



## Assign™ SBT v4.7.1 Update Document. Description of Changes from Assign™ SBT v4.7.0.232

This document details the significant changes to Assign™ SBT 4.7.1 since the last production release, Assign™ SBT v4.7.0.232. These include software improvements and bug fixes.

### 1. Group Specific Amplicon analysis

Assign™ SBT 4.7.1 has been improved to include the capability to analyse data derived from Group Specific Amplification methods alongside the already existing SBT analysis features of Assign™.

Users can now easily define their own GSA strategy in the software settings and choose whether to analyse against either genomic or cDNA references. All GSA data for a single sample can be imported and analysed together, allowing the software to produce a high resolution heterozygous typing result. This includes the analysis of two alleles by two separate GSA and/or multiple GSAs for a single allele if necessary.

For more information and instructions regarding the GSA analysis and capabilities of Assign SBT 4.7.1, please refer to *IFU057\_ GSA analysis\_Assign SBT 4.7.1 Instructions for Use (CE/IVD)*.

### 2. Auto save feature

#### How to use auto save:

The auto save function which has been added to Assign™ will create a backup copy of the user's layout 5 minutes after a change is made.

To initiate the auto save function, the user must load samples into a layout and save the layout manually. There after user edits and changes will be automatically saved after 5 minutes. These automatic saves are stored in a backup file which will be maintained until the user makes another manual save. When a manual save is undertaken the backup file will be removed and another one will be created 5 minutes after the next edit is made.

If you are working on a saved layout and the software is closed unintentionally (due to PC error or software crash etc.), the backup file will remain and can be loaded so that unsaved changes can be reapplied to your project. The next time the layout in question is opened in Assign™ the following backup file notification warning will appear:

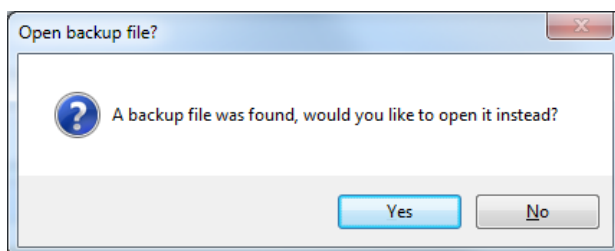


Figure 1 Back-up file notification



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If you select 'Yes' then the software will reapply the unsaved changes that have been made to the layout. It is recommended that the user then manually saves the project, which will remove the backup file.

If you select 'No' then the software will open the saved layout, and the backup file will subsequently be removed. If the user is opening a layout and they see the above message, but don't know why, it is advised to investigate with the previous user of this layout or a supervisor. If the user opted to open the saved layout and the user is unsure whether the back-up file should have been opened, it is recommended the layout is saved temporarily under a different name whilst seeking clarification, this will ensure the back-up file remains in the event it is needed.

The default time for an auto save to happen after a change has been made is 5 minutes. If you want to turn off the Auto Save function, please contact Conexio Genomics ([support@conexio-genomics.com](mailto:support@conexio-genomics.com)).

### How auto save works:

Auto save will normally create a backup copy of the user's layout 5 minutes after a change is made.

The exceptions are:

1. If the user has created a new layout and not yet saved it. **Assign cannot do an auto save for a layout that is not yet saved.**
2. If on opening a layout the user was given the option to open a backup layout but the user selected 'No', then the auto save function will not be initiated until after the user has done the first manual save. This is important as it prevents overwriting the backup file.
3. If you make 2 or more changes within 5 minutes, the auto save will occur after the first change saving all the subsequent changes made.

The automatically created backup files are removed if you do any of the following:

1. Manually save.
2. Manually save-as **unless** you elected to open the back up and "saved-as" the back-up layout under a new name. Then the backup file in the name of the original layout will still remain.
3. Close a layout and answer that you do not want to save.



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### 3. Navigator to launch only once samples are loaded

The Navigator will only appear when at least one sample is loaded into Assign™, as opposed to the functioning of previous versions of Assign™ where the navigator launched when the software was opened.

To change Navigator settings:

- 3.1 Ensure desired setting is selected and settings in toolbar are correct.
- 3.2 Load samples.
- 3.3 Change settings in navigator pad to desired user settings. Please refer to the Navigator section of the Operator's Manual for an explanation of the settings options.
- 3.4 Click the update button in the Settings section of the ribbon toolbar at the top of Assign to retain navigator settings.

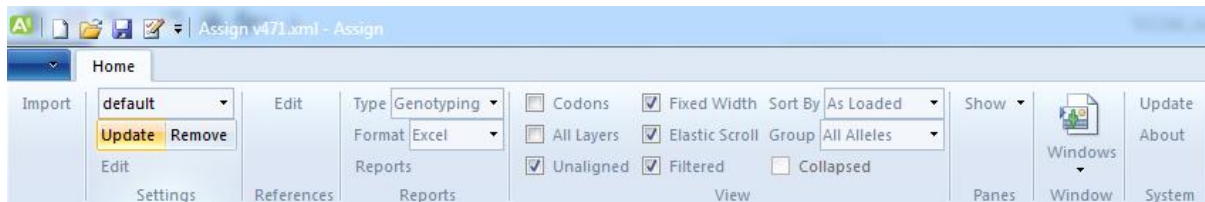


Figure 2 Assign™ ribbon toolbar



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## 4. Editing references

Changes to a reference within the Assign™ software are no longer applied to the original reference file. Instead all edits are only written to and read from the \_user file.

*Please note: If you are upgrading Assign™ SBT from version 4.7.0.232 or any previous versions, and have edited your references under the “Regions” or “Groups” sections as well as the “Primers” or “Variants” sections, it is recommended you remove your user file and reapply your edits to the “Primer” and “Variants” sections. “Regions” and “Groups” can no longer be edited.*

The previous version of Assign™ SBT 4.7 allowed users to carry out more edits than is necessary for SBT analysis. As such, user editing of the references has been brought back in line with Assign™ SBT 3.6+ functionality, so that only those fields that are necessary may be altered. This should not impact users as the areas they were able to edit before were not relevant.

The ‘Properties’ section in the General tab is no longer available to edit (other than to change the type between cDNA and genomic) and users cannot make any deletions (HARPs or aliases) to the reference file using the Reference Editor.

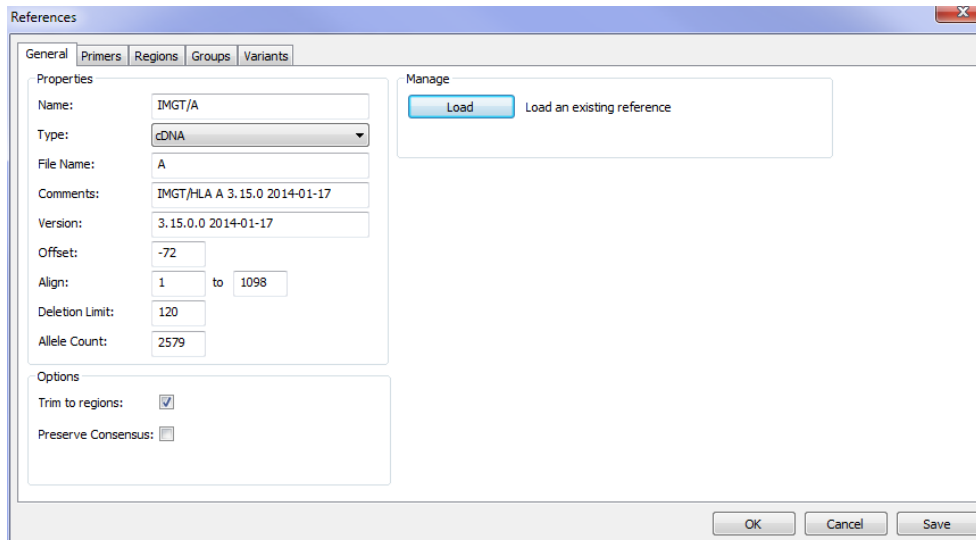


Figure 3 Assign™ SBT 4.7.0.232: Reference editor



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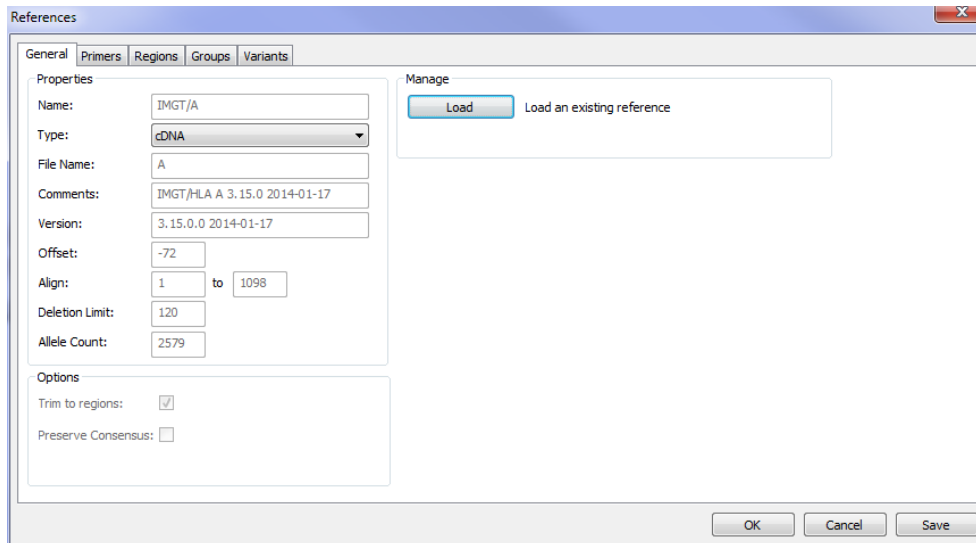


Figure 4 Assign™ SBT 4.7.1: Reference editor

As a result of these changes, any edits made to a reference using the Assign™ reference editor will not invalidate the references, since the edits are not written to the reference file themselves.

Upon saving edits made in the reference editor the user will be presented with the following message:

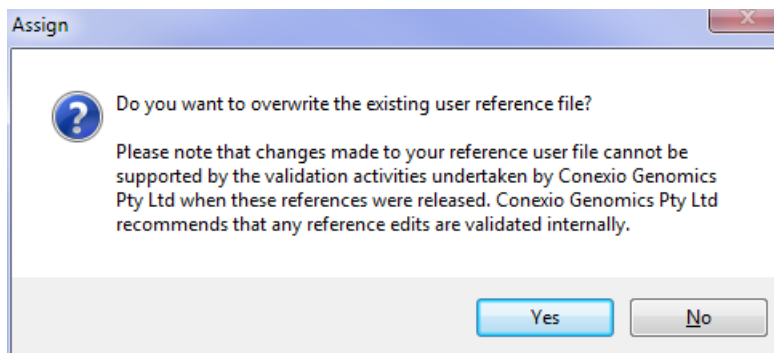


Figure 5 Reference Editor saving message



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However if the original reference xml file is edited manually or corrupted in anyway, the reference will be recognised as 'unsigned'. If the 'Reference Validation' Checkbox is ticked, when samples are loaded and aligned against an unsigned reference the usual warning message will appear:

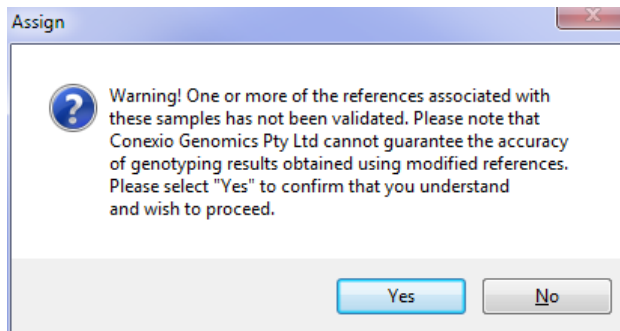


Figure 6 Invalidated references message

### 5. G group condensing

In the previous release of the software when the option to condense alleles into G groups was selected, in some cases, not all alleles in the results pane within the layout window were condensed into G groups correctly. However the G groups were reported correctly on all reports generated by Assign™.

In the latest version of Assign™ SBT, the results pane view has now been corrected and matches the output in the genotyping report; that is, all relevant alleles are correctly condensed into their appropriate G groups.

### 6. Sorting and selecting in sample and results pane

In some cases in Assign™ SBT v4.7.0.232 there was a discrepancy between the cursor position within the sample ID or results panes, and the highlighting or selection applied when clicking the mouse. This out of sync highlighting tended to occur when the samples or results were condensed by applying sort by sample, or G/P group options.

In the latest version of Assign™ SBT, this has now been fixed so the sample or genotype the cursor is hovering over is the one that is highlighted and selected when the mouse is clicked.



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## 7. Improvements to the Quick Print function

The Quick Print function is accessible using the button at the top of the Assign™ window or in the arrow list.

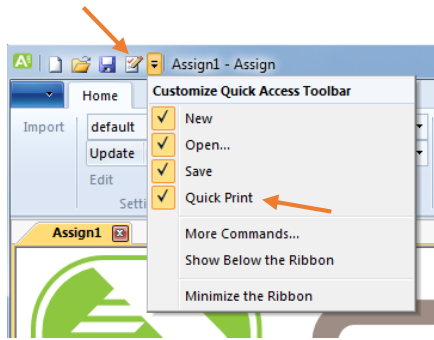


Figure 7 Quick Print function in Assign™

In Assign™ SBT v4.7.0.232 when selecting the Quick Print function, only one page could be printed – the beginning of the EPG read for the first loaded sample, even if all locus and all regions were selected.

The latest version of Assign™ SBT has been improved to print all the EPG sequences defined for print by the user.

## 8. CWD highlighting

The following issues were seen in some cases with version Assign™ SBT 4.7.0.232 in relation to CWD allele highlighting:

- HARPs reports: Highlighting of some non-CWD alleles.
- Genotyping reports: For some unusual samples, non-CWD alleles were displayed as un-highlighted in Assign™ (correct) but as highlighted in the genotype report (incorrect).
- P and G group CWDs: Only if the first allele in the pair was a CWD would the allele pair be highlighted.

All above issues are now resolved in the latest version of Assign™ SBT.

## 9. Quality Report

In Assign™ SBT 4.7.0.232 with no data imported, if the user tried to create a HARPS report for an individual HARP using the projects filter option, Assign™ would abort. Further to this, the BCS was not actually graphed on any of the quality reports generated using the projects filter option.

In the latest version of Assign™ both of these issues have been resolved.



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## 10. Improvements to EPG view

In previous Assign™ SBT 4.7 versions, artificial double or triple peaks appeared in the far left of the EPG display pane.

This problem with the EPG display has been fixed in the latest version of Assign™ so this artefact does not occur.

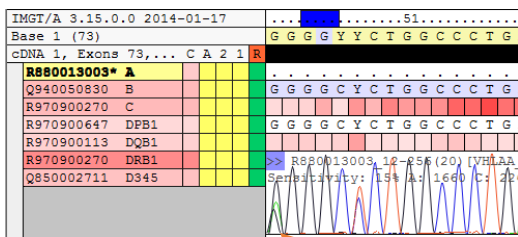


Figure 8 Assign™ SBT 4.7.0.232: EPG display

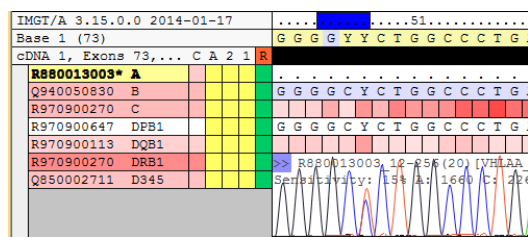


Figure 9 Assign™ SBT 4.7.1: EPG display

## 11. User email verification

As seen above, an additional box has been added for users to verify their email address. This is to ensure users receive their keys to the correct email address.

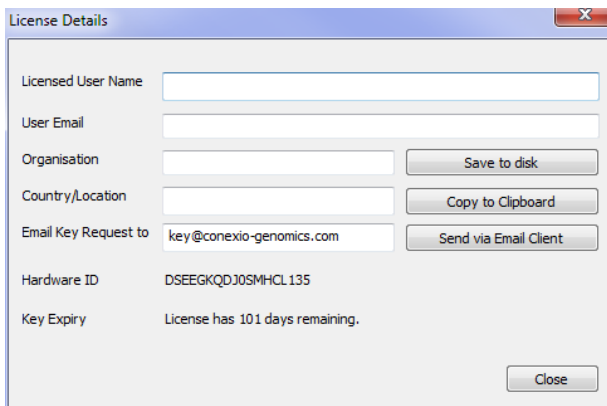


Figure 10 Assign™ SBT 4.7.0.232: License Details

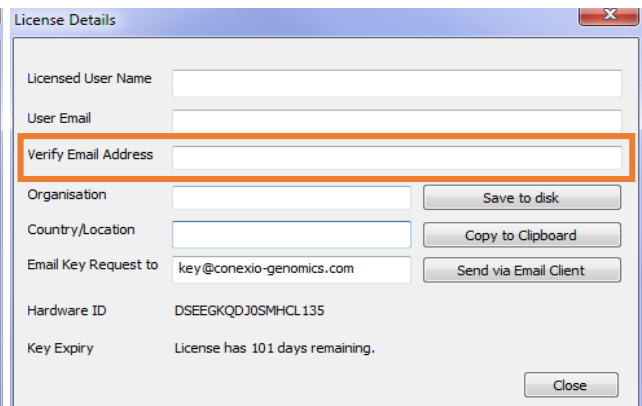


Figure 11 Latest Assign™ SBT 4.7.1: License Details





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### Customer Support

Assign™ SBT v4.7.1 is distributed with SBT Resolver™ assays by Olerup SSP and its local distributors.

For additional information, please contact Conexio Genomics Pty Ltd at [www.conexio-genomics.com](http://www.conexio-genomics.com) or your local Olerup representative.



Conexio Genomics Pty Ltd  
2/49 Buckingham Drive  
Wangara 6065  
Western Australia  
Australia  
[www.conexio-genomics.com](http://www.conexio-genomics.com)



Qarad bvba  
Cipalstraat 3  
B-2440 Geel  
Belgium

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