

OSIRIS Release Notes Version 2.8 & 2.9

Improvements in OSIRIS Version 2.8 & 2.9

Version 2.8 was an internal release version with no public final release. Version 2.8 release was combined with version 2.9 as both releases were going to be closely spaced.

Kit Improvements

Modified PowerPlex Y23 kit to allow DYS456 to be extended two repeats to the left of the allelic ladder. Custom lab settings (Operating Procedures) will inherit this ability to call those alleles on upgrading to version 2.9.

New Features

User Interface

1. Editing is greatly improved and simplified. Editing can be done by clicking peak labels on the graph, and there is a sample editing window that places all quality notifications in one location for easy acceptance and review while the graph is displayed.
2. Alleles are now displayed boxed.
3. Artifacts are now given specific labels to distinguish the type of artifact peak. These labels are customizable.

Improved allele and artifact calling

1. Vastly Improved pull-up analysis. Version 2.9 represents a huge improvement in pull-up analysis. Previously, each peak that might cause pull-up in other channels was analyzed in regard to any comigrating peaks in the other channels. So each pull-up 'event' was being analyzed in isolation from other pull-ups. In version 2.9, all of the possible pull-up events in a channel are analyzed together to develop a pattern for the pull-up across the channel and the entire sample. The pull-up pattern allows OSIRIS to distinguish true pull-up from actual alleles and even to identify allele peaks in which a pull-up peak overlaps an actual allele, so that the peak contains both allele and pull-up signal. Additionally, improvements have been made in identification of pull-up peak signals. These changes significantly reduce the amount of editing needed when very low analytical thresholds are being used so there may be many low level pull-up peaks, when spectral coloration matrix is not good, and when peaks have very high levels of signal, causing significant pull-up.
2. Peak information now includes peak width at half height.
3. Improved Ladder analysis.
4. Improved ILS (internal marker) analysis and added a setting to kit definitions to improve ILS analysis in situations where there are many noise or pull-up peaks in the ILS, particularly at the left of the electropherogram. (See "Internal Lane Standard Analysis Criteria: Scale ILS Primer Peak Search Based on Last ILS Peaks" on the Sample Limits tab of the lab settings.)
5. Added a notification that allows rare off-ladder alleles that fall within a neighboring locus to be edited to a correct allele/locus assignment.
6. Improved the analysis of noisy peaks which under rare circumstances might receive the same allele call twice.

Bug fixes

1. Fixed minor bug that would not affect allele calls, where a crater (split peak) could be erroneously designated as a noisy peak.
2. Fixed a bug that had no effect on analysis but in very rare cases might cause the display to show a high analyzed baseline.
3. Fixed a bug in version 2.7 where, if a locus specific plus stutter threshold was set and the default plus stutter was left blank or set to zero, the analysis would fail or give an anomalous result.*

*Users that continue to use version 2.7 and want to use a locus-specific plus stutter value with a zero default value should set the default value to 0.0001, which will prevent the bug and have the effect of a zero default value.