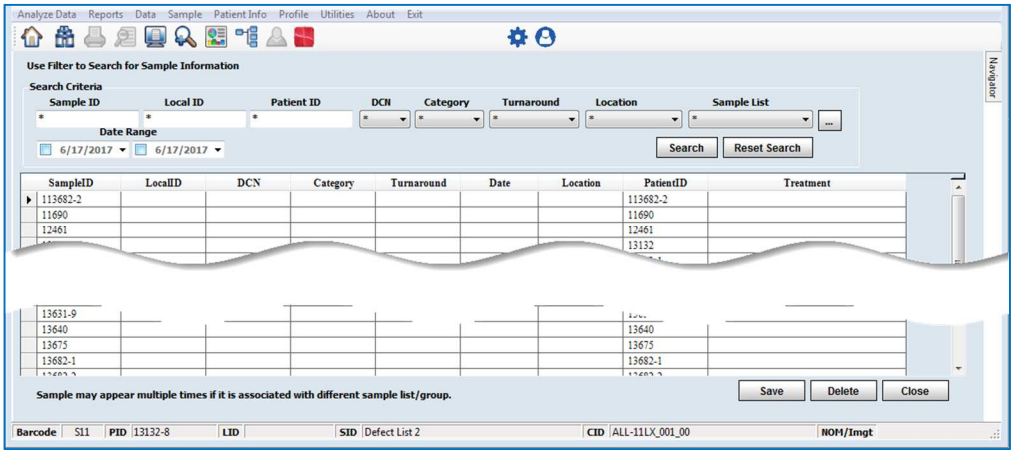
3. Sample List: XML Format

```xml
<SampleList xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance">
  <Patient ID="100">
    <Samples>
      <Sample ID="100001">
        <Date>2009-01-01</Date>
        <LocalID xsi:nil="true" />
      </Sample>
      <Sample ID="100002">
        <Date>2009-02-01</Date>
        <LocalID xsi:nil="true" />
      </Sample>
      <Sample ID="100003">
        <Date>2009-03-01</Date>
        <LocalID xsi:nil="true" />
      </Sample>
      <Sample ID="100004">
        <Date>2009-04-01</Date>
        <LocalID xsi:nil="true" />
      </Sample>
      <Sample ID="100005">
        <Date>2009-05-01</Date>
        <LocalID xsi:nil="true" />
      </Sample>
      <Sample ID="100006">
        <Date>2009-06-01</Date>
        <LocalID xsi:nil="true" />
      </Sample>
      <Sample ID="100007">
        <Date>2009-07-01</Date>
        <LocalID>24</LocalID>
      </Sample>
      <Sample ID="100008">
        <Date>2009-08-01</Date>
        <LocalID>25</LocalID>
      </Sample>
    </Samples>
  </Patient>
  <Patient ID="10092">
    <Samples xsi:nil="true" />
  </Patient>
</SampleList>
```


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.



2. Use the filters to find samples and click View Sample.
   a. Wildcards can be used in the Sample ID field to widen the results.

3. Edit sample information.
    a. 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.
    a. You are not allowed to delete a sample that is part of a session that has already been analyzed.

9

Patient Management

Patient Information

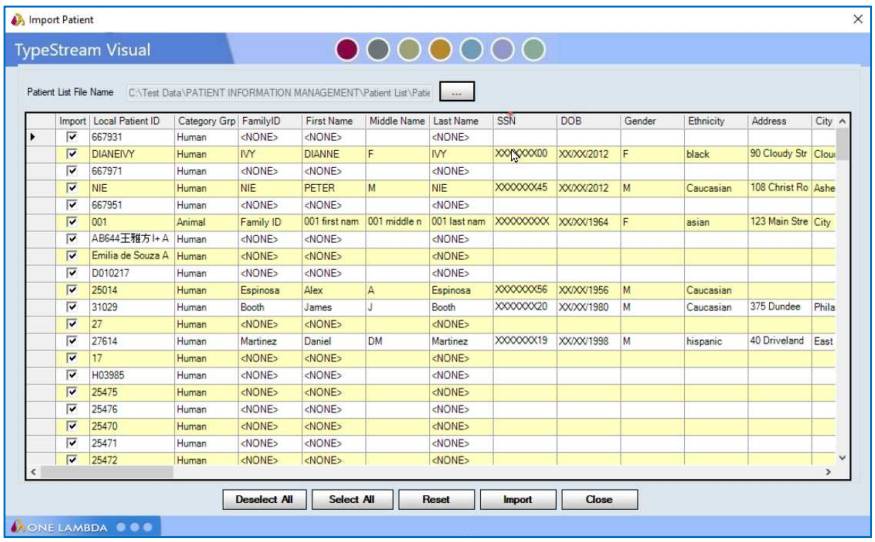
TypeStream Visual can store patient information and associate sample IDs with patients and donors. You can store all typing and screening information in one location for each patient.

> **NOTE:** Please verify all data you import. TypeStream Visual performs minimal data validation during import operations.

Importing Patient/Donor Lists

After creating a Patient/Donor List, you can import the information into TypeStream Visual.

1. From the Main Menu, select Patient Info > Import Patient List. The Patient Import window displays.



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.

The complete list of column headings for the Patient/Donor template is as follows:

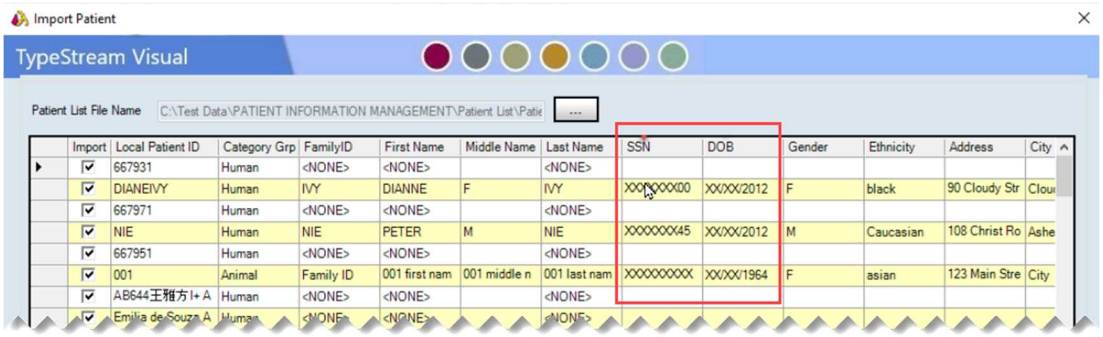
Patient ID	Category Grp	Family ID	First Name	Middle Name	Last Name	SSN
DOB	Gender	Ethnicity	Address	City	State	Region
Country	ZipCode	Email	Phone	Work Phone	Cellular	FAX
Employer	Spouse Name	Spouse Blood Type	Emergency Contact	Emergency Tel	DCN	Hospital Name
Division	Blood Type	Disease	Rh Blood Type	Patient/Donor Flag	Associated Sample IDs	Associated Donor IDs
HLA1_A	HLA2_A	HLA1_B	HLA2_B	SHLA1_Bw	SHLA2_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	HLA1_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	Unacceptable Antigens	Acceptable Antigens	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
Donor Type	Include in Donor PRA	Status	Transplant Type	From Other Facility	Donor Groups	PRA Donor Groups

NOTE: The TypeStream Visual system checks the patient/donor lists you attempt to import to verify that all characters contained in the data are supported by TypeStream. If your list contains unsupported characters, a warning message is displayed and the list is not imported.

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

New in v3.0

The Birthdate/DOB **(3)** and SSN fields **(4)** are partially covered by 'X' characters for security reasons. Only the last four digits of these fields are displayed.



Patient/Donor Management

The Patient/Donor Management function allows you to manage one record at a time via the Patient/Donor Information screen. From here you can do these operations and more:

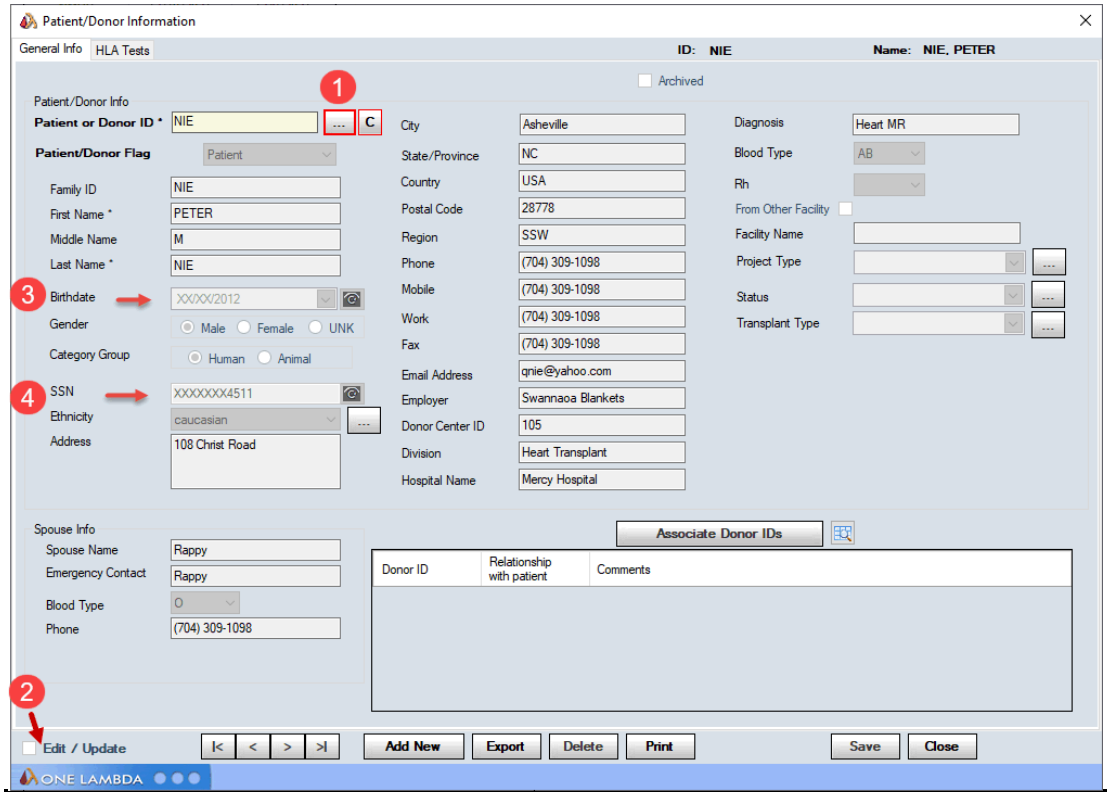
- Add new patient/donor records
- Search existing patient/donor records
- Edit patient/donor records, including Serological and Molecular test results
- Associate patient/donor IDs with sample IDs
- Associate patient and donor records
- Assign a donor to the Donor PRA
- Print, export and archive patient 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.

Steps to Add New Patient/Donor Records (please refer to numbered items in the figure):

1. From the Main Menu, select Patient Info > Manage Patient. Click the Ellipsis **(1)** to display a searcheable list of patients/donors in the database, and click one to select it:



2. Check the Edit/Update box **(2)** to permit editing.
3. Alternately, instead of using the searcheable list of patients **(1)**, enter an ID in the Patient or Donor ID field. The ID can be alphanumeric (contain letters and/or

number) or click Search and select a patient/donor from the list.

4. Enter patient/donor information to complete the form. Fields with an asterisk (*) are required.
5. Click Add New to save the data and add the patient/donor information to the TypeStream database.
6. Click Close to close the data entry form and return to the main menu.

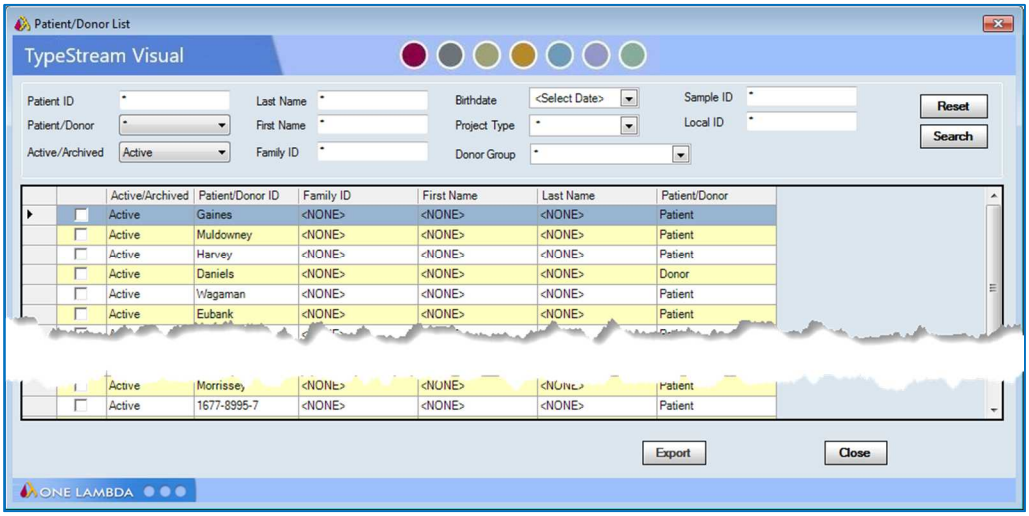
New in v3.0

The Birthdate **(3)** and SSN fields **(4)** are partially covered by 'X' characters for security reasons. Only the last four digits of these fields are displayed.

Search and Display Patient/Donor Records

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

1. From the Main Menu, select Patient Info > Manage Patient.
2. Click the Search button ... to browse patient records in the Patient/Donor List. You may look up Patient/Donor records by name, patient ID, whether it is active or archived, etc.:



3. Highlight a patient record in the results table and double-click to display or edit.
4. You can also find a record by typing the Patient ID or Donor ID directly into the Patient or Donor ID field next to the Search button, and pressing Enter:

5. If the Patient ID you typed is correct, the General Info tab (and other tabs as well) will be enabled and visible and will be populated with the information for that record.

Editing Patient/Donor Records

You must be a Supervisor in order to edit a patient/donor record. All patient/donor information (except patient/donor ID) can be edited.

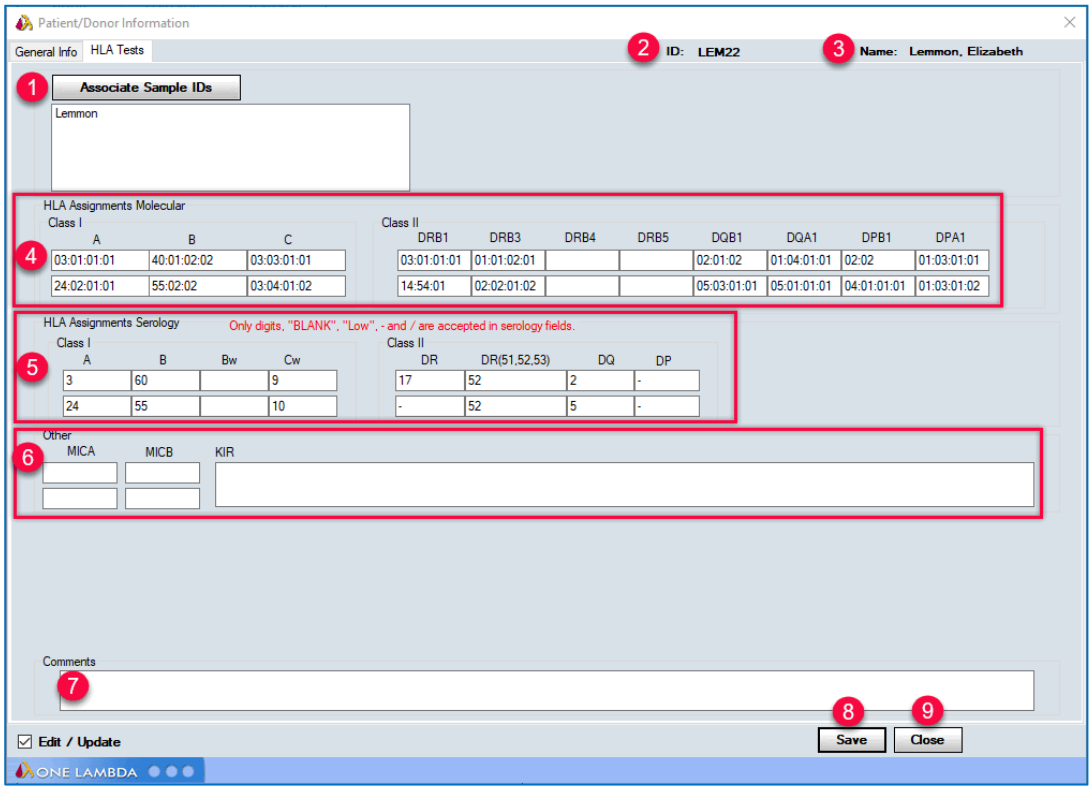
1. From the Main Menu, select Patient Info > Manage Patient.
2. Search for a Patient/Donor Record (see the search instructions shown immediately above) and select a record to edit.
3. Patient/donor information will appear on the General Info tab and any other tabs.
4. Before you can change information, you must select the check box next to Edit /Update on the lower left side of the screen.
5. Click Save to save your changes.
6. Click Close to return to the Main Menu.

Assigning Molecular and Serological Typing Information Manually

Molecular and Serological typing assignments can be entered manually for each patient or donor. To manually assign typing information, do the following:

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

1. From the Main Menu, select Patient Info > Manage Patient.
2. Open the Patient/Donor List using the search button ...
3. Select a Patient record using the filters and search mechanism, or simply double-click on a Patient record in the table.
4. Select the check box next to Edit /Update.
5. Click the HLA Tests Tab.
6. Enter Molecular and Serological typing values in the spaces provided, then click Save. The system will warn you to only use certain characters in data entry fields (warning appears in red text). You can also enter Comments here (at the bottom of the screen):



	Item	Description
1	Associate Sample IDs	Sample IDs already associated with this patient display in the text field. To associate more samples to this patient, click "Associate Sample IDs button. *(See below.)*
2	ID	Patient ID
3	Name	Patient Name
4	Molecular Assignments	May be manually assigned or automatically assigned from the analysis page.
5	Serological Assignments	May be manually assigned or automatically assigned from the analysis page
6	Other Assignments	MICA and MICB assignments, if relevant, must be manually assigned by the user.
7	Comments	User may optionally attach comments to the patient HLA tests

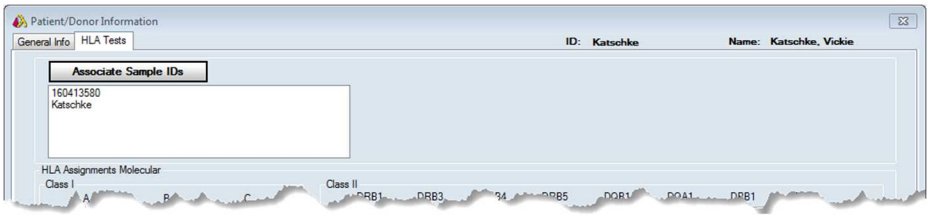
8	Save	Saves any changes made to the patient, including changes made to either of the tabs.
9	Close	Closed the patient management window.

Associating a Patient/Donor ID with Sample IDs

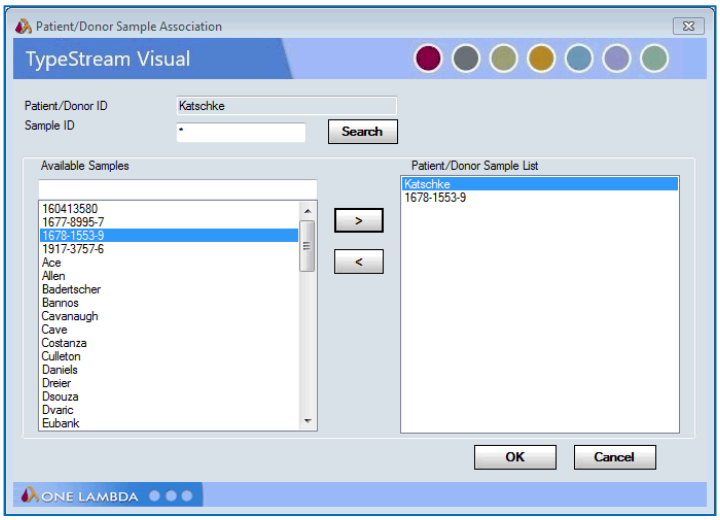
A Sample ID cannot be associated with more than one patient or donor record, but a patient or donor record can have more than one sample ID associated with it.

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

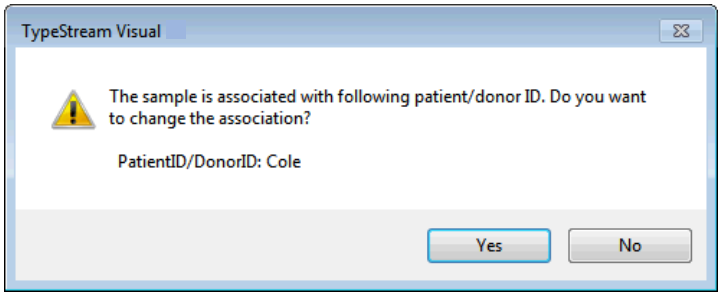
1. Select the HLA Tests Tab.



2. Click the Associate Sample IDs button.
3. 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:



4. When adding a sample ID to the Patient/Donor Sample List, you may receive this message. If you select Yes, the added sample will become part of the current Sample List for this Patient/Donor even though it is also associated with another Patient/Donor:



5. Click OK to return to the patient record and 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. Select a patient/donor record.
3. Click Edit/Update
4. Click the Test Info tab.
5. Click the Associate Donor IDs button.
6. 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.
7. Click Save to save data.
8. Click OK to return to patient record.
9. Click Close to return to the Main Menu.

Printing Patient/Donor Records

TypeStream Visual prints both Record Management tabs regardless of which tab is currently being viewed.

1. From the Main Menu, select Patient Info > Manage Patient**.**
2. Select a patient/donor record by clicking the Search button ... to browse patient records and lookup a record by name, patient ID, whether it is active or archived, etc. Select a patient in the results table and double-click to display it.
3. The General Info tab will appear with the desired information shown. Click Print to print the displayed record.
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 Patient Info > Manage Patient.
2. Select a patient/donor record by clicking the Search button ... to browse patient

records and lookup a record by name, patient ID, whether it is active or archived, etc. Select a patient in the results table and double-click to display.

3. The General Info tab will appear with the desired information shown. Click Export to export the displayed record.
4. A browse window opens. Select a location to save the CSV file to and enter a file name.
5. Click Save then click Close to return to the Main Menu.

Archiving or Reactivating 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 Archived check box, or you can archive records to remove them from system processing. To toggle the Archived status:

1. From the Main Menu, select Patient Info > Manage Patient.
2. Click the General Info tab.
3. Select a patient/donor record to reactivate by clicking the Search button ... to browse patient records and look up a record by name, patient ID, whether they are active or archived, etc. Then set the checkbox next to the record you wish to process and double-click it.
4. Click the Edit / Update checkbox.
5. Select the Archived checkbox (or unselect it) by single-clicking it.
6. Click Save to save, then 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 Patient Info > Manage Patient.
2. Click the General Info tab.
3. Select a patient/donor record by clicking the Search button ... to browse patient records and lookup a record by name, patient ID, whether it is active or archived, etc. Select a patient in the results table and double-click it.
4. The General Info tab will appear with the desired information shown.
5. Click Delete to remove the displayed record from the system.
6. If there are associations and references still active, you may receive a message that the record cannot be deleted. Check to make sure that there are no Associated Donors and no Associated Sample IDs (HLA Tests tab).
7. Click Delete. If Deletion is successful, you will receive a message confirming this operation.

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.

The first field/section must contain the names of the patient list fields, each separated by commas.

> **NOTE:** Creating a new patient list can be made easier by first exporting an existing list into CSV format, and using the fields in that to build your new list.

Patient List Field Names and Format

```
PatientID         CategoryGrp       FamilyID          FirstName         MiddleName        LastName          Ssn
Dob      Gender   Ethnicity         Address City      State    Region   Country ZipCode   Email    Phone    WkPhone
Cellular          Fax      Employer          SpouseName        SpouseBloodType   EmergencyContact
EmergencyTel      DCN      HospitalName      Division          BloodType         Disease  RhBloodType
PatientDonorFLg   Associated SampleIDs       Associated DonorIDs         HLA1_A   HLA2_A   HLA1_B   HLA2_B
SHLA1_Bw          SHLA2_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         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          Status   TransplantType    FromOtherFacility          FacilityName      DonorGroups
PRADonorGroups
```

Subsequent lines must list the actual patient information, alphanumerically, (can be letters and/or numbers) separated by commas. If there is no information for the patient in a particular field, that field still requires a comma as a placeholder.

For *all* manual serology entries, the locus must precede the value. For example, for an A locus of value 23, you must enter A23.

```
PatientID,CategoryGrp,FamilyID,FirstName,MiddleName,LastName,Ssn,Dob,Gender,Ethnicity,Address,City,State,Region,Coun
try,ZipCode,Email,Phone,WkPhone,Cellular,Fax,Employer,SpouseName,SpouseBloodType,EmergencyContact,EmergencyTel,DCN,H
ospitalName,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,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
38450,Human,Neely,Jason,,Neely,021-09-2987,2/17/2001,M,caucasoid,560 Waiting
Street,,CA,NWW,USA,91022,jneely@yahoo.com,(213) 567-0987,(213) 567-0987,(213) 567-0987,(213) 567-0987,MIT
Research,Evvonne,AB,Evvonne,(213) 509-0198,101,St Judes's Hospital,MARROW Transplant,O,bONE
MARROW+,,Patient,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,A2,-,B78,B56,,,,,,,DQ-,DQ-,DP14,DP9,,
27614,Human,Martinez,Daniel,DM,Martinez,032-11-1934,9/12/1998,M,hispanic,40 Driveland Road,East
LA,CA,NWW,USA,90222,mdaniel@aol.net,(324) 489-1430,(324) 489-1430,(324) 489-1430,(324) 489-1430,Joba
Juice,Maria,B,Maria,(324) 489-1430,103,East LA Hospital,MARROW
Transplant,O,Marrow,-,Patient,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,A2,-,-,B6,,,,,,,DQ8,DQ2,DP19,-,,
38557,Human,Phannudet,Keodone,PK,Phannudet,111-41-5432,12/30/2000,F,oriental,1009 Special
Road,Valencia,CA,NWW,USA,91355,kd@lions.net,(662) 234-1098,(662) 234-1098,(662) 234-1098,(662) 234-1098,Traveller's
Insurance,Kenneth,A,Kenneth,(662) 234-1098,221,Henry Mayo Hospital,,AB,Tissue,
+,Donor,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,-,A80,-,B37,,,DR15,-,DR52,-,,,DP5,DP5,,
44715,Human,Haigety,Jimmy,HJ,Haigety,111-94-1212,11/22/2000,M,caucasoid,7701 Christian Brothers
Road,Bellflower,CA,NNW,USA,91314,jh@msn.com,(323) 981-0916,(323) 345-1234,(323) 506-7771,(714) 556-1289,Verizon
Corporation,Juanna,O,Juanna,(323) 345-1098,103,St Michael Hospital,MARROW Transplant,O,Tissue,
+,Patient,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,B10,-,,,DR-,DR8,,,,,,,
44716,Human,Shoemaker,Cheryl,S,Shoemaker,111-13-1234,11/22/2002,F,black,1705  Brothers
Road,Canyonville,OR,NNW,USA,97417,sc@msn.com,(541) 839-4467,(541) 839-6509,(541) 299-1098,(541) 760-1986,Juniper
Creek,Elizabeth,O,Elizabeth,(323) 345-1098,103,St Michael Hospital,MARROW Transplant,O,Tissue,
+,Donor,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,A2,-,,,,,,,DR53,-,,,,,,
44717,Human,Dublin,Nikitta,D,Dublin,111-13-1234,11/22/2004,F,asian,345  Ashilly
Court,Canyonville,OR,NNW,USA,97417,sc@msn.com,(541) 839-4467,(541) 839-6509,(541) 299-1098,(541) 760-1986,Juniper
Creek,Elizabeth,O,Elizabeth,(323) 345-1098,103,St Michael Hospital,MARROW Transplant,O,Tissue,
+,Donor,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,-,A2,,,Cw4,Cw1,DR-,DR-,DR51,DR52,DQ7,DQ6,,,,
28198,Human,Sharpitis,Thomas,T,Sharpitis,023-18-0002,1/1/1950,F,caucasoid,9701 Bicycle Lane,Cystal
Village,CA,SWW,USA,91002,shar60@yahoo.com,(714) 978-1098,(714) 978-1098,(714) 978-1098,(714) 209-7812,Joseph
```

10

Database Utility

The TypeStream Visual Database Utility allows you to create and connect to SQL Server databases, as well as perform all of the following tasks.

- Create a new database
- Select/connect to an existing database
- Delete Database
- Attach Database
- Detach Database
- Back up Database
- Restore Database
- Merge Database
- Reconfigure Database
- Optimize Database
- Create/Select Audit Log Database
- Current Database Details
- Select/Connect To HistoTrac Database

It also has a new icon:

Opening the TypeStream Visual Database Utility

The TypeStream Visual Database Utility allows you to connect to any SQL Server on your computer or the network, depending on your permissions and your organization's security policies.

To use any of the TypeStream Visual Database Utilities, you must first connect to a SQL Server. With the exception of connecting to a database, the database tasks can be executed only on the server or on the computer on which the database resides.

The following are guidelines for using the TypeStream Visual Database Utility:

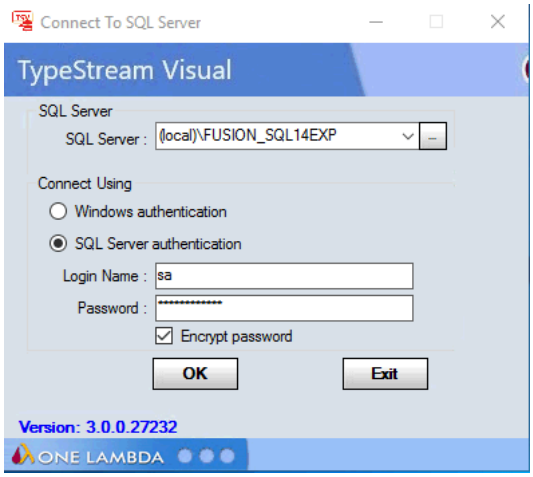
- You can connect to the SQL Server using either Windows Authentication or SQL Server Authentication. If you use SQL Server Authentication, the Server Dialog Box displays the default database administrator username and password for a local client/server installation.
- It is highly recommended that you do not switch collation and regional settings between databases. The collation of databases and the SQL Server play a major role during database merge and migration. (A *collation* encodes the rules governing the use of characters and numbers for a language or an alphabet).
- Please do not alter the permissions, (i.e., who has the right to make certain changes to the database).
- Double-click the TypeStream Visual DB Utility icon on your computer desktop.

The Connect to SQL Server dialog box is displayed.

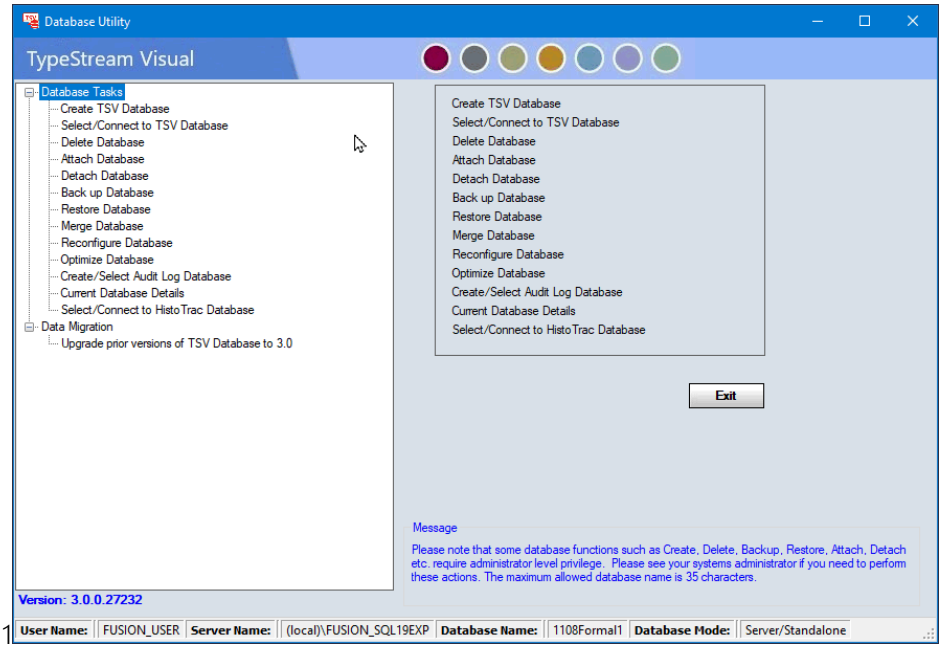
New in v3.0

In TSV 3.0, user has an option to encrypt the password to the database server. The encrypted information is stored in the application config file.

Note: You can also now use all editions of Microsoft SQL 2019.



Make sure your SQL Server information is correct and click the OK button. The Database Utility Main Window is displayed:



The status bar at the bottom of the TypeStream Visual Database Utility main window displays the Active User, Server Name, Database Name, and the Database Mode, (i.e., TypeStream Visual and the database are on the same computer, or the database resides on an external server).

- The Username field will say *Not Set* if you are using Windows Authentication.
- A Help button is available on every Database Utility window, or by pressing the F1 key.
- Click the +/- signs on the far left to display or hide related database utility menu options.

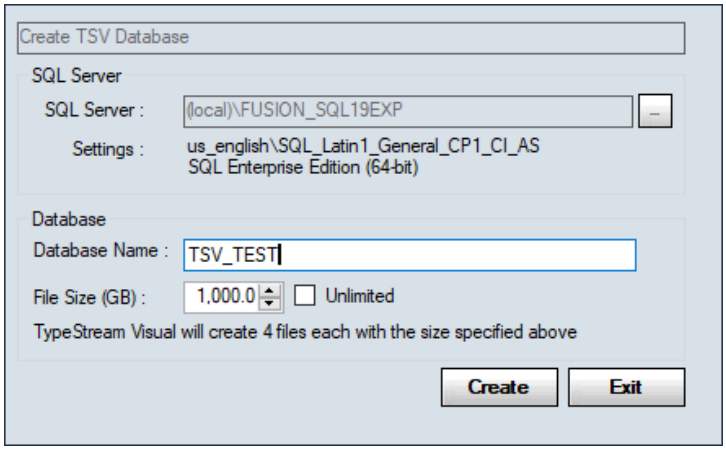
Database Tasks

The Database Tasks listed on the left side of the Main Window offer various means to configure, manage and maintain a TypeStream Visual database. These functions are described in the following sections.

Creating a New Database

A new database can be created only on the computer or server on which the SQL Server program resides.

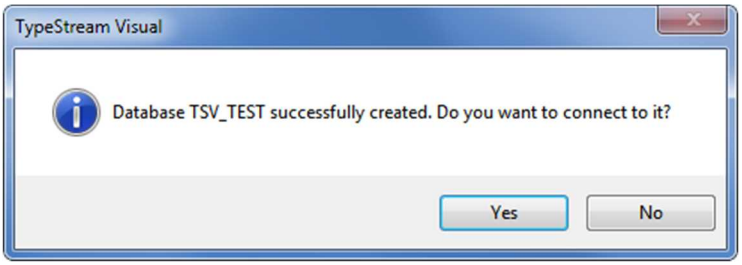
- On the left side of the Database Utility window, click Create Database:
- Using the SQL Server drop-down box, choose a SQL Server version that is correct for the database you want to create (SQL 2019 in this example)
- Enter a unique Name for the new database.
- Choose the maximum database size and click Create.



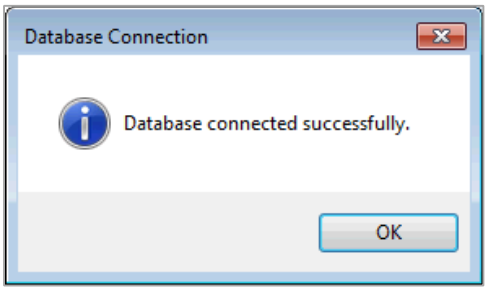
For a purchased, full-version of SQL Server, the maximum database size is one terabyte. Ensure that you have adequate storage space for a database of this size.

Also please note that currently if Microsoft SQL Express 2014 (default choice) is installed, the software will show FUSION_SQL14EXP in drop down lists.

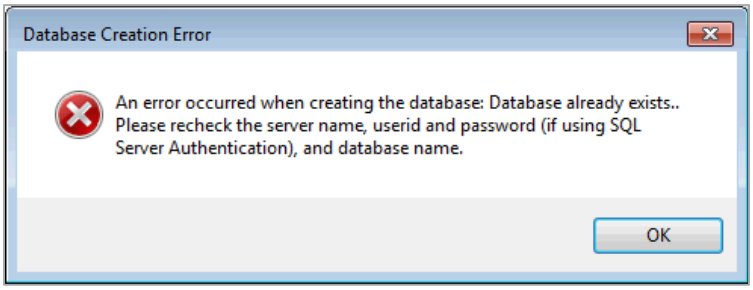
Provided the newly created database name does not already exist, the system creates the new database and displays the following message:



1. Click Yes to connect to it. Click No if you do not wish to connect to it at this time.
2. If you click Yes, a connection confirmation message is displayed:



3. Click the OK button.
4. If the newly created database name already exists, the Database Utility displays the following error message.



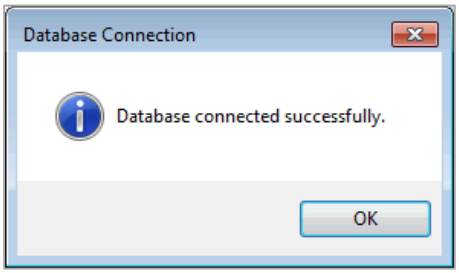
Click the OK button. Then verify that the database name you entered is unique to the selected SQL Server and retry.

The maximum length of a database name must not exceed 35 characters. Only alphanumeric characters and the underline character '_' are recommended for use when naming databases.

Selecting and Connecting to Database

From the Database Utility Window, you can choose to connect to a database that already exists on the selected server. The subsequent analysis with TypeStream Visual will use the selected database.

1. In the Database Utility window, click the Select/Connect to TSV Database option
2. Select a database from the Database Name dropdown selector.
3. Click Set.
4. The following message is displayed:



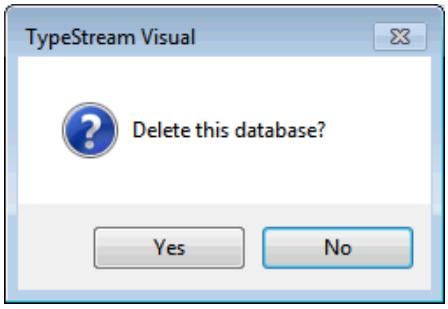
Click the OK button. The database you selected is now listed in the Database Name field in the Status Bar at the bottom of the Database Utility window. When the database connection is set the password to the database server is encrypted and saved in the config file if the Encrypt Password checkbox is selected when launching Database Utility .

Deleting a Database

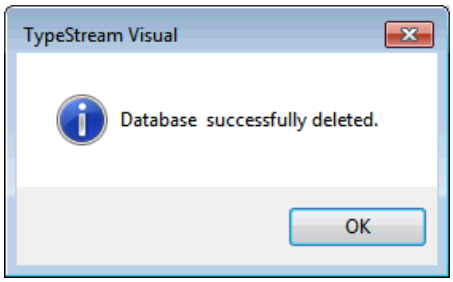
Click the OK button. The database you selected is now listed in the Database Name field in the Status Bar at the bottom of the Database Utility.

1. Within the Database Utility window, click Delete Database.
2. From the Database Name drop-down list, select a database and click the Delete button.
3. Click the Delete button:

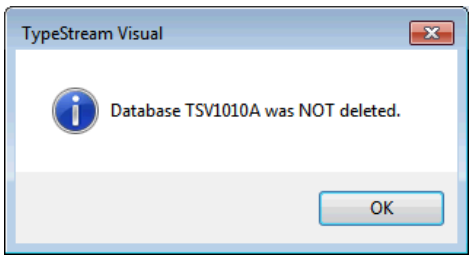
4. A confirmation message is displayed. Click the Yes button to continue with the database deletion.



5. The Database Utility confirms the deletion

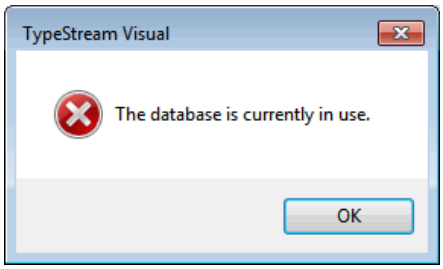


6. If you click No, a message verifying that the database was not deleted is displayed.



NOTE: If you receive a message that the selected database is in use, you must first detach the database from the interface (see Detach a database). You cannot delete an attached database.

7. Click the OK button to exit.



Attaching a Database

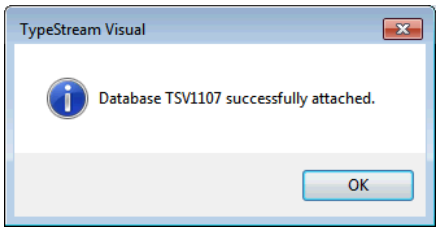
You may use the Attach and Detach Database options together when you want to move a database to another location and then link to that new location. Here is the sequence to follow if you want to do this:

- Detach the database, (see the section: *Detaching a Database* for more information)
- Move the database .mdf file, (which contains the database) to the desired location on another server.
- Attach the database using the steps below, specifying the new location of the moved database.

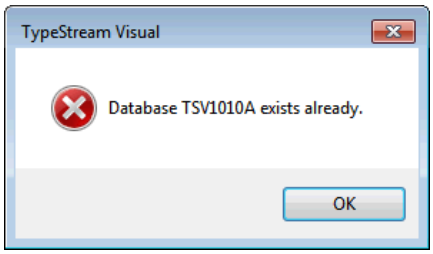
You can use the Attach database function to link to any TypeStream Visual database .mdf file. However, the database .mdf file you are attaching must reside on the selected server.

It is recommended that you back up the database before using the Attach feature.

1. Within the Database Utility window, click Attach Database.
2. Click the Browse button ... next to the MDF file to attach field and navigate to the database file you want to attach. Default location of databases is C:\Program Files (x86)\Microsoft SQL Server\MSSQL12.FUSION_SQL14EXP\MSSQL\DATA\.
3. Select the database (*.mdf) file and click the Open button. The path to the selected (*.mdf) file displays in the 'MDF file to attach' field.
4. Click the Attach button (above), then you will see this message:



If you attempt to attach a database that is already currently attached, you will receive a message like this:



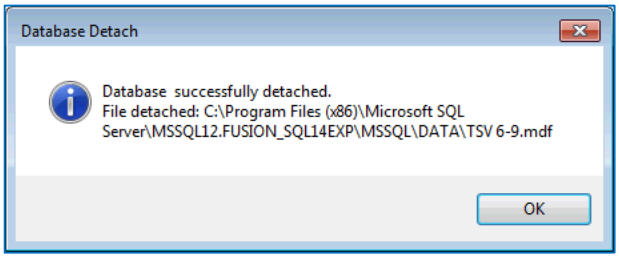
Detaching from a Database

If you wish to move a database file, (.mdf) to another location for disk space considerations or because you no longer want TypeStream Visual to link to it (but do not want to delete it yet),

NOTE: You cannot detach a database which is currently in use.

you must first detach it from TypeStream Visual. You can then relocate it and link to its new location, (see the database menu section entitled: Attaching to a Database).

1. Within the Database Utility window, click Detach Database.
2. From the Database Name drop-down list (above), select a database and click the Detach button. The following message is displayed.
3. Click the OK button.



NOTE: A detached database .mdf file is located in the directory where the TypeStream Visual instance of SQL was installed (e.g., for Microsoft SQL Express 2014, C:\Program Files(x86)\Microsoft SQL Server\MSSQL12.FUSION_SQL14EXP\MSSQL\Data

Creating a Database Backup File

It is recommended that you create regular, frequent backups of your TypeStream Visual database(s). If some event occurs that corrupts a database, or makes it inaccessible, having a backup copy of the database allows you to restore all data up through the date of the most recent backup. Use the Schedule Backup feature to set up automated regular backups of a specified database—any day or time, and as often as desired. For information on restoring a database with a backup copy, see the section, Restoring a Database.

The backed up database must be saved to the local drive of the server or the computer on which you are creating the backup copy. The filename of the backup file is the name of the database with a .bak extension.

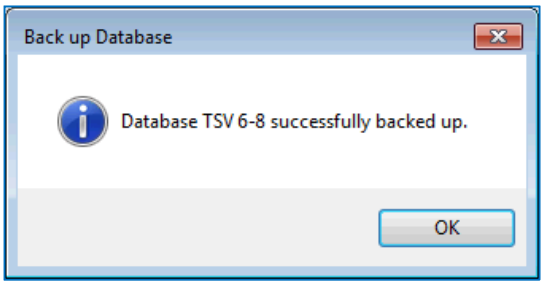
When setting up TypeStream Visual in a networked environment, the Sessions/Batch setting *(see General Settings > Paths)* must point to a networked, shared location.

You can use a shared or network mapped drive to store backups if the SQL agent is given the appropriate permissions to that directory. For more information, please refer to http://support.microsoft.com.

1. Within the Database Utility window, click Backup Database.
2. From the Database Name drop-down list (not shown open here, see arrow), select a database.

NOTE: Make sure you select a destination directory that is on the selected SQL Server. If you use your PC as a location for backups, it is recommended that you create a special folder for backups on the C: drive (e.g., C:\DB Backups) and do not store backups on the desktop.

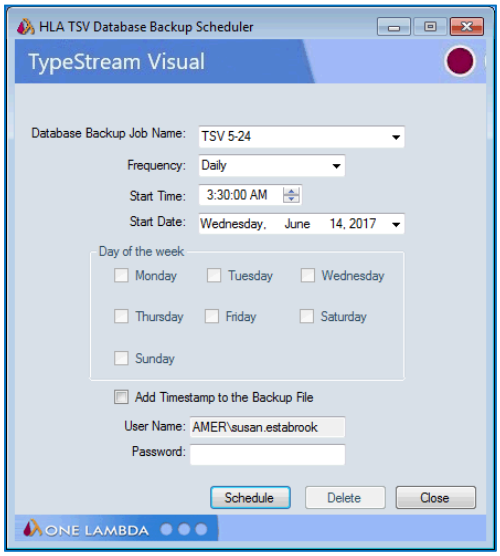
3. Click the Browse button ... next to the Destination field. A new window displays where you can navigate to a destination folder for the database backup.
4. Enter a database backup file name in the Backup File field (by default, it is the database name).
5. You may also click the Make New Folder button and create a special folder for your database backups. The backed up files are stored with a (.bak) file extension.
6. At this point you have two button options:
    a. 'Backup' – this will perform the backup immediately
    b. 'Schedule Backup' – this will open a window to schedule the backup for another day(s) and time:
7. To perform a backup of the database immediately, click the Backup button.
8. The following message confirms a successful database backup.
9. Click the OK button to exit.



Schedule a Backup

NOTE: The length of time required to back up a database is proportional to its size—the larger the database, the longer it takes to back it up.

To schedule backup(s) for a future date and time, or on an automated schedule, click Schedule Backup. The backup scheduler is displayed.



1. Complete the fields in the Database Scheduler to set the backup day and time:
2. Database Backup Job Name: Enter a unique name for the backup. Each scheduled backup task requires a unique name.
3. Frequency: Use the drop-down arrow to select the backup frequency (Daily, Weekly or Monthly).
4. Start Time: Use the up/down arrows to set the time at which to start the scheduled backup. Please note that the length of time required to back up a database is proportional to its size - the larger the database, the longer it takes to back up.
5. Start Date: Click the drop-down arrow and select the date on which you want the scheduled backup process to begin.
6. Days of the week: If you selected a frequency of weekly or monthly, select the check box for the day(s) of the week for which you would like to schedule backups. This option is grayed-out if the specified frequency is Daily.
7. Enter your Windows password in the Password field. You must enter this password to ensure you have the correct privileges to back up the database as specified.
8. Click the Schedule button.

It is not required to have the application running or to be logged-in to run scheduled backup tasks. However, you must have your computer on during the backup period.

NOTE: The directory you specified for the scheduled backups will contain the database backup file, (.mdf) as well as a log file that documents the backup job status.

If your scheduling is confirmed, a message is displayed.

Deleting a Scheduled Backup

Take the following steps to delete a scheduled backup job.

1. Click Schedule Backup. The backup scheduler is displayed.
2. Use the drop-down arrow in the Database Backup Job Name field to select a scheduled backup task to delete.

NOTE: The drop-down list may display more TypeStream Visual tasks than just backup jobs. Be careful to select only the TypeStream Visual database backup task you wish to delete. This list only displays the tasks assigned under the current windows username. Other user tasks should be viewed through the task scheduler function in the Windows.

3. Click the Delete button. You are asked to confirm the deletion of the task
4. Click the Yes button to delete the scheduled backup. If your scheduling has deleted, the following message is displayed.
5. Click the OK button to return to the main Database Utility Screen.

To create a new backup task, follow the steps for Scheduling a Backup in the prior section.

Restoring a Database

You can use database backups to restore, (replace) a database. The backup database copy contains all TypeStream Visual data up through the date of the backup creation.

You can restore a database backup to any existing, or new database - except for the current database.

Restoring a database can only be performed on the server or the computer where the backup database file resides.

1. Within the Database Utility window, click Restore Database.
2. Click on the browse button ... next to File To Restore text box. This brings up the File Selection window.
3. Browse to select the database backup file, (will have a .bak extension) to restore and click the Open button.
4. Enter a unique name for the restored database in the Restore as field and click Restore.
5. Click the Restore button. The database is restored to the specified filename and the following message is displayed.

NOTE: Microsoft SQL Server does not allow you to restore databases from certain locations, such as from a network drive or from a backup file on your computer desktop.

NOTE: If the user restores a database .bak file from one machine to another, the NGS Session folder must also be copied to the destination machine and the path in General Settings must point to the folder path.

Optimizing a TypeStream Visual Database

Optimizing a TypeStream Visual Database on a regular basis speeds up the analysis process by compacting wasted space, automatically repairing errors and optimizing data storage. To optimize a TypeStream Visual Database, do the following. First, open the TypeStream Visual Database Utility:

1. Select Optimize Database from the Database Tasks Menu.
2. Select the database you want to optimize from the Database Name drop-down.
3. Click the Optimize button.

When the database optimization is completed, you'll see a message indicating that the process was completed successfully.

Note that during optimization, SQL Server will temporarily require additional hard drive space to complete the process. If the additional hard drive space is not available, or your database exceeds the size limitations of SQL Express during optimization, the process may fail.

Here are a few suggestions to solve this problem:

- Reduce the size of the database by moving sessions from the current database to another database.

- If you're using SQL Server 2005 Express, (which has a four gigabyte size limitation) consider upgrading to SQL Server 2014 or 2019 Express, which each allow a larger ten gigabyte database size.
- Purchase the full version of MS SQL Server which offers a nearly unlimited database size.

A database can be optimized automatically in the same way that a database can be backed up on a pre-set schedule.

Scheduling Database Optimization

Setting the TypeStream Visual Database Utility to automatically perform database optimization is accomplished in exactly the same way as scheduling an automatic database backup.

1. Select Optimize Database from the list of database tasks in the TypeStream Visual Database Utility.
2. Select the database you want to schedule optimization for from the Database Name drop-down list.
3. Click the Schedule button.
4. The Scheduler window will appear (above). Create a new Database Optimization Job Name or select an existing Database Optimization Job Name from the drop-down list.
5. In the next field, Frequency, select the frequency that you want the optimization to run: Daily, Weekly or Monthly.
6. In the Start Time field, use the up and down arrows to select a time when the database optimization process will begin.
7. In the Start Date field, click the down arrow and choose the first day on which you want the database optimization to run.
8. If you selected Weekly in the Schedule Optimize field, select the day, or days, you want the database optimization to run in the Day of the Week section.
9. Enter your Username and Password and click the Schedule button.
10. The Database Utility will display a message indicating that the Database Optimization job has been successfully scheduled.

Reconfiguring a TypeStream Visual Database

Reconfiguring a Database allows you to increase the size of an existing database. To reconfigure and increase the size of an existing TypeStream Visual Database, please do the following:

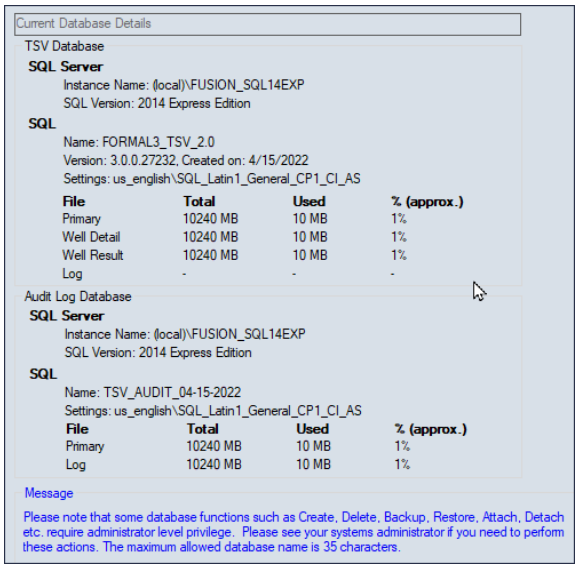
1. Select Reconfigure Database from the list of Database Tasks in the TypeStream Visual Database Utility.
2. Ensure that you're connected to the correct SQL Server.
3. If not, click the ... Browse Button in the SQL Server section to select the correct SQL Server.
4. Choose the database that you want to reconfigure by clicking the down arrow at the right side of the Database Name field to select it.
    a. Increase the size of the database by typing a new size, or by clicking the up and down arrows in the field just below the Database Name,

b. Or increase the database size to its allowable maximum size by placing an arrow in the Unlimited size checkbox provided for this purpose.

5. Click the Set button.
6. The Database Utility will display a message that the database reconfiguration was successful.

Current Database Details

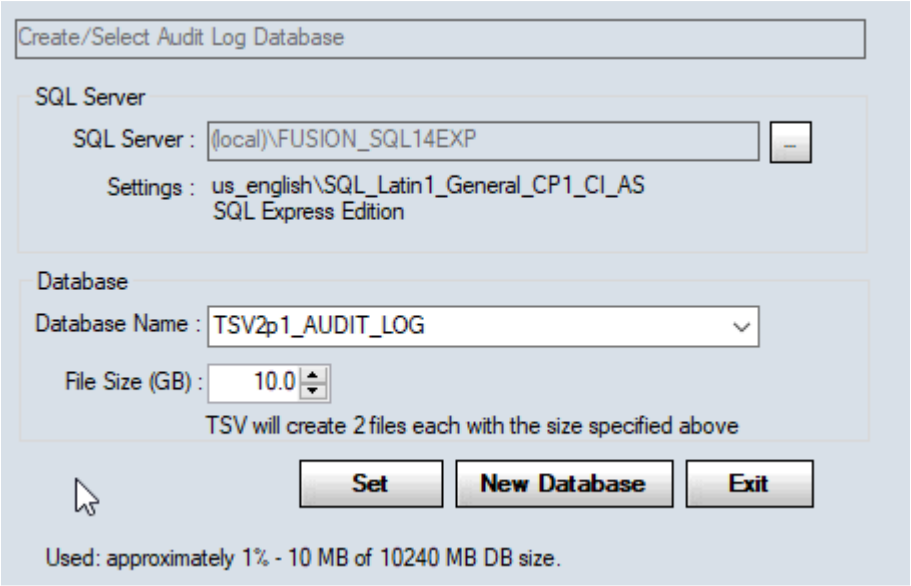
Selecting Current Database Details from the menu on the left side of the Database Utility brings up a detailed listing of the most important information concerning your TypeStream Visual databases.



The top part of this screen deals with the main TypeStream Visual database while the bottom section is devoted to the Audit Log database.

If the percentage of a database file exceeds 90%, it may be time to Optimize and/or Reconfigure the database to free up more space.

Create/Select Audit Log Database



A database for the audit trail log can be created or selected in much the same way as creating or selecting the main database.

- On the left side of the Database Utility window, click Create/Select Audit Log Database:
- Enter a unique Name for the new database (or select an existing one).
- Choose the desired database size and click Create.

Upgrading a TypeStream Visual Database

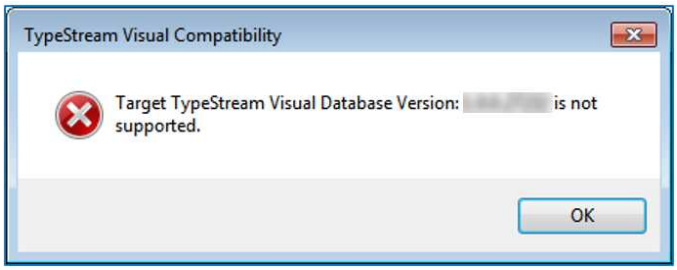
In the case of an update to TypeStream Visual that requires a change to the database structure, any current database will need to be upgraded before it can be used with the updated system.

New in v3.0

In Version 3.0, TypeStream Visual can upgrade databases from Version 1.3 and higher. Versions prior to v1.3 are no longer supported.

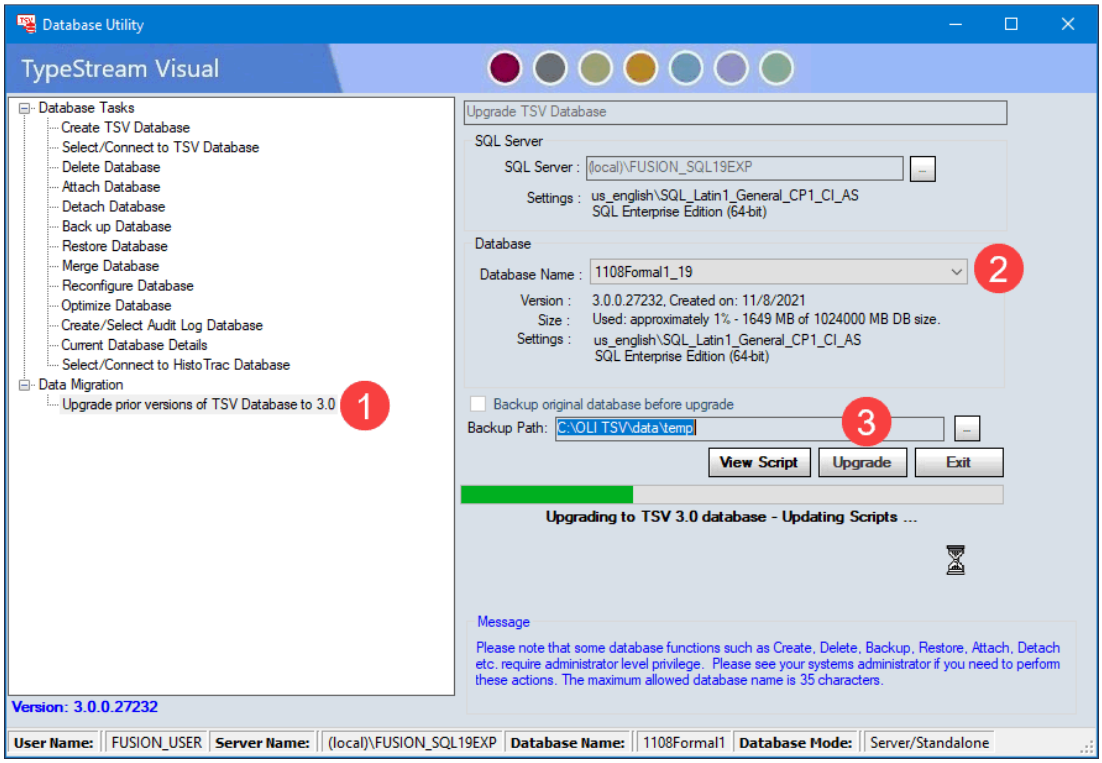
Note: For standalone configuration install, users migrating from one computer to another should make sure to move the /data/session folder to the new computer.

Attempting to connect to an older database through the database utility will return the following message:

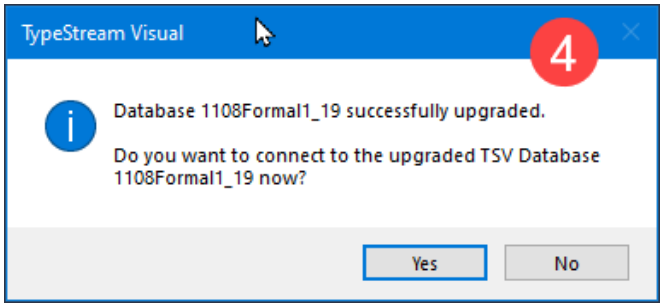


To upgrade your database to be compatible with the latest version of TypeStream Visual, do the following (please refer to the numbered sections in the screen image below the list of instructions):

1. Go to the Main Menu of the TSV Database Utility, and under Data Migration, select "Upgrade prior versions of TSV Database."
2. Use the Drop-down control to select your database. Version number, size, and settings for the selected database will display below the name.
3. Click the Upgrade button (you can also choose to backup the original database or view the script of upgrade actions, as described in the paragraph below). A progress bar will display during the upgrade process.
4. A message will display verifying a successful upgrade and giving the option to connect to the upgraded database now?



If you reply 'No,' you can always connect to it later using the TSV Database Utility.

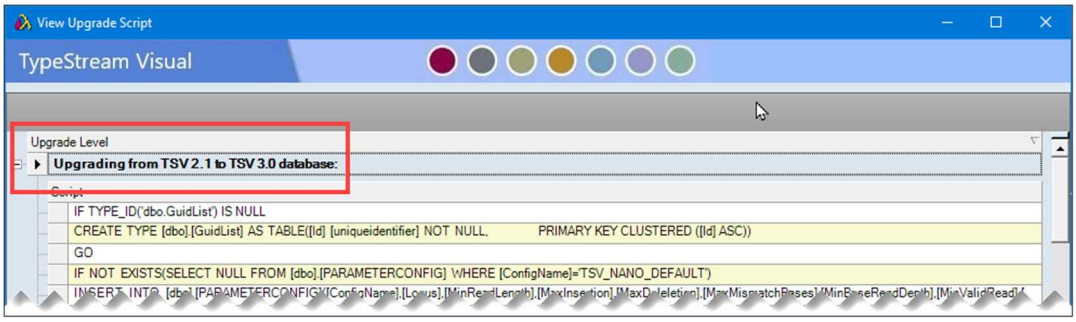


Create a backup

You may create a backup of your database before upgrading simply by checking the "Backup original database before upgrade" check box. The default location for storage of the backup is c:\OLI TSV\data\temp, but you may set the location to any local folder, with the exception of the desktop, My Documents directory, or a network directory.

View Script

If you would like to know the specific tables affected by the database upgrade, first select a database and click the "View Script" button. A table is displayed containing the available upgrades, e.g., "Upgrading from TSV 2.1 to TSV 3.0 database." Expand the '+' next to the appropriate upgrade. Full text of the database upgrade script displays.



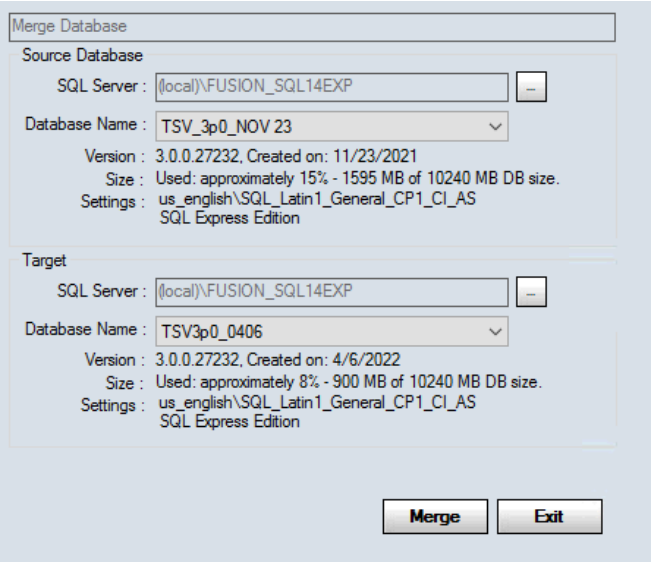
Merging a TypeStream Visual Database

This function allows you to combine two databases into one, regardless of their location. There are certain guidelines to follow when merging databases:

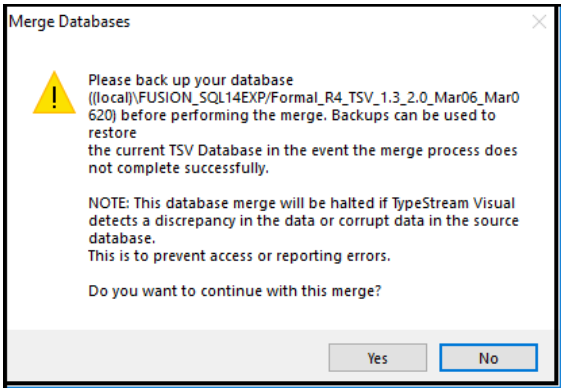
Both databases must be the same version of a TypeStream Visual Database.
Both databases should be backed up before performing a database merge.
The source database information is copied into the target database.
When merging into an *existing* TypeStream Visual Database, ensure that the destination database size is big enough to store the source database. By existing database, we mean that it has lab and user information at minimum.
The source database lab data will be copied if it is missing from the target

database.
When merging into a new TypeStream Visual Database, first create a new database using the Create Database function and make the size large enough to accommodate the source database.
Note that Donor Group Names, Patient ID's, Test Types, and Test Dates will not be merged if this information already exists in the Target Database.

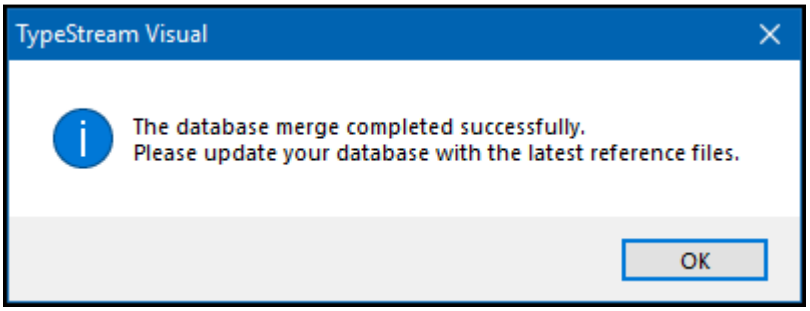
1. Within the Database Utility window, click Merge Database.
2. Select a database from the Database Name drop-down list under Source Database (assumed done; not shown here). The version, size, and settings for that database are then displayed:



1. Select a database from the Database Name drop-down list under Target. The version, size, and settings for that database are displayed once you select (not shown). (The system will prompt you to select a database, as shown by the red exclamation icon above).
2. You must look at the version, size, and settings of both the source and target database before merging to verify the version and settings match and that the size of the source database is not too large for the target.
3. Click the Merge button. You may see this message to please back up your database. If you are ready to continue with the merge operation, click the Yes button:

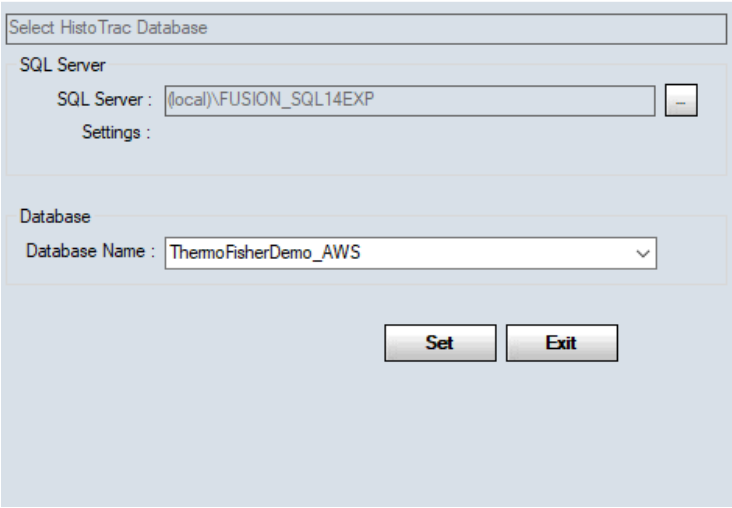


4. After the Merge, the following message is displayed:

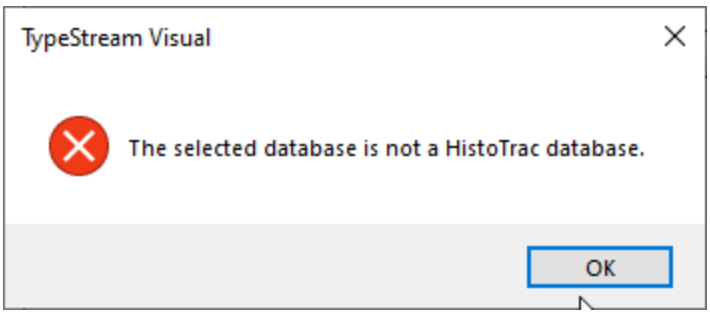


5. Click the OK button to return to the main Database Utility Screen.

Connect to HistoTrac database



Select a HistoTrac database from the Database Name drop-down list. The application will list all the databases from the selected SQL server. TSV will connect successfully if the selected database is a Histotrac database otherwise an error message as below would appear.
There should be sessions/samples imported into HistoTrac from TSV software for the selected database to be considered valid.



HistoTrac

What is HistoTrac?

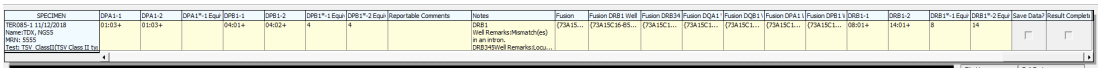
HistoTrac is a software package for HLA laboratories that automates your laboratory. It provides secure, role-driven access to your database and software functions. HistoTrac enables TSV users to do test tracking and creation of reports in tandem with TSV analysis. From TSV, user can send create PDF reports and screen shots and save these in the HistoTrac database directly.

Note: TSV 2.1 and TSV 3.0 is verified and validated with the current version of HistoTrac (2.53.3) but cannot claim future compatibility if HistoTrac version changes.

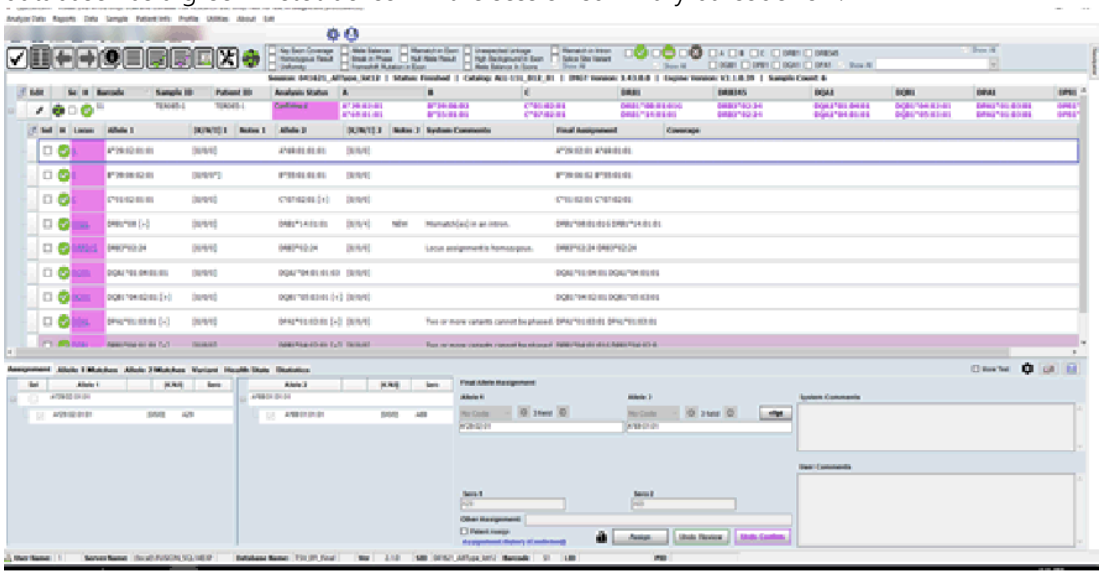
HistoTrac should be pre-installed on the client computer and connected to TSV database.

Opening TSV from HistoTrac

1. Samples associated to a TSV test have the below format for the sample record that includes information of the Well ID from the TSV database.



2. Users can click on the column to navigate to TSV. Samples associated in Histotrac database has a green Histotrac icon in the session summary barcode row.

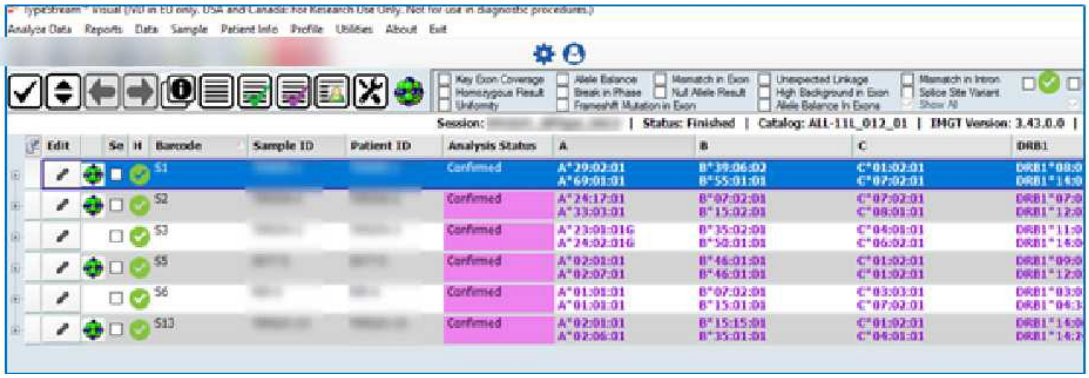


Note:	In order for a HistoTrac user to be able to navigate to TSV, the database information along with the user login details must be configured in HistoTrac application.

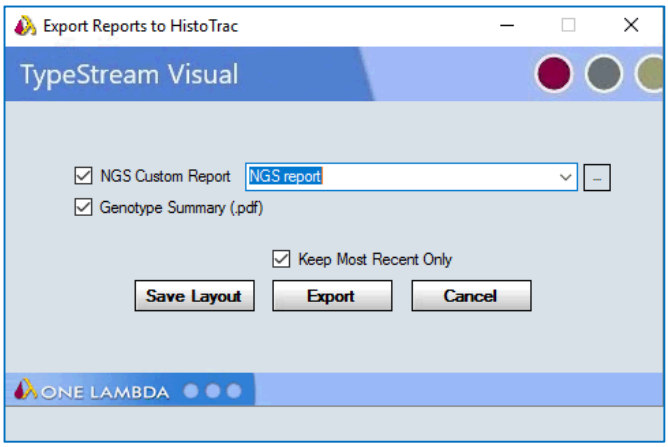
Exporting Report from TSV to HistoTrac

A green icon appears on the session summary header row, that indicates to the user if one / more samples in the session is associated to samples in the HistoTrac database. The icon is disabled if not samples are linked to HistroTrac.

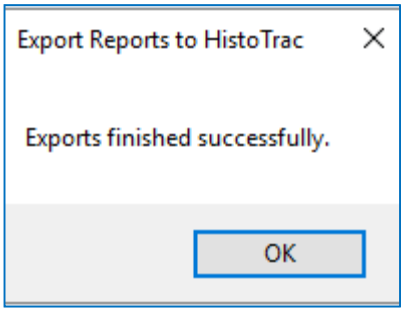
In addtion, to the icon the top of the summay row, individual barcode rows/ sample rows have the histotrac icon if they are linked to HistoTrac.



Selecting one or more samples that are associated and clicking on the HistoTrac icon on the session summary row, displays the below popup. Users have the ability to select the NGS custom report and genotype summary (.pdf) report.

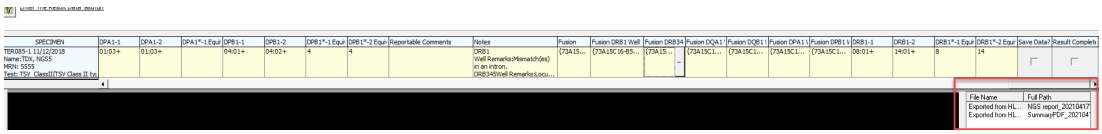


- NGS Custom Report: Select a predefined layout or create a new one using the box.
- Genotype Summary (.pdf)
- The option to Save Layout remembers your checkbox and list box selection choices and Keep Most Recent Only allows you to overwrite the most recent report instead of accumulating many reports.
- When you have made the choices you want, click Export. The selected items are exported into the HistoTrac database, and the following message appears:



To examine exported information within HistoTrac, do the following:

Close TSV and locate the HistoTrac window. On the Test Results screen, the results of the Export operation are now visible in a list on the right-hand side of the screen. Double-click any item to view the report or screen shot that was exported.



Appendix A

Copying BAM Files from Torrent Server

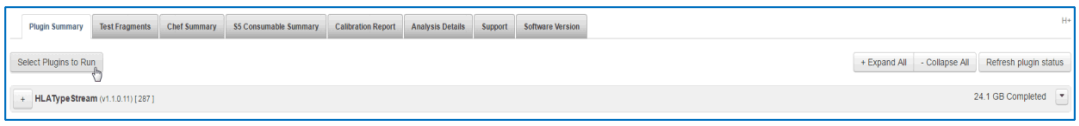
BAM files can be easily exported from the Torrent Server using the FileExporter Plugin.

BAM files can be exported as individual files or as a single compressed file containing all BAM files.

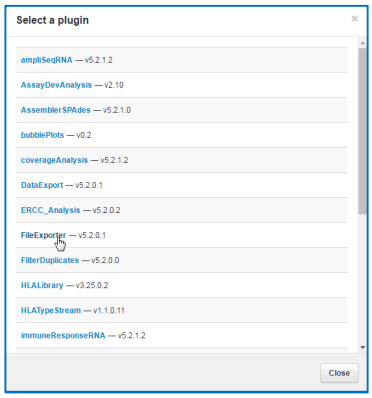
Custom renaming of files is also possible.

Copying Files using FileExporter Plugin:

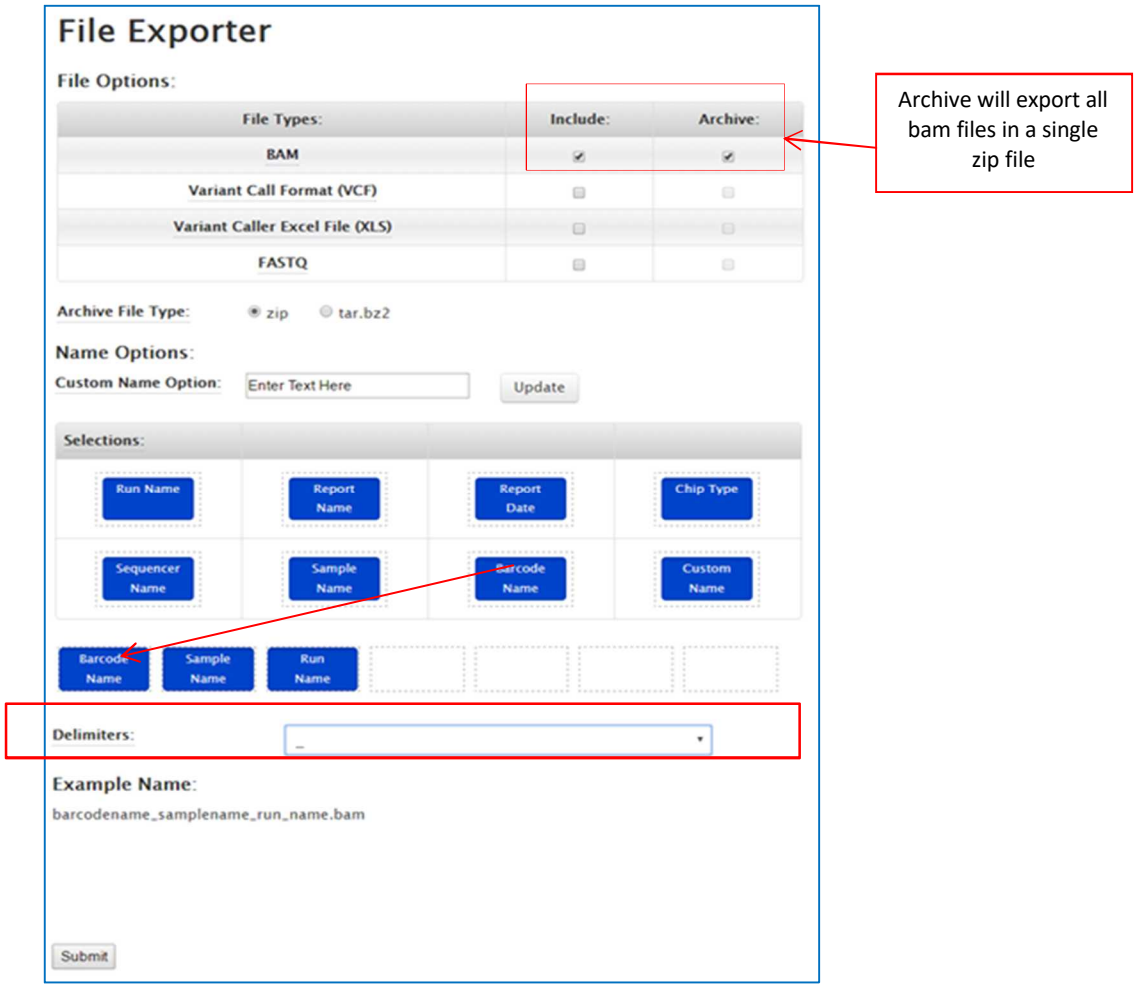
1. Select Plugin to Run



2. Select FileExporter

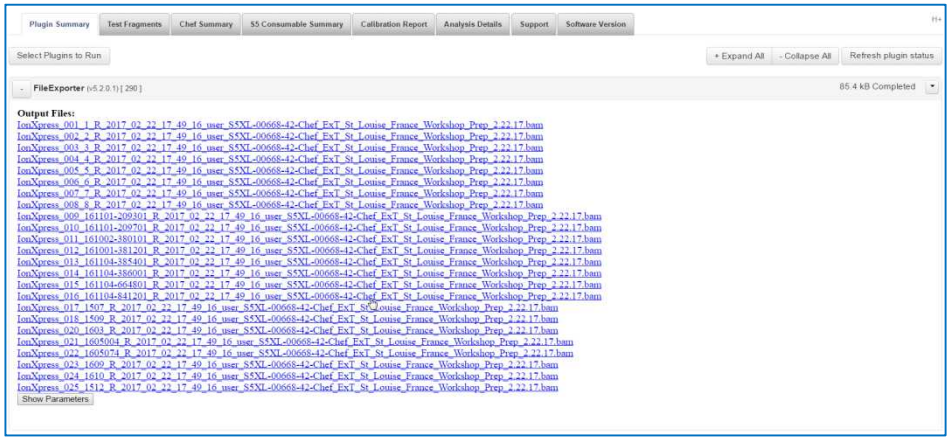


3. Enter File Exporter information
    a. Select a desired file type:
        i. To export individual BAM files, check BAM and leave Archive unchecked
        ii. To export all BAM files as a single zip file, check both BAM and Archive
    b. Select File Naming format by drag & drop in desired order
    c. Select delimiter



4. Click Submit
5. Results of FileExporter are displayed:

6. Click each link to download BAM files individually



7. Or Click Compressed Files link to download BAM files in .zip file format (Archive option)

Reference Documents

Software version	Document Name	Document ID
TSV 2.0	TypeStream Visual NGS Analysis Software v2.0 Release Notes	TDX-OLI-DMR-PS-3248
TSV 2.0	TypeStream Visual NGS Analysis Software v2.0 Installation Guide	TDX-OLI-DMR-PS-3226
TSV 2.0.1	TypeStream Visual NGS Analysis Software v2.0.1 Release Notes	TDX-OLI-DMR-PS-4134
TSV 2.0.1	TypeStream Visual NGS Analysis Software v2.0.1 Installation Guide	TDX-OLI-DMR-PS-4109
TSV 3.0	TypeStream Visual NGS Analysis Software v2.0.1 Release Notes	TDX-OLI-DMR-PS-4767
TSV 3.0	TypeStream Visual NGS Analysis Software v3.0 Installation Guide	TDX-OLI-DMR-PS-4768

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EXPLANATION OF SYMBOLS

(Reference EN ISO 15223-1: medical devices – symbols to be used with medical device labels, labeling and information to be supplied.)

Symbol	Description
ISO 7000 Reg No. 1641	Consult instructions for use. An eIFU indicator can be a manufacturer's website URL or some other appropriate indication that the instructions for use are available in an electronic format.
REF *ISO 7000 Reg No. 2493*	Catalog number
IVD	In vitro diagnostic medical device
ISO 7000 Reg No. 0434A	Caution
ISO 7000 Reg No. 3082	Manufacturer
EC REP	Authorized representative in the European Community
ISO 7000 Reg No 2497	Date of Manufacture

Batch field on the label is for traceability of manufacturing event.

For Summary of Safety and Performance, contact TDX Customer Service

Revision History

Revision	Date	Description of Change
01	Current	Initial Release

This software is for In Vitro Diagnostic Use in the European Union Only. In the USA and Canada this software is For Research Use Only, not for use in diagnostic procedures.

For Research Use Only, this software is not intended to provide information for the diagnosis, prevention or treatment of disease or to aid in the clinical decision-making process. One Lambda Research Use Only software products are designed to assist personnel experienced in genotyping analysis. However, any research results must be carefully reviewed by a person qualified in genotyping. This software may be used to aid in research but should not be used as the sole method for determining reportable research results. This software is meant as a laboratory aid, not as a source of definitive results. The laboratory director or technologist trained in histocompatibility testing is required to review all data to detect any problems with the software. Please note that this document was prepared in advance of the TypeStream™ Visual software release. Therefore, you may notice slight differences in the content of the actual application screens.

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