

Feature	Description	Risk	Algorithm Change
Added second positive control concordance	Automatic concordance check for two different genotypes – most commonly: Extraction positive and Amplification positive	Moderate	No
AT for peaks outside marker by dye	Additional option in the analysis template – especially beneficial for low concentration samples where AT varies significantly by dye	Major	Yes
Peak width at half-height	Report column for peak width at half height - provides a measurement for evaluating resolution in samples with decreasing peak height and increasing width	Moderate	No
Improvements to Size Quality (SQ Flagging)	Improved UI for Size Quality settings can use auto-allele call range and provides detail of conditions that fire the rule	Major	Yes
Automated evaluation of Quality Sensor peaks	New sample quality setting includes automated evaluation of Q and S fragments of Quality Sensor markers to provide feedback for potential degradation, amplification and DNA quantity issues. Optimized for Qiagen Investigator®24plex samples.	Major	Yes
Improved UI Preferences settings	Grouped sample quality settings in a separate view-preferences tab. Provided additional options for location of Program Data folders (optimize sharing commonly used settings and flexibility to save to appropriate location for the lab's IT security).	Minor	No
Improved report scaling	Optimized screen display and pdf report scaling for computers with 4K hi res monitors	Moderate	No

Changes in minor release version 2.9.9**May 2019**

Feature	Description	Risk	Algorithm Change
CODIS export	Added the setting DAT (CMF 1.0 Style) which also allows 36 loci per sample	Moderate	No

Changes in minor release version 2.9.8**April 2019**

Feature	Description	Risk	Algorithm Change
Additional Mutation allowance setting	Added the setting to use the mean mutation rate / mean PE for the PI of a locus with allele conflict.	Major	Yes

Feature	Description	Risk	Algorithm Change
PI calculation detail table	Display the Markers and results in the kit order, rather than the order of the allele frequency table	Moderate	No
UI Locus Name group	Added alternative spellings of TH01 and CSF1PO to the locus name group to avoid conflict with allele frequency or mutation rate table locus characters.	Moderate	No
Auto-start raw data setting	Reinstated the auto-start raw data detection to locate the region after the ion front rather than start at frame 0 – results in removal of pull up and saturation detection conflict seen with some data	Moderate	No
Bug Fix	Repaired the import/export function of the Preferences.ini file and improved setting Program Data Folders for shared files and windows 10 compatibility	Moderate	No

Changes in the minor release version 2.9.7**October 2018**

Feature	Description	Risk	Algorithm Change
Allele Specific Stutter	Added a rule for edge cases to detect stutter and apply designated allele specific stutter filter	Major	Yes
User Interface Allele Importing data	Improved the user interface for dye channel designation; includes ability to add new supplier and dye names.	Moderate	No

Changes in the minor release version 2.9.6**April 2018**

Feature	Description	Risk	Algorithm Change
Import mtx file	Improved compatibility with 310 CE matrix files to accept mtx file that does not contain a header	Moderate	No
User Interface Allele Comments	Increased the character limit of the allele comment field to 63	Minor	No
User Interface	Improved UI for technical review – samples that have the ? resolved by the analyst are now designated with E. Provides streamlined workflow for technical review of only samples that required intervention for CODIS expert system	Minor	No
Print Bug Fix	Reactivated the auto-scale marker function	Minor	No

Description of risk categories:

Minor - cosmetic; such as changes to the graphic user interface and reporting options (no algorithm change)
Moderate - includes additional parameters or functions that may affect the final report (no algorithm change)
Major - includes algorithm change(s) and is evaluated by concordance testing.