Assign^{TM} v2.0

TruSight HLA Analysis Software

Customer Release Notes

May 2016

Introduction

These Release Notes detail the key changes to software components for the Assign TruSight HLA software since the package containing v1.0.

For more information about operating the Assign 2.0 Software, see the [Assign 2.0 TruSight HLA Analysis Software Guide (document # 1000000010450)](#).

For frequently asked questions, see the [TruSight HLA v2 Sequencing Panel Questions & Answers page](#).

The software package includes:

- Assign TruSight HLA v2.0.0.920

NEW FEATURES (FROM V1.0):

- Updated references to IMGT 3.23.0 (January 2016).
  - See IMGT 3.23.0 Reference Release Notes for more information.
- Added the ability to analyze data with new HLA-B.2 and HLA-DRB.2 primers.
- Algorithm enhancements resulting in faster analysis of sequence data.
- Supports analysis of pooled amplicons from the TruSight HLA v2 workflow.
- Backwards compatible with the TruSight HLA v1 workflow and HLA-B.1 and HLA-DRB.1 primers.
- Addition of the Phase Block display. Grey block are used to denote regions where mixed bases are linked by at least 30 single or paired reads (see Figure 1).

Figure 1

phased   nonphased
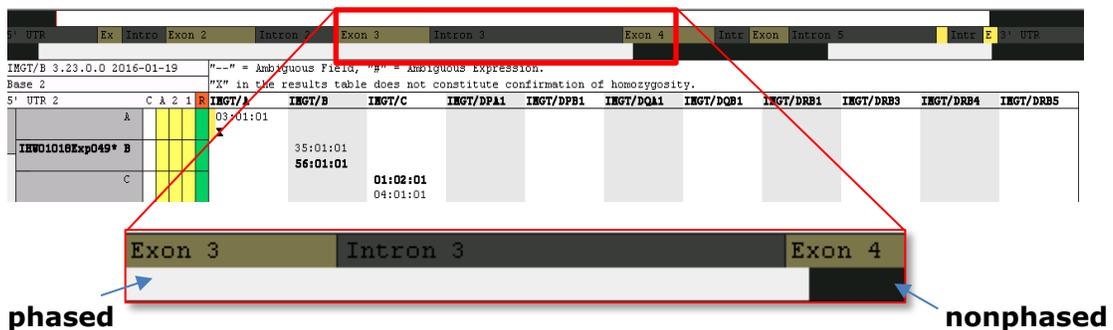
- Added minimum coverage metric that varies depending on the portion of the gene used to make the typing call.
- Added functionality to display CWD alleles in bold text on the summary screen.
- Updated the CWD list. For more information about the CWD list, see the IMGT 3.23.0 Reference Release Notes.
- Modified reporting for putative homozygous loci to display X for the second allele when a heterozygous base is not used in the sequence to make the typing call.

DEFECT REPAIRS:

- Repaired the reference update functionality in the user interface, now allowing user to import new reference updates without a separate installer.

- Fixed NMDP code generation in the summary report.

- Modified bolding of CWD alleles when the user selects fewer fields than the CWD allele. For example, if the CWD allele is 01:01:01:01 and the user is displaying only two fields, 01:01, the allele will be bolded regardless if the fourth field typing is 01:01:01:01 (CWD) or 01:01:01:03 (non-CWD).

KNOWN ISSUES:

- Importing additional FASTQs into an open project is not permitted. Attempting to do so causes an "Out of Memory" error and will close the software.

- Assign 2.0 does not allow the user to create an individual report for a sample named "Sample1".

- When 2 or more projects are open in the same instance of Assign 2.0, the fields combo box will not update when switching between them. You will need to update each project separately. The Results display is not affected.

- Box A in the sample panel does not always turn green after a sample is verified at all positions indicated in the Navigator.

- The text option for a report is not always be available when reopening a saved project. To generate a text report, close and reopen the report dialog.

- FASTA report settings are not saved as default after clicking Update in report dialog.

NOTES:

- The first import after initial install and after a reference update takes slightly longer to analyze. During this first import, only a single user can be using the software.

- CWD sets cannot be toggled and changed dynamically in the UI. User must select Update in the Settings tab and restart the software for the CWD file to be changed.

- CWD alleles are not bolded in the xml report options.