OSIRIS Release Notes Version 2.14

Improvements in OSIRIS Version 2.14

Version 2.14 includes substantial improvements over previous versions

New Features

Simplified printing

Version 2.14 introduces Simplified printing of both individual views and entire analysis batches. Single samples may be printed and is customizable via the onscreen view so that labels, thresholds, channels and views will print as displayed on the screen. Entire analysis batches can be printed and customized to display as the user desires, including labels, thresholds, Y-axis ranges, X-axis range in base pairs or time, and the number of channels per page. The number of channels per page can be customized individually for ladders, negative controls and samples to optimize the display of peak peaks and peak labels for ladders and samples with many peaks. Print color intensity can be optimized for different printers.

Peak and label colors

Peak and label colors have been adjusted to make both more easily distinguishable if a label overlays a peak.

Improved analysis robustness

Analysis has been improved to prevent poor quality samples from causing an entire analysis to fail. Additional error messages have been added to explain why samples or analyses failed.

Analysis correction function for artifact peaks

Occasionally, poor data quality in the ladder controls or sample internal marker ILS makes it impossible for OSIRIS to analyze. The ability has been added to accept a list of peaks in the ladder or in the sample ILS that should be ignored to allow the software to recognize the correct known peaks and complete the analysis. This allows users to rescue ladders and samples.

Running OSIRIS from the command line

An explanation of how to run OSIRIS from the command line has been added to the User's Guide, so that OSIRIS to be called by other software without the need to start the user interface first. This allows OSIRIS to be incorporated into a computing workflow or into other software.

Added homozygote threshold settings

- Added a setting that prevents a "Homozygote too low" artifact in positive control samples.
- Added a homozygote threshold above which a peak is considered to be a valid homozygote even if peaks are found between the Min RFU Analysis threshold and the Detection threshold.

Removed off ladder allele setting

- The setting "Do not call OL allele if pull-up" was removed to prevent the possibility of a valid allele not being called if it also contained signal from a pull-up, given that the current pull-up analysis algorithm deals appropriately with that situation.

Changed uncertain pull-up artifact priority

- Changed the artifact priority of "Partial Pull-up Uncertain" peaks, where the pull-up algorithm is unable to determine a pull-up pattern, from non-critical to conditional. If the peak is pure pull-up or partial pull-up corrected below minRFU from another channel, pull-up uncertain is non-critical. Otherwise, it is a critical artifact to ensure analyst review.

Bug Fixes

- Fixed a bug that in certain circumstances could have prevented the maximum threshold artifact from being triggered when a peak's height exceeded the maximum RFU threshold.
- Fixed a bug in the baseline offset calculation that would prevent analysis in rare circumstances where dynamic normalization was not selected.
- Fixed a bug that caused off-ladder alleles to trigger a non-critical artifact at the peak level, but a critical artifact at the locus and sample level. Off ladder peaks now give a critical artifact at all levels.
- Fixed a bug introduced in v. 2.12.2 which caused sigmoidal pull-up to be called as partial pull-up rather than pure pull-up and to receive an allele call in addition to the artifact, if above the analytical threshold.