

Assign SBT 3.2.7 Release Notes

1 Updates

1.1 Enhanced Auto-Editing

The auto-editing function has been enhanced with improved filtering to prevent incorrect re-calling. The auto-editing feature can also be launched from the sample and electropherogram menus. The auto-editor has now replaced the insertion/deletion filters.

1.2 Warning System

Sample ID's will be shaded red (left hand frame) when one or more of the conditions listed below are met.

- Any of the component electropherograms has a mean BCS of less than 35.
- The discrepancy between forward and reverse sequences exceeds 10%.
- The editor detects that there may be preferential amplification.
- The measured sequence does not intersect with one or more reference sequences.
- The number of possible matches exceeds the limit of 4096.

NB The warnings are to assist in the detection of problem samples. The absence of warnings does not imply that the sequence does not have any of these problems. For example, preferential amplification may have occurred and remain undetected.

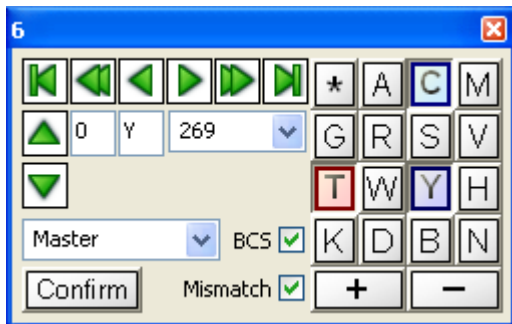
1.3 Highlighting

Highlighting has been added to notify the operator of edited positions.

- Blue markers indicate that a position has been edited manually.
- Red markers indicate that a position has been edited automatically.

1.4 Updated Navigator

The Navigator has been updated to make highlighted positions easier to identify.



1.5 Keyboard editing

Use “Ctrl+Left/Right” Arrow to move between bases and type in the IUB code to edit without the navigator.

1.6 Sequence Direction

The reversed electropherograms are now identified by the identifier “Rev” after the name.

1.7 Short Sequences

The minimum consensus length required for matching has been reduced from 100 to 60 bases.

1.8 Sample Sorting

Samples are now imported alphabetically.

1.9 Reports

- Summary reports can now be filtered to disqualify samples that cannot be edited to give zero mismatches.
- Page breaks can now be inserted at the end of each sample in Excel®.
- Sample names are highlighted in bold type.

1.10 NMDP codes

- The NMDP file used by Assign can now be downloaded directly from the NMDP at <http://www.nmdpresearch.org/HLA/numeric.zip>. This file can be unzipped and placed in the Assign references folder (usually C:\Program Files\Conexio Genomics\Assign\data\references). This will result in an NMDP code interpretation of the allele assignment and will appear in the reports
- Changed the behaviour of the code generator so that the broad type is always listed. For example, 01WEY will be given instead of WEY for the combination 0101/2601.

1.11 Manual

The manual has been updated to version 3.2.7. This describes the changes in more detail.

2 Fixes

2.1 Short Sequences

A possible error for short sequences that do not intersect with any polymorphic positions in the reference has been fixed. This behaviour resulted in a mismatch appearing outside of the consensus sequence. This can never result in an incorrect allele pair forming the best match for a sample.

2.2 Consecutive mismatches in 0301 versus 0304

Fixed a problem where the sequence for homozygous 0301 would produce a single mismatch at position 196 against homozygous 0304 instead of two mismatches at positions 196 and 197. If the base at position 196 is edited, the mismatch at position 197 is correctly identified. This can never result in an incorrect allele pair forming the best match for a sample