



Assign™ SBT v4.7.1.853 Update Document. Description of Changes from Assign™ SBT v4.7.1.745

This document details the significant changes to Assign™ SBT 4.7.1.853 since the last production release, Assign™ SBT v4.7.1.745. These include software improvements and bug fixes.

1. Significant improvements to the HARPS reporting functionality.

The Resolution/HARPs reports within Assign™ now replicate the report outputs produced by the HARPSFinder™ website, which indicate the HARPs capability to resolve each ambiguity i.e. the new report format provides the user with a breakdown of how each HARP resolves the ambiguity. For full instructions for how to use HARPSFinder™ within Assign™ and the new reports format, please see *Appendix 1* of your Assign™ SBT 4.7.1 IFU.

The major changes, improvements and bug fixes to the HARPs reports within Assign™ are listed below:

- 1.1 HARPs reports can now list more than two HARPs in cases where more than two HARPs are required to resolve an ambiguity.
- 1.2 HARPs reports no longer tries to consider allele ambiguities and intronic information when reporting HARPs.
- 1.3 As part of the improved reporting format the **Trim to Reference Defaults** and **Trim to Regions** parameters have been removed in favour of the user defined parameters so users have full control to define their report outputs. **Trim to Reference Defaults** and **Trim to Regions** parameters for HARPs reports have been greyed-out in both the Resolution Reports tab and the Settings>Engine tab (shown below).

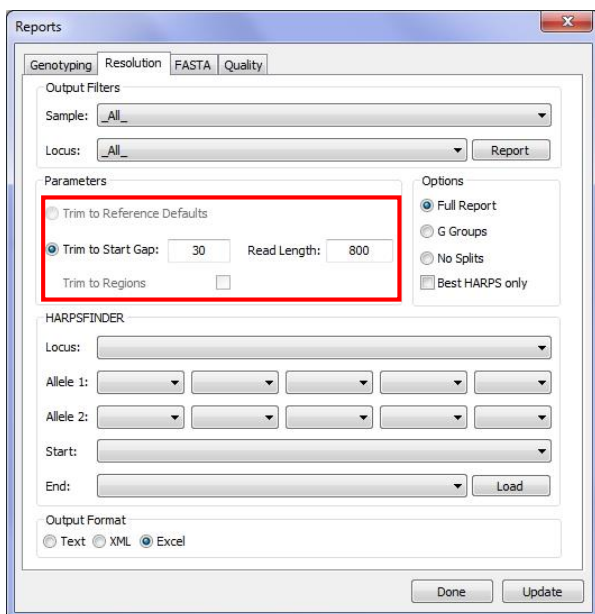


Figure 1: Assign SBT 4.7.1.853 Resolution Reports

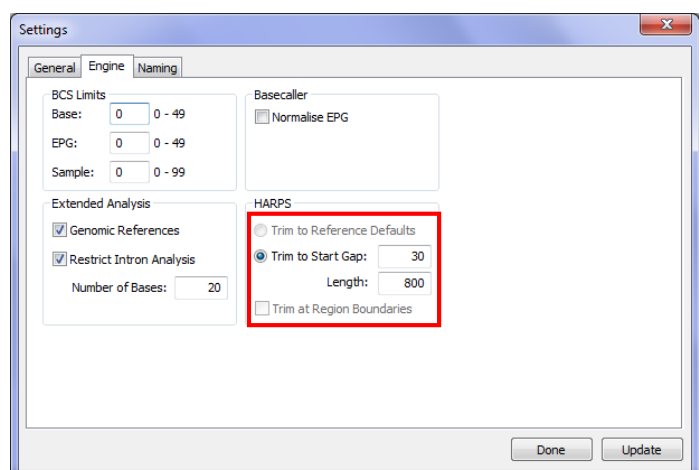


Figure 2: Assign SBT 4.7.1.853 Engine tab within Settings window



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2. **Improved Resolution Report tab loading speed**

The loading speed when clicking on the Resolution Report tab has now been significantly increased. This has been achieved by delaying loading of the references until Assign™ is prompted to do so by the user by clicking the **Load** button. The references are required for using the HARPSFinder™ functionality within Assign™. Please see *Appendix 1* of the Assign™ SBT 4.7.1 IFU for more details.

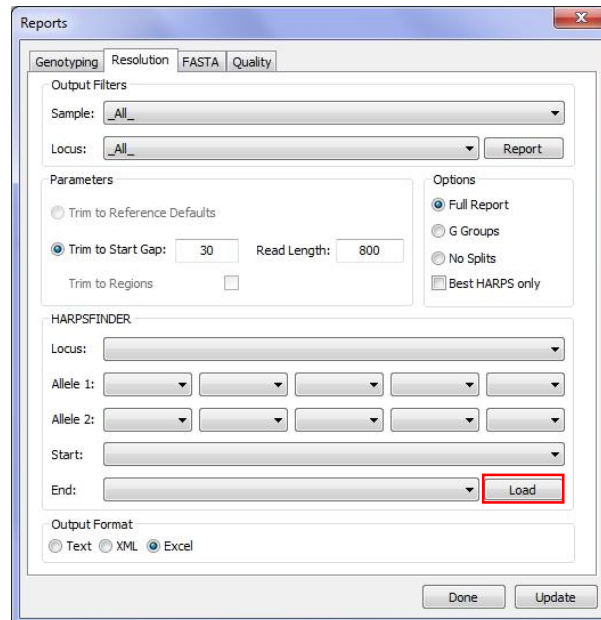


Figure 3: Resolution Reports tab in Assign SBT 4.7.1.853

3. **Improved allele sorting and results pane display**

Please see *Section 6.4* of the Assign™ SBT 4.7.1 IFU for information on the results pane.

3.1 In Assign™ SBT 4.7.1.745 and previous versions, allele pairs in the results pane are sorted according to their mismatch number against the reference library then numerically; mismatches in the non-coding regions are included if the N-C layer is active.

In Assign™ SBT 4.7.1.853 allele pairs with 0 mismatches are sorted on the basis of coverage in the reference database, not numerically. That is alleles with 0 mismatches and full coverage in their reference will be sorted to the top of the list. When analysing data in genomic settings, the number of mismatches in the non-coding layer is also taken into account when sorting allele pairs.

3.2 Orange shading over an allele display depicts where reference information is missing for that allele relative to the sample sequence i.e. allele information has not been described in the latest IMGT/HLA reference update.



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In Assign™ SBT 4.7.1.853, the shading has been changed to distinguish between the presence of cDNA and genomic library information for the alleles:

3004 gA							
Start: 98 (98) IMGT 5UTR -203, 5' UTR 98							
Stop: 2196 (2196) IMGT 1875, Intron 4 30							
Allele 1	Allele 2	MM 0	N-C	IND	MM 3	MM 4	Diff
A*02:01:01:01	A*24:02:01:01	0			0	0	
A*02:01:01:01	A*24:02:01:02L	0			0	0	Intr
A*02:01:01:04	A*24:02:01:01	0			0	0	Intr
A*02:01:01:04	A*24:02:01:02L	0			0	0	Intr
A*02:01:01:01	A*24:02:40	0			0	0	Exon
A*02:01:01:02L	A*24:02:01:01	0			0	0	5' U
A*02:01:01:04	A*24:02:40	0			0	0	Intr
A*02:01:01:01	A*24:02:01:03	0			0	0	Intr
A*02:01:01:02L	A*24:02:01:02L	0			0	0	5' U
A*02:01:01:03	A*24:02:01:01	0			0	0	Intr
A*02:01:01:04	A*24:02:01:03	0			0	0	Intr
A*02:01:01:03	A*24:02:01:02L	0			0	0	Intr
A*02:36	A*24:03:01	0			0	0	Exon
A*02:01:01:03	A*24:02:40	0			0	0	Exon
A*02:01:01:02L	A*24:02:40	0			0	0	5' U
A*02:01:01:02L	A*24:02:01:03	0			0	0	5' U
A*02:01:01:03	A*24:02:01:03	0			0	0	Intr
A*02:01:02	A*24:02:58	0			0	1	Exon
A*02:01:52	A*24:02:76	0			0	1	Exon
A*02:04	A*24:52	0			0	0	Exon
A*02:12	A*24:13:01	0			0	0	Exon
A*02:70	A*24:29	0			0	1	Exon

Figure 4: Results pane in Assign SBT 4.7.1.853

Dark Orange indicates a region is missing from the genomic sequence for these alleles.

Bright Orange indicates only cDNA information is available for that allele and some exon information is missing.

The coverage of shaded area over the allele display represents the region/s within the sample sequence for which reference sequence is unavailable. In the figure above, A*24:02:01:03 is missing library information for some portion of sequence in the 5'UTR. Whereas A*24:13:01 is missing library sequence for exon 1 and exon 4 onwards.

4. Editing positions in the non-coding region of the HARPs layer

A bug existed in the previous version of Assign™ SBT 4.7.1 where a non-coding position could not be edited whilst the active layer was the HARP layer (e.g. MM2 or MM3 etc. was active). This has been corrected so positions in either the coding or non-coding regions can be edited in the HARPs layer.

5. Increased max start gap to 100bp

In previous versions of Assign™ SBT 4.7.1 the max start gap for HARPs was set to 40bp. For users with start gaps greater than 40bp, the reported HARP couldn't produce data to cover the right nucleotide position and therefore couldn't allow resolution of the ambiguous allele pairs.

To resolve this issue the max start gap has been increased to allow up to a 100bp start gap. The default start gap for HARPs is still set to 40bp within Assign™.



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6. G & P Group condensed view

Please see *Section 6.1.5.8* of the Assign™ SBT 4.7.1 IFU for allele pair group condensing. Within the results pane, allele pairs can only be condensed into G or P groups if the Non-Coding layer (N-C) in the results pane is deactivated. If the allele pairs are set to be displayed in G or P groups, activating the N-C layer will automatically convert the allele pairs to the full allele list view.

7. Genotype Report Headers

The layout of the genotyping reports has been improved to included descriptive headers above the tables. The red highlight below shows the new headers in reports produced in Assign™ SBT 4.7.1.853 compared to reports generated in previous versions of Assign™. The genotyping report headers have been added to excel and text report outputs but not xml outputs.



Created: CWD 2012 v3.19 cat 1-2.cwd; CWD 2012 File; 0.02

Sample: A*02:01:01:01 + A*31:01:02:01
Reference: IMGT/A 3.21.0.0 2015-07-06

G Group Summary

The allele pairs listed below are compatible with the consensus sequence.

Allele 1:	Allele 2:	Full:	Part:	Full:	Part:
A*02:01:01G	A*31:01:02G	546	0 Yes Yes	546	0
A*02:20:01	A*31:02	546	0 Yes Yes	546	0 Exon 2
A*02:24:02	A*31:68	546	0 Yes Yes	546	0 Exon 3
A*02:40:01	A*31:41	546	0 Yes Yes	546	0 Exon 3
A*02:243:01	A*31:21	546	0 Yes Yes	546	0 Exon 2

Figure 5: Genotyping report produce in Assign SBT 4.7.1.853 with report headers



Created: CWD 2012 v3.19 cat 1-2.cwd; CWD 2012 File; 0.02

Sample: A*02:01:01:01 + A*31:01:02:01
Reference: IMGT/A 3.21.0.0 2015-07-06

G Group Summary

The allele pairs listed below are compatible with the consensus sequence.

A*02:01:01G	A*31:01:02G	546	0	Yes	Yes	546	0
A*02:20:01	A*31:02	546	0	Yes	Yes	546	0 Exon 2
A*02:24:02	A*31:68	546	0	Yes	Yes	546	0 Exon 3
A*02:40:01	A*31:41	546	0	Yes	Yes	546	0 Exon 3
A*02:243:01	A*31:21	546	0	Yes	Yes	546	0 Exon 2

Figure 6: Genotyping report produce in Assign SBT 4.7.1.745 without report headers



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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 or your local Olerup representative.

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