

TruSight HLA Assign 2.1 RUO

Software Guide

For Research Use Only. Not for use in diagnostic procedures.

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Introduction

The TruSight HLA Assign™ 2.1 software (hereafter referred to as "Assign 2.1") assists with the assignment of a human leukocyte antigen (HLA) type. The software is designed to analyze data from libraries prepared with the Illumina® TruSight® HLA v2 Sequencing Panel for DNA and then sequenced on the Illumina sequencing system.

Using Assign 2.1, you can import sequence data, perform base calling, edit sequences, and compare a consensus sequence with a library of sequences of HLA alleles.

Assign 2.1 has the following features and functionality:

- ▶ Import sequences from multiple samples and multiple loci per sample into a user-friendly interface
- ▶ View sample identifiers, loci headers, sequence reads, base calls, and allele assignments
- ▶ Complete analysis audit trail
- ▶ Sort allele assignments based on regions of each locus, such as core exons, all exons, or entire sequences
- ▶ Generate reports that include CWD alleles, G groups, and P groups
- ▶ Phase-resolve paired-end sequence data from Illumina TruSight HLA libraries sequenced on the Illumina sequencing system

IMGT/HLA Database

Assign 2.1 compares a sample sequence with a library of sequences from known alleles listed in the IMGT/HLA database, which comprises sequences of the human major histocompatibility complex, known as the human leukocyte antigen (HLA). The IMGT/HLA database includes sequences for the World Health Organization (WHO) Nomenclature Committee for Factors of the HLA System. The IMGT/HLA database is part of the international ImMunoGeneTics (IMGT) project (www.imgt.org).

Performance Characteristics

Assign 2.1 can import sequence data from samples generated by the TruSight HLA v2 Sequencing Panel into a single project.

Base Call Accuracy

Assign 2.1 contains a unique base caller that improves the accuracy of heterozygous base calls. However, sequence data quality and depth of sequencing coverage can influence base call accuracy.

Limitations

Poor quality data including sequences with background noise or low depth of sequencing coverage might result in incorrect base calls and incorrect typing. Assign 2.1 includes a simple visual interface to view read quality and depth of sequencing coverage, which enables rapid identification of poor read quality and low depth of sequencing coverage.

Assign 2.1 compares a sample sequence with a library of sequences from known alleles listed in the IMGT/HLA database. The report lists those allele combinations in the library that are identical to the sample sequence. However, the same sequence might be derived from alleles yet to be described and whose sequence is not yet part of the library. Therefore, caution is advised when interpreting the genotype report as an HLA type.

Computing Requirements and Compatibility

To ensure optimal performance, use the following minimum computing requirements:

- ▶ 1 GHz or faster 64-bit Intel quad-core processor, or equivalent
- ▶ 16 GB RAM, minimum
- ▶ 16 GB available hard disk space
- ▶ Recommended screen resolution—1920 × 1080 pixels

Sequence data files can be stored locally or on a network location. Depending on network performance, the software might experience a significant delay in processing while files are imported from a network location.

Computer Operating System and Software

Assign 2.1 runs on Windows and requires Windows Vista, Windows 7, Windows 8, Windows Server 2008, or Windows Server 2012 operating systems.

Assign 2.1 is not compatible with the following editions of Windows: Embedded (including Windows on the Illumina sequencing system), RT, Starter, Mobile, and Phone, or any hardware that does not support a standard keyboard, mouse, and monitor.

Microsoft Excel 97, or later, is required for generating Excel reports from Assign 2.1.

Compatible Data File Formats

Assign 2.1 is compatible with the FASTQ file format, either zipped (*.fastq.gz) or unzipped (*.fastq). The Illumina sequencing system generates these file formats. For more information about the FASTQ file format, see the MiSeq Reporter Generate FASTQ Workflow Reference Guide (document # 15042322).

Installation

Illumina recommends administrator access to the computer before installing Assign 2.1. Make sure that the computer is connected to the internet to facilitate system updates with new libraries and other files when needed.

- 1 Double-click the installer (*.msi) file and follow the prompts to install the software.
- 2 Review the License Agreement.
- 3 Accept the terms in the License Agreement, and then click **Next**.
- 4 Select the Installation Folder location. Illumina recommends that you accept the default location. Click **Next**.
- 5 Select shortcut options, and then click **Next**.
- 6 Click **Install** to begin the installation.
- 7 When the installation is complete, click **Finish**.



NOTE

In a default installation, the reference library files, as well as the CWD, P, and G group files are also installed. Updated reference files are available semiannually from the Illumina TruSight HLA support website. At a minimum, updating annually is recommended.

Getting Started

- 1 Double-click the Assign 2.1 icon on the desktop or in the installation location.
- 2 In the Operator Login dialog box, select the operator from the drop-down list. The default operator is **admin**.
- 3 Enter the password. The default password for the admin operator is **cg01**.

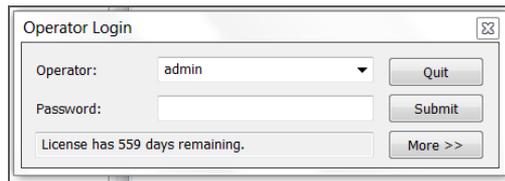


NOTE

Illumina recommends that you do not change the admin password.

- 4 Click **Submit** to start the software.

Figure 1 Operator Login



Add License

- 1 In the System group, click **Update**.
- 2 Browse to the Assign 2.1 license file obtained from Illumina, and then click **Open**. Licenses can also be stored in the software installation folder.
- 3 Click **Done**, and then restart the software.



NOTE

License keys are provided with a fixed time frame (eg, 6 months). To obtain a new license key, contact Illumina Customer Service.

Add Operators

- 1 Double-click the Assign 2.1 icon on the desktop or in the installation location.
- 2 In the Operator Login dialog box, from the **Operator** drop-down list, select an operator. The default operator is **admin**.
- 3 Enter the password. The default password for the admin operator is **cg01**.
- 4 Click **More** to expand the Operator Login dialog box and access the Edit Users section.
- 5 In the **Edit Operator** field, enter a new operator name.
- 6 Enter a password for the new operator and retype the same password for verification.
- 7 From the **Default Settings** drop-down list, select **TruSight HLA**. Select this setting for all operators analyzing TruSight HLA data. Operators with sufficient privileges can modify settings directly in Assign 2.1.
- 8 From the **Operator Level** drop-down list, select from the following options.

Operator Level	Permissions
First Reviewer (edit only)	Cannot change settings. Can edit sequences not yet approved by a final reviewer. Cannot sign the final review checkbox.
First Reviewer (with access to settings)	Can change settings. Can edit sequences not yet approved by a final reviewer. Cannot sign the final review checkbox.
Final Reviewer (with full access)	Can change settings. Can edit sequences not yet approved by a final reviewer. Can sign the final review checkbox.

Figure 2 Add Operator

- 9 Click **Add/Update**.

Import and Analyze Sequences

- 1 Click an open document tab to choose the import destination. To create a document, click the File button  and select **New** or press Ctrl+N.
- 2 On the Home tab, in the Data group, click **Import and Analyze**.
- 3 Navigate to the folder containing the FASTA/FASTQ/GZ files.
The software automatically detects the version of the HLA-B and HLA-DRB primers used.
- 4 Use the Ctrl or Shift keys to highlight the desired files. Click **Open** to begin import and analysis.



NOTE

Each sample generates a FASTQ file for Read 1 and Read 2. Make sure that you select both FASTQ files.

Importing sequences can take from minutes to hours depending on the number of files imported and the computer system performance. During import, Assign 2.1 is unavailable and the application title bar indicates that the software is not responding. The software responds after import and analysis is complete.

The first import takes slightly longer to analyze after the initial installation and after a reference update. During the first import, only a single user can use the software.



TIP

To abort an import and close Assign 2.1, from the computer Task Manager, highlight the application and click **End Task**.

After you import sequences into Assign 2.1, analysis begins automatically. Analysis includes alignment of reads, base calling, phasing, IMGT/HLA reference alignment, and HLA typing.

Importing Errors

After the analysis of imported sequences is complete, either of the following warnings appear to indicate that the files were not successfully imported.

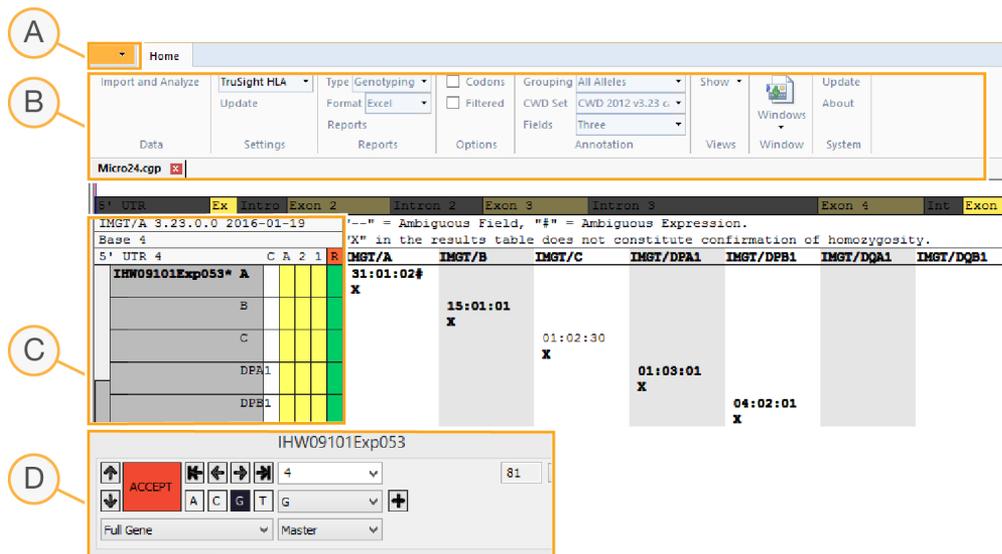
- ▶ No sample identifier/delimiter
 - ▶ There are no dashes (-) in the file name as expected.
 - ▶ There are no appropriate characters before the first dash to name the sample.
- ▶ No target identified/delimiter
 - ▶ An appropriate gene name is missing or incorrect (eg, A, B, C, DPA1, DPB1, DQA1, DQB1, DRB1, HLA).
- ▶ Unable to combine 1 or more paired end files.
 - ▶ Only a single read was imported for 1 or more samples.

FASTQ sample file names typically have the following format:

- ▶ *samplename-HLA-date_S1.FASTQ.gz* (eg, 00001234-HLA-04262016_S5_L001_R1_001.fastq.gz, 00001234-HLA-04262016_S5_L001_R2_001.fastq.gz)
- ▶ For more information, see the *TruSight HLA v2 Sample Sheet Template (part # 1000000012322)*.

Navigating the Interface

Figure 3 Assign 2.1 Interface

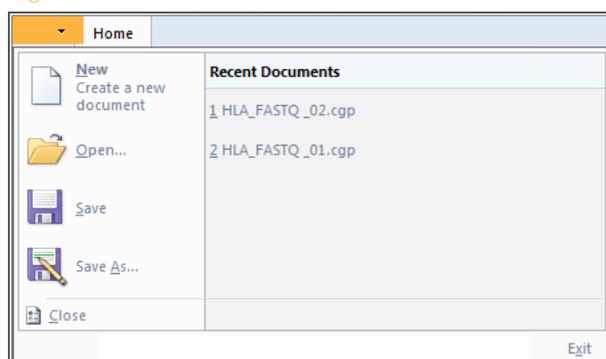


- A **File menu**—Allows you to create new, open, and save sequences in Assign 2.1.
- B **Home tab**—Provides access to change settings and views.
- C **Sample panel**—Lists the samples in a project, expands to show each locus typed, and tracks reviewer comments and the laboratory analysis pipeline. For more information, see *Sample Panel* on page 12.
- D **Navigator**—Helps you navigate to base positions of interest. For more information, see *Navigator* on page 15.

File Menu

The File menu is located to the left of the Home tab. Click the down arrow to open the File menu. Use the File menu to create new, open, and save projects.

Figure 4 File Menu

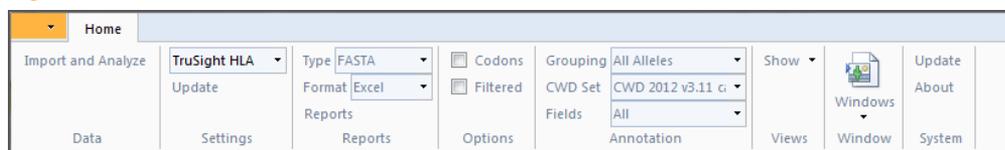


Click **Save** or **Save As** to save aligned reads, the Sample Consensus Sequence, and user edits.

Home Tab

The Home tab is divided into the following groups: Data, Settings, Reports, Options, Annotation, Views, Window, and System.

Figure 5 Home Tab



Data

The Data group allows you to import and analyze sequence data.

- 1 In the Data group, click **Import and Analyze**.
- 2 Navigate to the folder containing the FASTQ files.
- 3 Use the Ctrl key to select individual files or the Shift key to select a group of files that you want to import and analyze. Use Ctrl + A to select all the files in a folder. The search box at the top right of the import dialog can also be used to find a particular sample or locus for analysis. When searching for files, it is possible to create a project with input files from multiple folders.
- 4 Click **Open**.



NOTE

Each sample generates a FASTQ file for Read 1 and Read 2. Make sure that you select both FASTQ files. For optimal analysis, both Read 1 and Read 2 FASTQ files are imported and analyzed simultaneously.

Settings

The TruSight HLA setting is the default configuration for the Results panel. To change the default configuration, select customized settings in the Reports, Options, and Annotation groups, and then click **Update** in the Settings group.

Reports

The Reports group allows you to generate 2 types of reports.

- ▶ Report types are Genotyping and FASTA.
 - ▶ Genotyping report file formats are text, Excel, or XML.
 - ▶ FASTA reports are saved in FASTA format.

For more information, see *Generating Reports* on page 33.

Options

The Options group allows you to switch between viewing options.

- ▶ **Codons**—Switches views between nucleotide and codon numbering.
- ▶ **Filtered**—Removes allele pairs from the Results panel that are not consistent with base calls that have been confirmed.

Annotation

The Annotation group allows you to consolidate annotations into the following groups:

- ▶ **G Groups**—Consolidates the Results panel list into G groups.
- ▶ **P Groups**—Consolidates the Results panel list into P groups.
- ▶ **All Alleles**—Shows all allele matches in the Results panel.

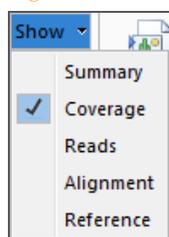
The CWD Set shows a list of the Common and Well-Documented (CWD) alleles, which are indicated in bold in the Results panel.

The Fields dropdown allows you to limit the view of alleles in the results list to the specified number of fields. The default is set to 3. If you select **All**, the sequence used for the typing is automatically expanded to the entire gene for all loci. When the number of fields is decreased, alleles can appear several times in the results table. Identical allele pairs can occur because there are 3rd or 4th field differences with resulting mismatch differences.

Views

The Views group allows you to navigate between panels to view sequence data in different ways. Use the Show drop-down list to choose the **Summary**, **Coverage**, **Reads**, **Alignment**, or **Reference** view.

Figure 6 Views Group



- ▶ **Summary**—Comprises 3 panels.
 - ▶ Typing Summary panel—Shows the types assigned.
 - ▶ Quality Summary panel—Shows the percentage of base calls with quality \geq Q30.
 - ▶ Coverage Summary panel—Shows the mean depth of sequencing coverage. For more information, see *Summary View* on page 18.
- ▶ **Coverage**—Shows the mean coverage and base call composition across the amplicon. For more information, see *Coverage View* on page 21.
- ▶ **Reads**—Shows reads used in base calling. For more information, see *Reads View* on page 31.
- ▶ **Alignment**—Shows a comparison of the Sample Consensus Sequence and the allele pairs lists in the Results panel. For more information, see *Alignment View* on page 32.
- ▶ **Reference**—Shows a comparison of the Sample Consensus Sequence and the reference sequences for a locus. For more information, see *Reference View* on page 32.

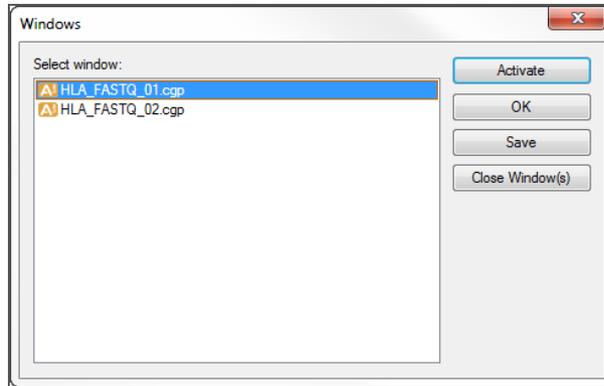
Window

In the Window group, the **Windows** list allows you to control open file windows.

Click **New Window** to duplicate the active window in a new tab. The active window file name appears in bold on the tab.

Click **Windows** to open a dialog box that allows you to activate, save, or close a currently open window.

Figure 7 Windows Dialog Box



- ▶ **Select window**—Lists the open file windows. Click a file name to highlight it.
- ▶ **Activate**—Click to activate the highlighted file window.
- ▶ **OK**—Click to close the dialog box without applying changes.
- ▶ **Save**—Click to save the highlighted file.
- ▶ **Close Windows**—Click to close the highlighted files.

System

The System group allows you to update and view information within the Assign 2.1 software.

Click **Update** to open a dialog box that allows you import keys, references, NMDP codes, and CWD files.

Click **About** to open a dialog box that provides the software version and licensing information.



NOTE

CWD sets cannot be toggled and changed dynamically in the user interface. To change the CWD file, select **Update** in the Settings tab and restart the software.

Sample Panel

The Sample panel shows the sample names, the loci sequenced for each sample, the IMGT/HLA reference release, and the status of the review for each locus.

Figure 8 Sample Panel

IMGT/A 3.23.0.1 2016-01-19		C	A	2	1	R
Base 3318						
3' UTR 94						
IHW01018Exp049						
IHW01040Exp049* A						
B						
C						
DPA 1						
DPE 1						
DQA 1						
DQB 1						
DRE 1G03						
DRE 3						

- A IMGT/HLA reference
- B Samples and Loci

C Review hierarchy, report enabling, and locus-specific commenting

IMGT/HLA Reference

The first row in the Sample panel shows the IMGT/HLA reference database used for assignment of HLA nomenclature to the sample sequence. For more information, see *IMGT/HLA Database* on page 3.

The following example indicates specific information about the database:

IMGT/A 3.23.0.0 2016-01-19

- ▶ IMGT is the reference database
- ▶ A is the gene name
- ▶ 3.23.0 is the IMGT/HLA database release version
- ▶ 2016-01-19 is the date of the IMGT/HLA release

Assign 2.1 converts sample sequences into HLA nomenclature version 3.0, established in 2010, in agreement with the WHO Nomenclature Committee for Factors of the HLA System.

The HLA nomenclature uses the following format:

HLA-A*02:01:01:02L

HLA	The HLA Prefix
-	The hyphen separates the gene name from the HLA prefix.
A	The gene name. For TruSight HLA, the gene name can be A, B, C, DRB1, DRB3, DRB4, DRB5, DQB1, DPB1, DQA1, or DPA1.
*	The asterisk separates the gene name from the sequence information.
02	Field 1—The allele group; alleles that encode an antigen.
:	A colon separates fields.
01	Field 2—Specific alleles that differ at the protein level from DNA substitutions and result in nonsynonymous amino acid substitutions.
:	A colon separates fields.
01	Field 3—Synonymous DNA substitutions within coding regions of the gene.
:	A colon separates fields.
02	Field 4—Differences in the noncoding regions of the gene.

L

This expression modifier is present regardless of the number of fields reported. As of date, the following modifiers are possible:

- N denotes Null—An allele that is not expressed.
- L denotes Low—An allele encoding a protein with significantly reduced or low cell surface expression.
- S denotes Secreted—An allele encoding a protein that is expressed as a secreted molecule only.
- Q denotes Questionable—An allele with a mutation that has previously been shown to have a significant effect on cell surface expression, but is not confirmed. Therefore, its expression remains questionable.

Samples and Loci

Click a sample name to view the loci that have been identified for the selected sample. Click a locus to view information for the selected locus in the Sequences and Results panels.

Review Hierarchy

The review hierarchy section of the Sample panel includes 5 columns, which allow for multiple levels of review and comment for each sample and each locus listed. The columns are labeled C, A, 1, 2, and R. Each review level is tracked and audited.

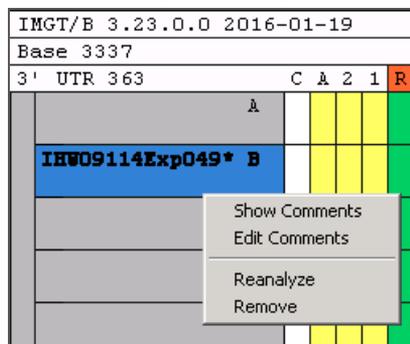
- ▶ **Column C**—By default, the box in column C is white. Right-click the sample or locus to add a comment related to the review. When comments are present, the box changes to light blue. Comments added in column C are included in the full genotyping report.
- ▶ **Column A**—By default, the box in column A is yellow. When the sample is verified at all positions indicated in the Navigator, the box in column A changes to green automatically.
- ▶ **Column 2**—By default, the box in column 2 is yellow. When the second review is complete, click the yellow box to change it to green, indicating the second review is complete and locking the sample. No further edits are possible unless the box is cleared manually.
- ▶ **Column 1**—By default, the box in column 1 is yellow. After the first review is complete, click the yellow box. The box changes to green, which indicates that the first review is complete.
- ▶ **Column R**—A green box in column R indicates that the locus is included in generated reports. Click the red box to prevent reporting on the locus.

Sample Panel Options

Additional options are available for any locus listed in the Sample panel. To view options, right-click on a locus name. The following options are available:

- ▶ **Show Comments**—Shows any quality warnings or comments about a sample.
- ▶ **Edit Comments**—Opens a field to add or edit comments about the selected sample. These comments appear on the report. A light blue box in column C indicates that a comment is present.
- ▶ **Reanalyze**—Removes any edits and trims made to the selected locus. This function does *not* completely restore the locus to its original state after import.
- ▶ **Remove**—Removes the selected locus from the project.

Figure 9 Sample Panel Options



Navigator

Use the Navigator to navigate to a base position of interest, confirm base calls, or make base call edits. You can drag the Navigator anywhere on the screen.

Figure 10 The Navigator

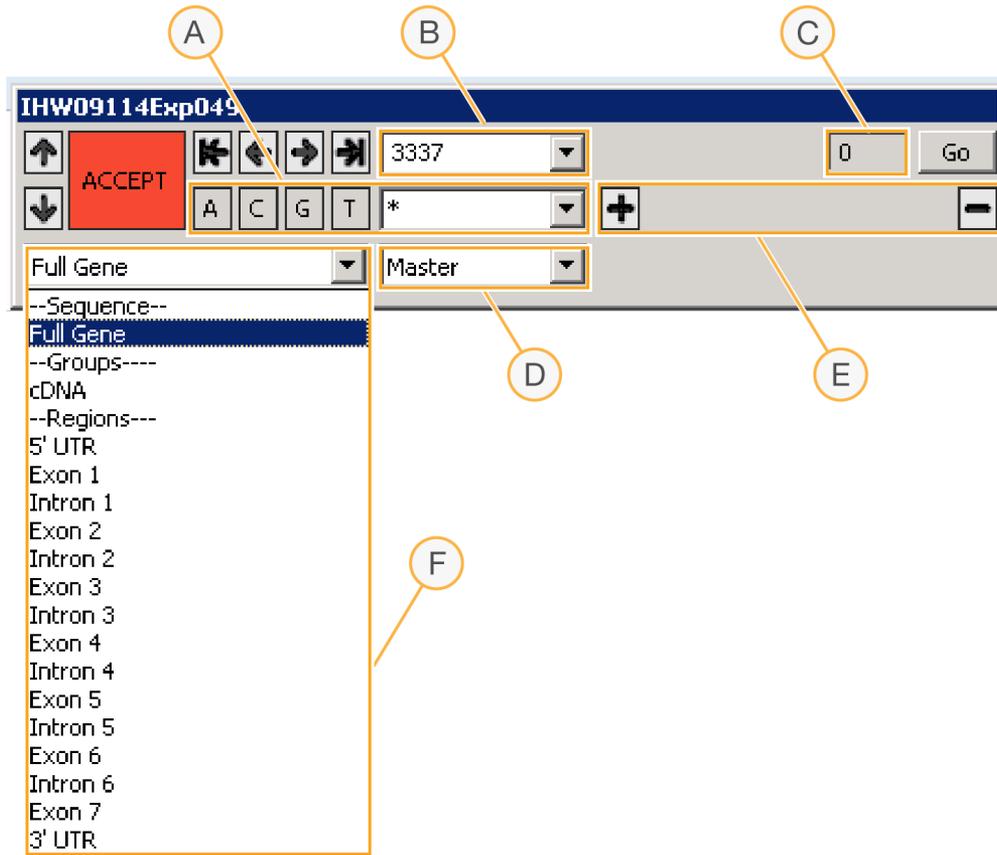


Basic Navigation

Navigation Icon	Description
 	Click the up and down arrows to navigate between loci in the Sample panel.
 	Click Accept to confirm a base call at a specific position. Click Reject to change a previously accepted base call.
 	Use the previous and next arrows to navigate between base positions highlighted in the Confidence Indicator. For more information, see <i>Confidence Indicator</i> on page 25.
 	Use the first and last arrows to navigate to the base positions highlighted at either end in the Confidence Indicator.
	Click Go to make a selection.

Advanced Navigation

Figure 11 Advanced Navigation



- A Base Selection
- B Active Nucleotide Position and Mismatch List
- C Confidence Indicator
- D Phase Tracks List
- E Indel Details
- F Nucleotide Position Field Change

Base Selection

The highlighted base indicates the base call at the current position. Multiple highlighted bases indicate that more than one base was positively identified at the current position.

A highlighted **+** indicates an insertion. A highlighted **-** indicates a deletion.

- 1 To add or remove a base at the current position, click **A**, **C**, **G**, or **T**, or select from the base selection list.
- 2 Click **Accept** to accept the selected base and move to the next low confidence position.
- 3 To change a previously accepted base call, click **Reject** to enable editing.

Use with the **Filtered** option in the Options group to eliminate allele pairs from the Results panel that are not consistent with confirmed base calls. For more information, see *Options* on page 10.

Mismatch List

The Mismatch list shows the selected position. Select the down arrow to show all mismatch positions for the selected allele pair in the active mismatch columns.

To move the cursor to a selected position, enter a number in the nucleotide position field and click **Go**, or select an option from the list to move to that position.

Confidence Indicator

The Confidence Indicator shows a numerical value from 0 to 99 for the selected base. A value of 0 indicates low confidence and a value of 99 indicates high confidence.

The Confidence Indicator value is associated with the coloring on the Confidence Indicator. Dark red indicates low confidence and white indicates high confidence. For more information, see *Confidence Indicator* on page 25.

Phase Tracks List

Use the Phase Tracks drop-down list to switch between layers (sequence and phase tracks) in a locus.

Indel Details

At a position where an insertion or deletion is present, the appropriate + (insertion) or – (deletion) box is highlighted in blue. The length of the insertion or deletion and the bases included in that insertion or deletion are indicated in the space between those symbols.

Nucleotide Position Field Change

The default numbering begins at the first base of the gene. Use the drop-down list to change the numbering system. You can also view the position of a base within an exon. Use cDNA numbering to determine the position within the coding sequence.

- ▶ **Full Gene**—Position in gene sequence based on the locus consensus sequence.
- ▶ **Groups**
 - ▶ **cDNA**—Position in cDNA. In this view, introns are numbered individually beginning at 1 in each intron.
- ▶ **Regions**— For a particular position of interest, choose the region of the gene, enter the relative position in the mismatch list, and then click **Go**. Use this feature for quick navigation.

Summary View

After imported files have completed analysis, the default view is the Summary view. To see the Summary view later, click **Show** in the Views group, then click **Summary**. Alternatively, hover the mouse cursor over the blue box in the upper-left corner of the view in the Coverage, Reads, Alignment, or Reference views, and then click the blue arrow that appears.

The following Summary panels are available within the Summary view:

- ▶ Typing Summary panel
- ▶ Quality Summary panel
- ▶ Coverage Summary panel

Navigating the Summary Panels

To move between Summary panels, hover over the blue box in the upper-right corner of a Summary view and click the blue arrow that appears. This arrow cycles through the Summary panels.

Typing Summary Panel

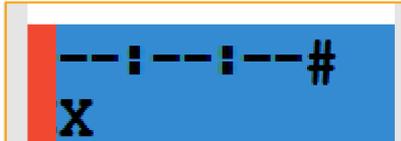
The Typing Summary panel shows the samples and types assigned to each locus for each sample. In addition to the typing results, this panel shows whether sequence or expression ambiguities exist, each of which warrant further investigation.

Use multiple monitors or increase the screen resolution on your monitor to expand the number of viewable fields for each locus. The recommended screen resolution is 1920 x 1080 pixels.

Figure 12 Typing Summary Panel

“-” = Ambiguous Field, “#” = Ambiguous Expression.
“X” in the results table does not constitute confirmation of homozygosity.

IMGT/A	IMGT/B	IMGT/C	IMGT/DP1A	IMGT/DP1B	IMGT/DQA1	IMGT/DQB1	IMGT/DRB1	IMGT/DRB3	IMGT/DRB4
03:01:01 X	35:01:01 56:01:01	01:02:01 04:01:01	01:03:01 02:01:01	04:02:01 11:01:01	01:01:01 04:01:01	04:02:01 05:01:01	01:01:01 08:01:--		



The Typing Summary panel uses the following markers:

- ▶ **Active sample**—A blue highlight indicates the active sample. Click the highlighted area to open the sample and locus in the Coverage view for further investigation. Complete fields indicate an unambiguous typing result.
- ▶ **Ambiguous expression**—A # indicates an ambiguous expression in an allele typing.
- ▶ **Ambiguous fields**—A double dash (--) indicates an ambiguous field in the typing result. For example, --:01 indicates an ambiguity in the first field, 01:-- indicates an ambiguity in the second field, and 01:01:-- indicates an ambiguity in the third field.

- ▶ **Confidence warning, red**—A red box immediately to the left of an allele pair indicates a locus that might warrant further investigation. This warning can indicate insufficient coverage or read quality.
- ▶ **X shown for second allele**—An X shown for the second allele indicates that no heterozygous positions were detected in the analyzed sequence. The presence of an X in the summary screen does not constitute confirmation of homozygosity.
- ▶ **Bold text**—Indicates a CWD allele.

Quality Summary Panel

A quality score, or Q-score, is a modified Phred score that measures the probability of an incorrect base call. During Illumina sequencing, each base in a read is assigned a Q-score. A higher Q-score indicates a smaller probability of error. For example, a Q-score of 30, indicated as Q30, represents a 1 in 1000 chance of an incorrect call with a corresponding 99.9% call accuracy.

The Quality Summary panel shows the percentage of base calls with Q30 or higher scores for each locus. A confidence warning appears for loci when the percentage of base calls with a Q30 score is 75% or less.

Figure 13 Quality Summary Panel

Percent base calls with Q30 or better.										
IMGT/A	IMGT/B	IMGT/C	IMGT/DPA1	IMGT/DPB1	IMGT/DQA1	IMGT/DQB1	IMGT/DRB1	IMGT/DRB3	IMGT/DRB4	IMGT/DRB5
		99%	99%	99%	99%	98%	96%	94%		96%

Coverage Summary Panel

The Coverage Summary panel shows the mean depth of sequencing coverage for each locus in the project. The depth of sequencing coverage is the number of observations of a particular base in the sequence data. Warnings are present when loci do not meet specifications of 100x average coverage. If the 2 alleles of a locus are split between 2 groups (eg, DQB1 and DQB1G06), a warning appears when the group does not meet specifications of 50x average coverage.

Figure 14 Coverage Summary Panel

Average sample coverage.										
IMGT/A	IMGT/B	IMGT/C	IMGT/DPA1	IMGT/DPB1	IMGT/DQA1	IMGT/DQB1	IMGT/DRB1	IMGT/DRB3	IMGT/DRB4	IMGT/DRB5
		310	297	312	317	293	272	267		259

Gene Summary

Hover the mouse cursor over an allele typing to see the following summary information.

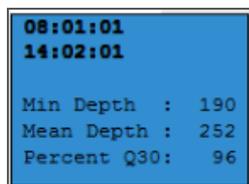
- ▶ **Min Depth**—Minimum sequence coverage across the sequence used for the typing call. The default minimum depth is all exons.
- ▶ **Mean Depth**—Average depth of sequencing for the locus.
- ▶ **Percent Q30**—Percentage of bases > Q30.



NOTE

When alleles from more than 1 group are present, the summary shows results for the first listed allele.

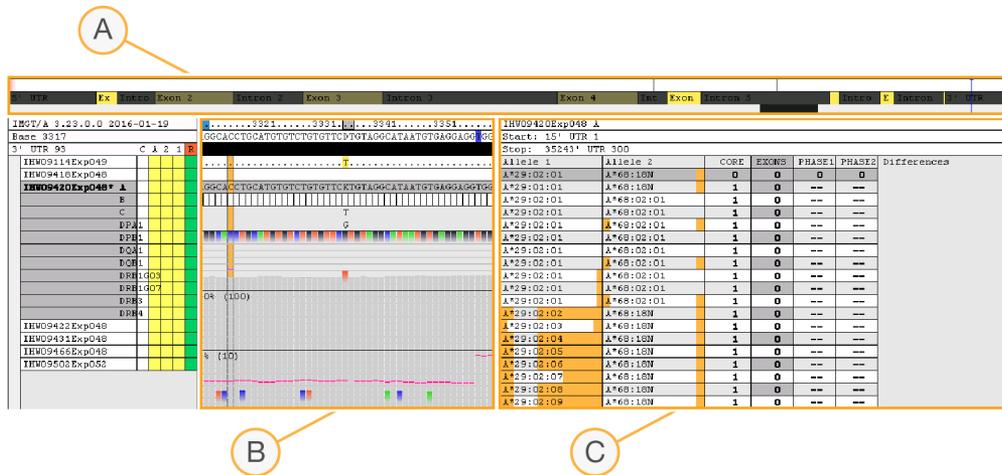
Figure 15 Gene Summary Popup



Coverage View

The Coverage view comprises the Confidence Plot, Locus Structure, and Phase Block Display, the Sequences panel, and the Results panel. To see the Coverage view, in the Views group, click **Show**, and then click **Coverage**.

Figure 16 Coverage View



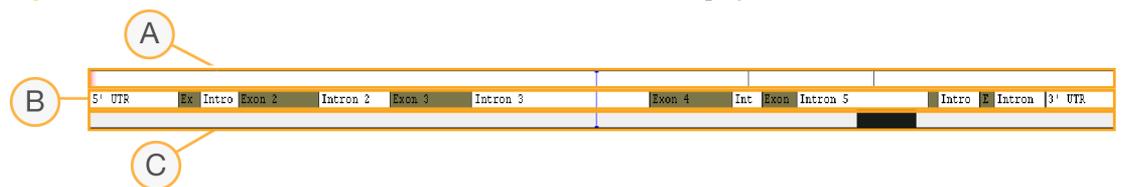
- A Confidence Plot, Locus Structure, and Phase Block Display**—Shows a view of the high-level locus structure, such as UTRs, introns, and exons, indicates base call confidence and position, and indicates blocks of phased sequence. For more information, see *Confidence Plot, Locus Structure, and Phase Block Display* on page 21.
- B Sequences Panel**—Shows consensus reference sequence, sample sequence, base calls, depth of sequencing coverage, base call quality, and alternate sequence reads. For more information, see *Sequences Panel* on page 22.
- C Results Panel**—Shows the allele combinations that most closely match the sample sequence, and shows the mismatches between the sample sequence and the reference sequence when present. For more information, see *Results Panel* on page 28.

Move the Coordinate scroll box in the Sequences panel to find positions where base call confidence is low. Use the Results panel to find mismatches with allele pairs.

Confidence Plot, Locus Structure, and Phase Block Display

Three rows span the width of the screen at the top of the Coverage view.

Figure 17 Confidence Plot, Locus Structure, and Phase Block Display



- A Confidence Plot**
- B Locus Structure**
- C Phase Block Display**

Click a row to move the blue line, which indicates the region in view in the Sequences panel.

Confidence Plot

The Confidence Plot uses colors to show positions where base call confidence might warrant further investigation.

Figure 18 Confidence Plot colors

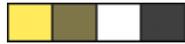


- ▶ Black indicates no coverage. Common reasons for no coverage include the following:
 - ▶ The amplicon does not cover the full genomic sequence for the analyzed locus
 - ▶ The reference sequence contains an insertion that is absent in the sample
- ▶ Increasing shades of red indicate any of the following conditions:
 - ▶ Sequence coverage \geq Q30 is below 100x
 - ▶ Mean quality score for base calls at this position is low
 - ▶ A base above noise threshold is not called in consensus
 - ▶ A base below noise threshold is called in consensus
- ▶ White indicates complete coverage.

Locus Structure

The Locus Structure uses yellow to indicate an exon/coding sequence and white or gray to indicate an intron/noncoding sequence.

Figure 19 Locus Structure colors



- ▶ **Bright yellow**—Exons that are in the active Mismatch Column of the Results panel.
- ▶ **Dark yellow**—Exons that are not currently in the active Mismatch Column of the Results panel.
- ▶ **White**—Noncoding regions that are in the active Mismatch Column of the Results panel.
- ▶ **Gray**—Noncoding regions that are not in the active Mismatch Column of the Results panel.

Phase Block Display

In the Phase Block Display, regions are either light gray or black.

Figure 20 Phase Block Display colors



- ▶ **Light Gray**—Regions where bases are phased together
- ▶ **Black**—Sections where phase linkage is lost

The first phasing block begins at the beginning of the gene and extends until the last heterozygous position that is able to be phased. The last phasing block continues from the last heterozygous position through to the end of the gene.

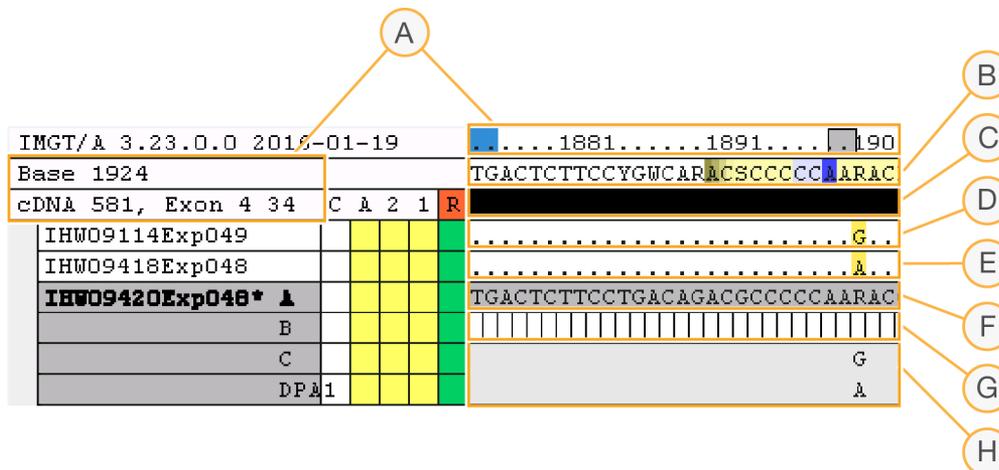
Sequences Panel

The Sequences panel on the Coverage view is composed of the Sequences section and the Base Calling section.

Sequences Section

The Sequences section of the Sequences panel includes information from comparisons of reference sequences with sample sequences. These rows are updated when you select different allele pairs in the Results panel.

Figure 21 Sequences Section



- A Coordinates
- B Locus Consensus Sequence
- C Sequence Edit Indicator
- D Allele 1 Reference Sequence
- E Allele 2 Reference Sequence
- F Sample Consensus Sequence
- G Confidence Indicator
- H Phasing Track



TIP

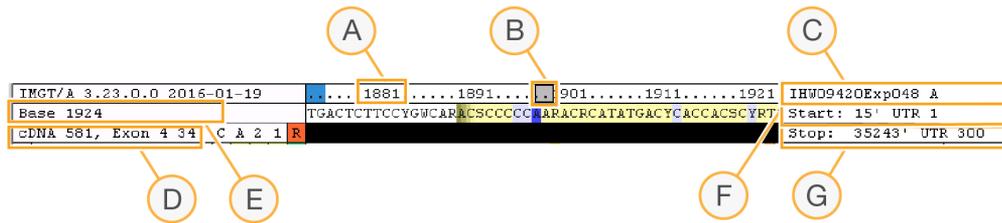
If **cDNA** is selected for Groups, press CTRL+A in the Sample Consensus Sequence to alternate between nucleotide and amino acid views.

The consensus sequence rows in the Sequences section (rows B and E) include International Union of Pure and Applied Chemistry (IUPAC) degenerate base designations.

Code	Bases	Description
W	A T	Weak
S	C G	Strong
M	A C	Amino
K	G T	Keto
R	A G	Purine
Y	C T	Pyrimidine
B	C G T	not A
D	A G T	not C
H	A C T	not G
V	A C G	not T
N	A C G T	all bases
*		no base call

Coordinates

Figure 22 Coordinates



- A Gene coordinates
- B Coordinate scroll box—Drag the gray box to scan along coordinates
- C Sample name and locus
- D Highlighted base coordinate in the exon, intron, or UTR (from Sequences panel)
- E Highlighted base associated codon coordinate in the gene (from Sequences panel)
- F Amplicon start position and location
- G Amplicon stop position and location

Locus Consensus Sequence

The Locus Consensus Sequence represents a collection of common variants and motifs. Rare variants are not included.

- ▶ Yellow indicates exonic/coding sequence
- ▶ White indicates intronic/non-coding sequence
- ▶ Blue indicates insertions or deletions present in some alleles

For HLA-DRB1 and HLA-DQB1, the Sample Consensus Sequence is compared with sequences of alleles that have been divided into groups with similar intronic sequence structure. Therefore, the consensus sequence represents the consensus of the best matched allele group.

- ▶ HLA-DRB1 alleles are split into 4 groups: DRB1G01, DRB1G03, DRB1G04, and DRB1G07
- ▶ HLA-DQB1 alleles are split into 2 groups: DQB1 and DQB1G06

Sequence Edit Indicator

The Sequence Edit Indicator row shows a color-coded edit status and acceptance status of each base in the sequence. The base edit status changes when you edit the originally called sequence using the Navigator.

Color Code	Edit status	Acceptance status
■ Black (default)	Not edited	Not accepted
■ Green	Not edited	Accepted
■ Blue	Edited	Not accepted
■ Blue/Green	Edited	Accepted

Allele 1 Reference Sequence

The Allele 1 Reference Sequence shows the IMGT/HLA reference for an allele in the highlighted allele pair selected in the Results panel.

- ▶ A base is displayed in this row when the allele sequence differs from the Sample Consensus Sequence for the sample, or the position is heterozygous.
- ▶ Blank positions indicate that the reference sequence is missing for the selected allele.
- ▶ A dot (.) indicates that the allele sequence is identical to the observed sequence at the selected position.

Allele 2 Reference Sequence

The Allele 2 Reference Sequence shows the IMGT/HLA reference for an allele in the highlighted allele pair selected in the Results panel.

- ▶ A base is displayed in this row when the allele sequence differs from the Sample Consensus Sequence for the sample, or the position is heterozygous.
- ▶ Blank positions indicate that the reference sequence is missing for the selected allele.
- ▶ A dot (.) indicates that the allele sequence is identical to the Sample Consensus Sequence at the selected position.

Sample Consensus Sequence

The Sample Consensus Sequence shows the consensus sequence of the sample sequenced with the TruSight HLA Sequencing Panel.

Confidence Indicator

The Confidence Indicator is a per-base representation of the Confidence Plot. The confidence of a base call at any given position can vary based on several factors, including balance of the alleles, noise threshold, depth of coverage, and sequence quality.

White in the Confidence Indicator denotes a high confidence base call. A bright red Confidence Indicator denotes base calls in which any of the following conditions have occurred:

- 1 Sequence coverage \geq Q30 is below 100x
- 2 Mean quality score for base calls at this position is low
- 3 A base above noise threshold is not called in consensus
- 4 A base below noise threshold is called in consensus

Use the Navigator to move between red confidence flags. For more information, see *Basic Navigation* on page 15.

Phasing Track

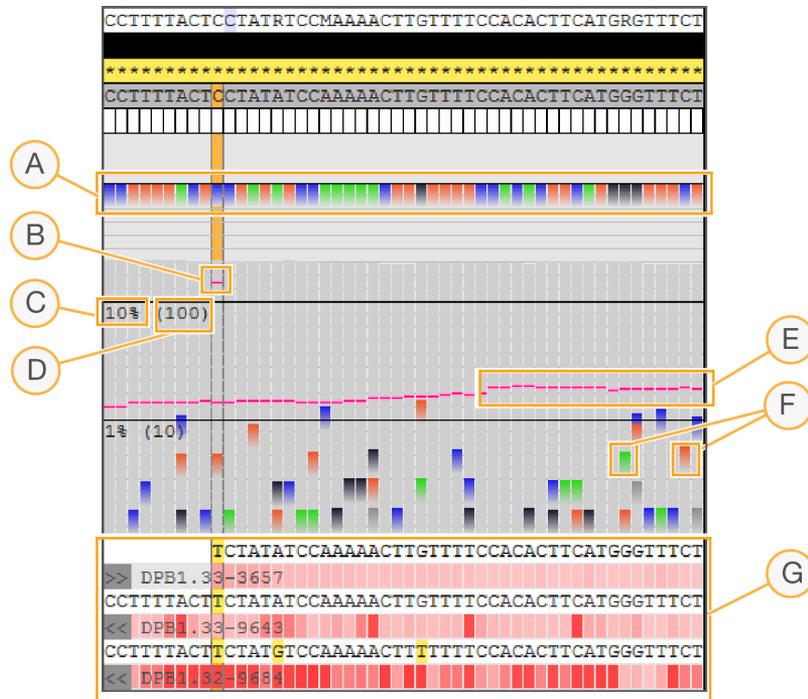
For heterozygous allele combinations, the Phasing Track rows show the phase relationship between bases connected by single reads or paired reads. A phase assignment is made only when most phasing sequences are concordant.

The top row corresponds to Allele 1/PHASE1 in the Results panel and the bottom row corresponds to Allele 2/PHASE2. If there is a large distance between heterozygous positions and the software is unable to link phase, there might be rare instances where the top row corresponds to Allele 2/PHASE2.

Base Calling

Base-level information appears below the Sequences section of the Sequences panel.

Figure 23 Base Calling



- A Primary base called
- B Approximate allele ratio
- C Base call ratio
- D Depth of sequencing coverage
- E Approximate noise threshold
- F Other base calls
- G Sequence reads covering that base position that were not included in the consensus sequence for the sample

Right-click on a read to open a menu.

- ▶ **Copy Sequence**—Places all the bases in the read on the clipboard
- ▶ **Copy Aligned**—Places the bases used during alignment on the clipboard
- ▶ **BLAST Sequence**—Submits the full sequence to NCBI BLAST
- ▶ **Copy Pair**—Places the sequence of a read pair on the clipboard
- ▶ **Show Warnings**—Shows Q30 coverage or mean quality warnings for the sample

Primary Base Called

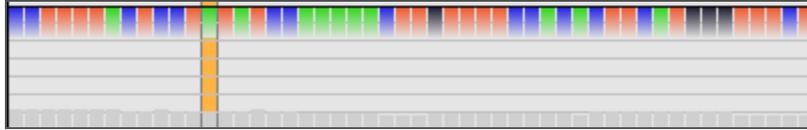
In the Primary Base Called section, the following colors indicate the most frequently occurring base call for a given position.

Figure 24 Primary Base Called Color Indicators



- ▶ A—Green
- ▶ C—Blue
- ▶ G—Black
- ▶ T—Red

Figure 25 Primary Base Called



Approximate Allele Ratio

When a base location is highlighted, the top pink line indicates the approximate mean read depth ratio of the second allele present in the sample for heterozygous loci.

Base Call Ratio

Base calls are shown using a logarithmic scale, as follows:

- ▶ Lowest section has a ratio between 0% and 1%
- ▶ Middle section has a ratio between 1% to 10%
- ▶ Highest section has a ratio between 10% to 100%

Depth of Sequencing Coverage

The depth of sequencing coverage is shown with gray bars for each base using the logarithmic scale in parentheses:

- ▶ Lowest section shows coverage depth between 0x and 10x
- ▶ Middle section shows coverage depth between 10x and 100x
- ▶ Highest section shows coverage depth between 100x and 1000x



NOTE

If the coverage is below 30, no call is shown.

Approximate Noise Threshold

Noise is a common byproduct of amplification fidelity, specificity, sequencing errors, and sequence alignment. Assign dynamically sets a threshold for noise at any given base position. A pink dashed line indicates the Approximate Noise Threshold at all base locations. Typically, base calls below the noise threshold are not called.

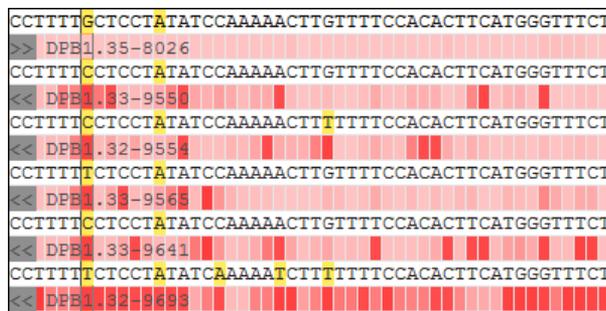
Other Base Calls

The Other Base Calls section shows the base calls that differ from the most frequently occurring base call for a given position and use the same color indicators used in the Primary Base Called section.

Sequence Reads

The Sequence Reads section contains calls that are not included in the Sample Consensus Sequence at the highlighted base position.

Figure 26 Sequence Reads



The quality of the base call for alternate reads, as reported in the FASTQ file, is shown below the sequence in a gradient of red.

- ▶ **Dark red**—Lowest quality base call.
- ▶ **Light pink**—Highest quality base call.

Results Panel

In the Coverage view, the Results panel lists all the IMGT/HLA allele pairs that exactly match or closely match the Sample Consensus Sequence. The Results panel also provides information for each of the allele pairs listed.

Figure 27 Results Panel

Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2	Differences
DPB1*04:01:01:01	DPB1*14:01	0	0	0	0	0	
DPB1*04:01:01:02	DPB1*14:01	0	0	0	0	0	Intron 2
DPB1*23:01:01:01	DPB1*76:01	0	0	0	1	1	Exon 2
DPB1*35:01:01	DPB1*72:01	0	0	0	1	1	Exon 2
DPB1*45:01	DPB1*215:01	0	0	0	1	1	Exon 2
DPB1*67:01	DPB1*214:01	0	0	0	3	3	Exon 2
DPB1*98:01	DPB1*306:01	0	0	0	3	3	Exon 2
DPB1*108:01	DPB1*125:01	0	0	0	5	5	Exon 2
DPB1*57:01	DPB1*66:01	0	0	0	6	6	Exon 2
DPB1*03:01:01	DPB1*04:01:01:01	1	0	2	--	--	
DPB1*03:01:01	DPB1*04:01:01:02	1	0	2	--	--	
DPB1*04:01:01:01	DPB1*35:01:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*45:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*70:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*76:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*104:01	1	1	0	--	--	
DPB1*04:01:01:01	DPB1*119:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*197:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*242:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*243:01	1	0	0	--	--	
DPB1*04:01:01:01	DPB1*266:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*35:01:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*45:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*70:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*76:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*104:01	1	1	0	--	--	
DPB1*04:01:01:02	DPB1*119:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*197:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*242:01	1	0	0	--	--	
DPB1*04:01:01:02	DPB1*243:01	1	0	0	--	--	

- A Allele columns
- B Common and Well-Documented (CWD) alleles (in bold)
- C IMGT/HLA reference coverage (regions that are *not* orange indicate reference coverage)
- D Mismatch columns
- E Differences column

Allele Columns

In the Alleles columns, all allele pairs appear in order based on the number of mismatches they contain when compared to the Sample Consensus Sequence. Allele pairs with no mismatches appear at the top of the columns followed by pairs with increasing numbers of mismatches.

When no heterozygous positions are detected in the sequence used for the typing (default is all exons), the Allele 2 column contains an X. The presence of an X does not constitute confirmation of homozygosity. When a heterozygous position is found in the active sequence, a second allele is reported. When the results table or report is truncated to 2 or 3 fields, the second allele can appear identical.

Common and Well-Documented (CWD) Alleles

In the Results panel and Summary panel, CWD alleles are shown in bold.

IMGT/HLA Reference Coverage

The allele pairs are banded white and gray by alternating rows for ease of viewing. Sometimes, the allele includes orange, which indicates that a part of the reference sequence is missing in the IMGT/HLA reference for that allele. The allele container width is directly proportional to the amplicon length.

The shading represents only exon sequence coverage and does not indicate coverage in noncoding regions.

Figure 28 IMGT/HLA Reference

Allele 1	Allele 2
DPA1*01:03:01:05	DPA1*02:01:01
DPA1*01:03:03	DPA1*02:01:02
DPA1*01:06:01	DPA1*02:03
DPA1*01:03:01:02	DPA1*02:01:01
DPA1*01:03:01:01	DPA1*02:01:01
DPA1*01:03:01:03	DPA1*02:01:01
DPA1*01:03:01:04	DPA1*02:01:01
DPA1*01:03:01:01	DPA1*02:01:02
DPA1*01:03:01:01	DPA1*02:01:04
DPA1*01:03:01:01	DPA1*02:01:06
DPA1*01:03:01:01	DPA1*02:01:07

Mismatch Columns

The number of mismatches in the selected regions appear in the columns to the right of the allele pairs.

Figure 29 Mismatch Columns

Allele 1	Allele 2	A	B	C	D	E
Allele 1	Allele 2	CORE	EXONS	N-C	PHASE1	PHASE2
DPB1*108:01	DPB1*125:01	0	0	0	5	5
DPB1*57:01	DPB1*66:01	0	0	0	6	6
DPB1*03:01:01	DPB1*04:01:01:01	1	0	2	--	--
DPB1*03:01:01	DPB1*04:01:01:02	1	0	2	--	--
DPB1*04:01:01:01	DPB1*35:01:01	1	0	0	--	--

- A Mismatches in core exons; additional positions for expression mutations that are known. For a list of core exons, see the customer release notes for the reference used.
- B Mismatches in remaining exons.
- C Mismatches in noncoding sequence (introns and UTRs).
- D Mismatches in phasing of Allele 1.
- E Mismatches in phasing of Allele 2.

Navigating the Mismatch Columns

Of the 5 possible mismatch columns, the **Core** and **Exons** columns are activated upon import. Click the **Core** column header to expand or collapse the **Exons** column. Click the **Exons** column header to expand or collapse the **N-C** column. The phase mismatch columns are present only if necessary to resolve a sequence ambiguity.

Phasing mismatches are only calculated for the allele pairs with the lowest number of mismatches in the core regions.

Differences Column

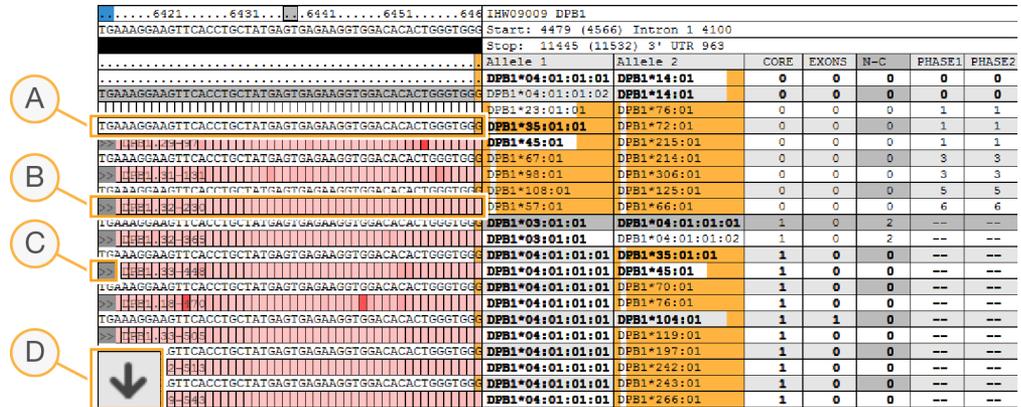
The Differences Column indicates the location of differences between the allele pairs relative to the first allele pair listed.

Where ambiguities exist, the regions in which they might be resolved are indicated in this column.

Reads View

The Reads view shows the sequence reads used in base calling for the selected position. To see the Reads view, in the Views group, click **Show**, and then click **Reads**.

Figure 30 Reads View



- A Nucleotide Sequences
- B Base call quality from FASTQ file—Quality is shown in light pink (highest quality) to dark red (lowest quality).
- C Read direction arrow—Indicates the direction of the read (ie, forward or reverse).
- D Read scroll arrows—Use the scroll arrows to view the next batch of reads. You can also navigate by pressing Page Up and Page Down on your keyboard.

To hide reads for a specific nucleotide at the base selected, press the Shift key and the nucleotide letter simultaneously. The reads reappear using the same keys. For example, press Shift + A to hide the reads calling A at the selected position.

Right-click on a sequence to open a menu that includes the options to copy the sequence to the clipboard, send the sequence to BLAST for alignment, or display warnings for a sample.

Alignment View and Reference View

The Alignment view and Reference view provide comparisons of the Sample Consensus Sequence and your data against the IMGT sequences.

Alignment View

The Alignment view shows a comparison of the Sample Consensus Sequence and the allele pairs listed in the Results panel. Click the headings **Allele 1** or **Allele 2** to add or remove the contribution from the alleles in that column. To see the Alignment view, in the Views group, click **Show**, and then click **Alignment**.

Reference View

The Reference view shows a comparison of the Sample Consensus Sequence and the reference sequences for a locus. To see the Reference view, in the Views group, click **Show**, and then click **Reference**.

You can limit the reference alleles that appear in the Reference view. Enter the reference alleles of interest into the lower field of the Navigator, and then click **Filter** to the right of the text field. Alleles that contain the text entered in the box are shown. You can enter multiple entries, separated by commas, into the filter field.

Figure 31 Limiting Reference Alleles

The screenshot displays a sequence alignment interface. At the top, it shows the IMGT/A 3.23.0.0 2016-01-19 version and a sequence starting with 'CYGWCARCSGCCCC'. Below this, a table compares the sample sequence 'IHWO9420Exp048' against reference alleles 'IHWO9114Exp049', 'IHWO9418Exp048', and 'IHWO9420Exp048'. The table has columns for 'Allele 1' and 'Allele 2'. A 'Filter' control panel is overlaid on the right, showing 'ACCEPT' and 'Full Gene' dropdowns, and a text input field containing '01:01:01' with a 'Filter' button.

Sample	Allele 1	Allele 2
IHW09114Exp049	CTGACAGCGCCCAARACGCATATGACTCACCAACGCTG	CTCTGACCATGARGCCACCCCTGAGGTGCTGGGCCCTGAG
IHW09418Exp048	C.T...C...G..A...G...C...C.CA	...G...A...G...C.CA
IHW09420Exp048*	C.T...C...G..A...G...C...C.A	...G...A...G...C.CA

Generating Reports

Types of Reports

Assign 2.1 generates a genotyping report or a FASTA report.

- ▶ Genotyping Report—Reports on a single sample or locus or all samples and loci in the project.
- ▶ FASTA Report—Reports the Sample Consensus Sequence using the IUPAC designations.
- ▶ Fragment Analysis—Reports for the distribution of DNA fragments clustered and read by the Illumina sequencer and imported into Assign 2.1.

Reports can be customized with a logo, page numbers, date and time, and other references about the report. For more information, see *Changing the Full Report Logo* on page 35.

Genotyping Report

Click **Reports** to launch the reporting tool.

Figure 32 Genotyping Report

Generating a Full Report

A full genotyping report includes a header with your preferred logo, page numbers, created date and time, sample name and references used, and the CWD set used.

- 1 On the Genotyping tab, in the Filters section, use the **Sample** list to select the samples to include in the report. Select **All** to include all samples in the project.
- 2 From the **Locus** list, select an individual locus to include in the report. Select **All** to include all loci in the project.
- 3 In the Sorting section, select either sample **Name** or **Locus** to sort the report.

- In the Fields section, select the number of fields to report from the list.

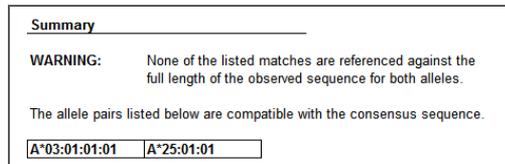


NOTE

By default, the results panel is set to 3 fields. Reporting more fields than the results panel gives all possibilities at the additional field level.

- In the Full Report section, use the **Sample** lists to select **Summary** or **Auditing** from the list. Select **Empty** if a selection list is not needed.
 - ▶ **Summary**—Includes any warnings regarding the typing and the allele pairs that are compatible with the Sample Consensus Sequence (as edited) for each locus selected in the Filters section. Additional modifications to this section of the report are available in Summary Options.

Figure 33 Warning Description



- ▶ **Auditing**—For each Locus selected in the Filters section, the Auditing report includes the reviewer status as either Pass or Fail and whether all positions have been confirmed as either Pass or Fail. The report stamps the date, time, and user for each item passed. Additional modifications to this section of the report are available in Audit Options.
- In the Full Report section, use the **Layers** lists to select the level of layer detail to include in the report. Select **Empty** if a selection list is not needed.
 - ▶ **Sequences**—For each locus selected in the Filters, the Sequences report prints the Sample Consensus Sequence (as edited).
 - ▶ **Edit List**—For each locus selected in the Filters, the Edit List report shows the edited positions, the edit that was made, and the user that made the edit.
 - ▶ **Mismatch List**—When selecting the Mismatch List layer for reporting, set values in the **Mismatch Limits** section. To obtain the desired mismatch list in the report, enter the desired combination of number of mismatches and select the relation to best match from the list. The mismatch limits apply to the entire gene sequence. This feature is useful for novel alleles.
 - [Optional] Select **Table** to export an Excel workbook with separate worksheets for the 3 summary screens instead of a Full Report. In addition to the 3 summary screens, the Table report includes a worksheet that displays the allele balance for each locus, in which the frequency of the second allele is displayed. The Table report also includes a worksheet that displays the frequency of reads that were determined to be the result of a PCR crossover event and have been removed from the analysis.
 - In the Summary Options section, select the checkbox for each option to include in the report.

Summary Option	Description
Full Allele List	Includes all alleles.
P Groups	Includes P groups. For more information, see hla.alleles.org/alleles/p_groups.html .

Summary Option	Description
G Groups	Includes G groups. For more information, see hla.alleles.org/alleles/g_groups.html .
NMDP	Provides the NMDP code corresponding to the matching allele pair for a locus.
Differences	Includes the information in the differences column of the Results panel.
Trim Introns	When the “Sequences” layer is selected for reporting, intron sequences are removed from the sequences and only cDNA sequence is provided in the report.



NOTE

When 2 or more perfect matches are available, creating an ambiguous result, the software first checks whether the alleles share a G group and then shorts them by G group. If no G group relationship exists, then Assign 2.1 shorts by P group and if no P group relationships exist, then the software shorts sequentially lowest to highest. When G groups are present (or P groups when G groups are not present), these groups are displayed on the Summary screen and in the Summary Report. In addition, the ambiguity strings are then reported on a new “Ambiguities” tab on the Summary Report.

- In the Audit Options section, select **Save** to generate a history of save and load events. Select **Confirm** to include a history of reviewer confirmations.

Figure 34 Auditing Report

Auditing
First Review: Pass
Final Review: Pass
Confirmed All Positions: Fail
Aug 16 2014 13:5£ admin set the first review to pass
Aug 16 2014 13:5£ admin set the final review to pass

- In the Output Format section, select from the following formats:
 - ▶ **Text**—Generates a report of the selected options into text format.
 - ▶ **Excel**—Generates a report of the selected options into an Excel spreadsheet.
 - ▶ **XML**—Generates a report of the selected options into a tagged *.xml file that is best suited for importing into an external database.
 - ▶ **Page Breaks**—Adds page breaks to the Excel spreadsheet.
- [Optional] Select **Duplicate Homozygote Calls** to print 2 alleles instead of allele 1 and X for putative homozygous samples.
- Click **Report**. Excel reports generate and open automatically in Excel. Text or XML reports generate when you choose a save location on your computer.

Changing the Full Report Logo

You can alter the image by directly editing the Excel template included with Assign 2.1. To change the logo, open Excel then choose the Genotyping.xlt template file. In a default installation, the template is located in C:\ProgramData\Conexio Genomics\Assign TruSight HLA v2.1\data\templates. For a custom installation folder, navigate to the appropriate folder and then choose data\templates\Genotyping.xlt. To replace the logo image, under Print, view Page Setup and edit the header and footer.

FASTA Report

The FASTA file format is a simple text-based format that has become a standard bioinformatics tool for representing genetic sequences. The FASTA format begins with a description line that includes a greater than symbol (>). The next line in the FASTA is the Sample Consensus Sequence using the IUPAC designations.

- 1 On the Home tab, in the Reports section, select **FASTA** from the **Type** list.
- 2 Click **Reports** to launch the reporting tool.
- 3 On the FASTA tab, in the Output Filters and Numbering section, use the **Sample** list to select an individual sample to include in the report. Select **All** to include all samples. The sample name is included automatically in the FASTA description line preceding the sequence.
- 4 From the **Locus** list, select an individual locus to report on the selected samples. Select **All** to include all the loci for the samples selected. Select the checkbox to insert the locus name into the FASTA file (eg, > SampleName_IMGTA).
- 5 From the **Layer** list, select a single layer to restrict output. Select the checkbox to insert the layer name into the FASTA file.
- 6 From the **Group** list, select a designated group of regions to restrict output.
- 7 From the **Region** list, select a designated region, such as an exon. Select the checkbox to insert the region name into the FASTA file.
- 8 In the Sort by section, select either sample **Name** or **Locus** to sort the report.
- 9 In the Options section, select the **Pad Ends** checkbox to add N base calls to each sequence to cover the entire amplicon.
- 10 Click **Generate Report**, and then choose a save location on your computer.

Fragment Analysis

The Fragment Analysis is an Excel report that provides details of the distribution of fragment sizes imported into Assign for each sample and locus.

- 1 Click **Reports** to launch the reporting tool.
- 2 On the Fragment Analysis tab, do 1 of the following:
 - ▶ Select a single sample in the project
 - ▶ Select all the samples and select a single locus or all the loci from the dropdown lists
- 3 Click **Report** to generate the fragment analysis.
The Fragment Analysis automatically opens in Excel.

Revision History

Part #	Date	Description of Change
Document # 1000000010450 v01	October 2016	Updated for Assign 2.1 RUO TruSight HLA Software. Added Fragment Analysis section and information about PCR crossover.
Document # 1000000010450 v00	May 2016	Initial Release.

Notes

Technical Assistance

For technical assistance, contact Illumina Technical Support.

Table 1 Illumina General Contact Information

Website	www.illumina.com
Email	techsupport@illumina.com

Table 2 Illumina Customer Support Telephone Numbers

Region	Contact Number	Region	Contact Number
North America	1.800.809.4566	Japan	0800.111.5011
Australia	1.800.775.688	Netherlands	0800.0223859
Austria	0800.296575	New Zealand	0800.451.650
Belgium	0800.81102	Norway	800.16836
China	400.635.9898	Singapore	1.800.579.2745
Denmark	80882346	Spain	900.812168
Finland	0800.918363	Sweden	020790181
France	0800.911850	Switzerland	0800.563118
Germany	0800.180.8994	Taiwan	00806651752
Hong Kong	800960230	United Kingdom	0800.917.0041
Ireland	1.800.812949	Other countries	+44.1799.534000
Italy	800.874909		

Safety data sheets (SDSs)—Available on the Illumina website at support.illumina.com/sds.html.

Product documentation—Available for download in PDF from the Illumina website. Go to support.illumina.com, select a product, then select **Documentation & Literature**.



Illumina

5200 Illumina Way

San Diego, California 92122 U.S.A.

+1.800.809.ILMN (4566)

+1.858.202.4566 (outside North America)

techsupport@illumina.com

www.illumina.com