OSIRIS Release Notes Version 2.6

Improvements in OSIRIS Version 2.6.

New Features

Channel specific thresholds

Version 2.6 allows the user to set channel-specific Analytical and Detection thresholds. The thresholds can be set as a default or as overrides to the default settings. This affects the Lab Settings and New Analysis windows displays.

Calling alleles between loci

A new setting has been added that automatically extends the region in which Osiris calls Off Ladder alleles to cover the entire region between the loci. This also allows users to edit those off-ladder alleles to assign them to the appropriate locus. A second setting allows previously defined extended locus boundaries that overlap a neighboring locus ladder region to extend this setting further to allow overlap of the neighboring ladder. See the user's guide for a complete description.

User Interface

- Users may now enter the search value for laboratory custom controls in the File Name Search box in the Positive Controls list on the Lab Settings Assignments tab for Osiris to recognize the control. It is no longer necessary to also add it to the File Name search criteria in the Positive Controls list on the File/Sample Names tab.
- 2. The Laboratory Settings tabs have been renamed to accommodate the channel-specific thresholds settings. The former "Locus/ILS Thresholds" tab has been renamed the "Thresholds" tab and the Analysis, Detection, Minimum Interlocus, and Maximum RFU thresholds have been moved there. The former "Sample Thresholds" tab has been renamed the "Sample Limits" tab.
- 3. Pull-up peak hover information now displays the channels causing the pull-up and the percentage of the primary peak causing the pull-up.

Improved allele and artifact calling

- 1. Eliminated "Pull-up with excess residual" artifact to ensure valid alleles are called.
- 2. Added option to reduce notification of data saturation ("Laser off scale").
- 3. Eliminated some redundant artifact notices.

Bug fixes

1. Fixed a bug that under very rare circumstances could have eliminated a valid allele call on a low level peak, when using the Fractional Filter.