Improved STR Artifact Recognition in Mixtures Using OSIRIS v. 2.8

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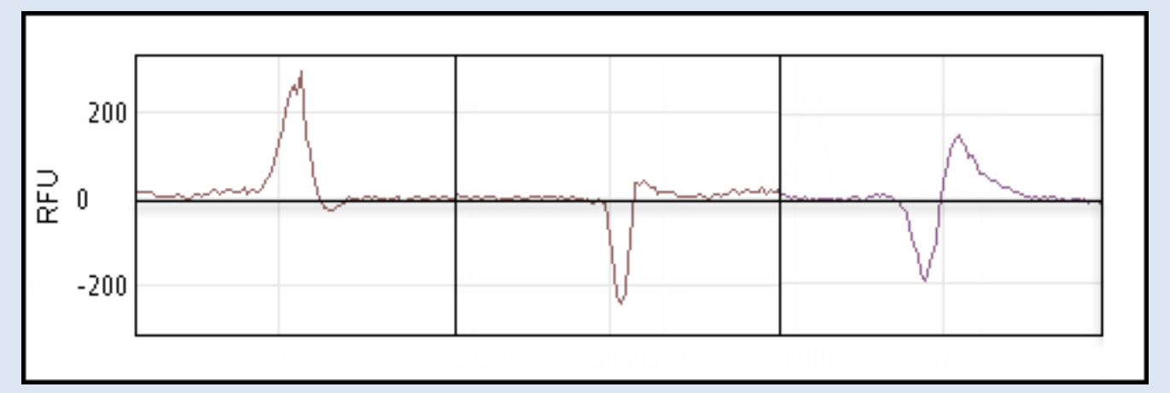
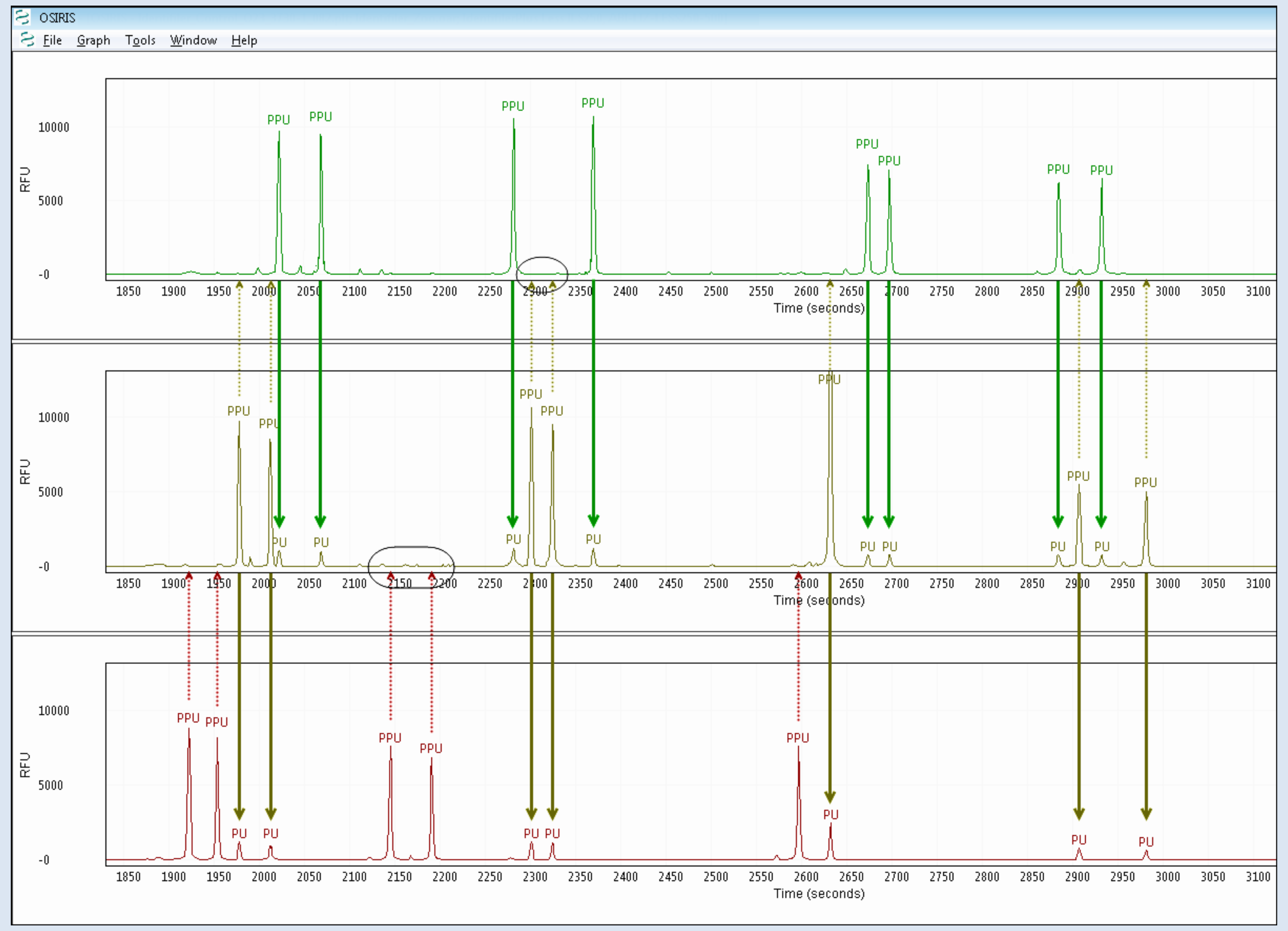
Data analysis



Pull-up Pull-down Sigmoidal

Pull-up causes characteristic signals in raw data. Osiris analyzes these, along with cross-channel alignment, noise and other factors to determine the pattern of pull-up in the entire sample.

OSIRIS Analyzes the Sample-wide Pull-up Pattern

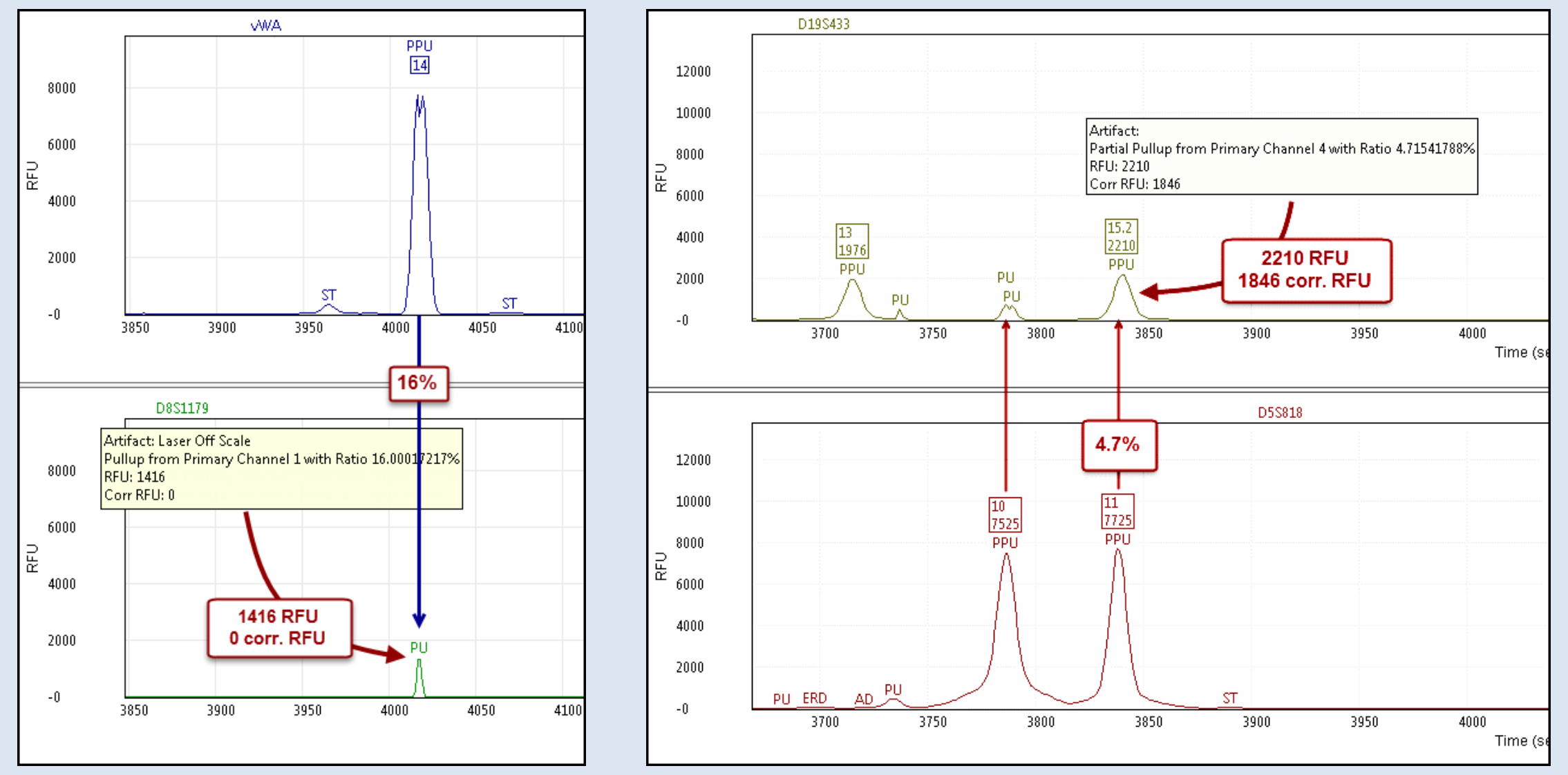


Similar-sized peaks cause similar-sized pull-up in other channels.

In this sample the pattern is shown with solid arrow indicating pull-up and dashed arrows and circles indicating lack of pull-up.

PU – pull-up, solid arrows; **PPU** – peak causing pull-up;
Other artifacts not labeled. Identifiler, analyzed data.

OSIRIS Analyzes Partial Pull-up



Pure pull-up Partial pull-up (15.2)

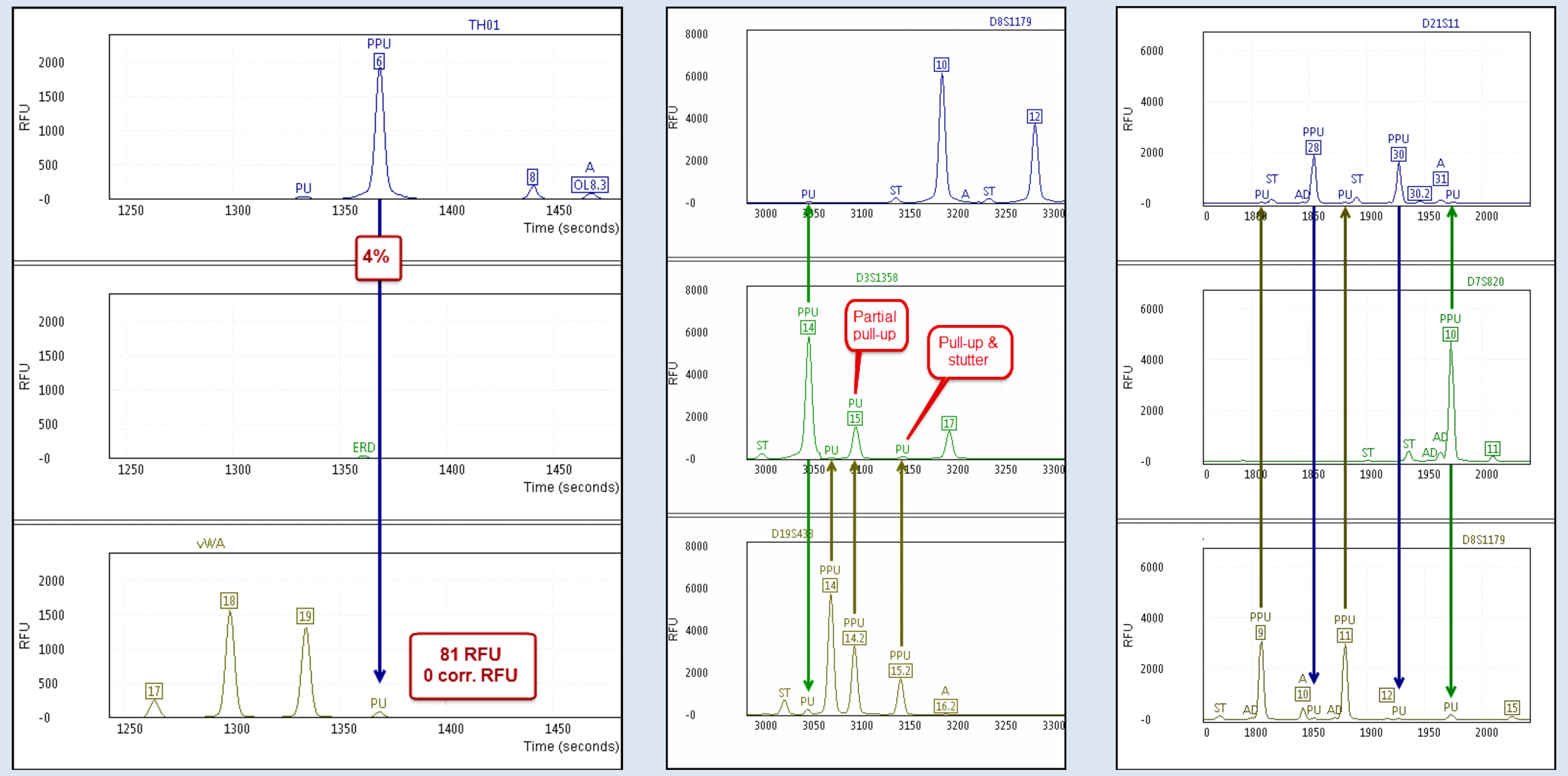
OSIRIS calculates corrected RFU for alleles that contain some pull-up (15.2 is 1846 corr. RFU).

Pull-up is difficult to determine in mixtures with minor alleles based solely on single occurrence - whether a peak is truly pull-up or simply comigrates by coincidence. Pull-up shows a sample-wide pattern - peaks with equivalent amounts of DNA will cause equivalent pull-up.

OSIRIS v. 2.8 checks for a pull-up pattern and which are outlier peaks – alleles – in the pattern (least median of squares). OSIRIS removes alleles from pattern analysis, then uses regression to determine pull-up pattern. Off-scale data exhibit a different pattern and are considered separately.

This gives an accurate assessment of which peaks are pull-up (no allele call), and which are alleles (with pull-up correction for comigrating alleles), reducing editing and freeing up time for case interpretation.

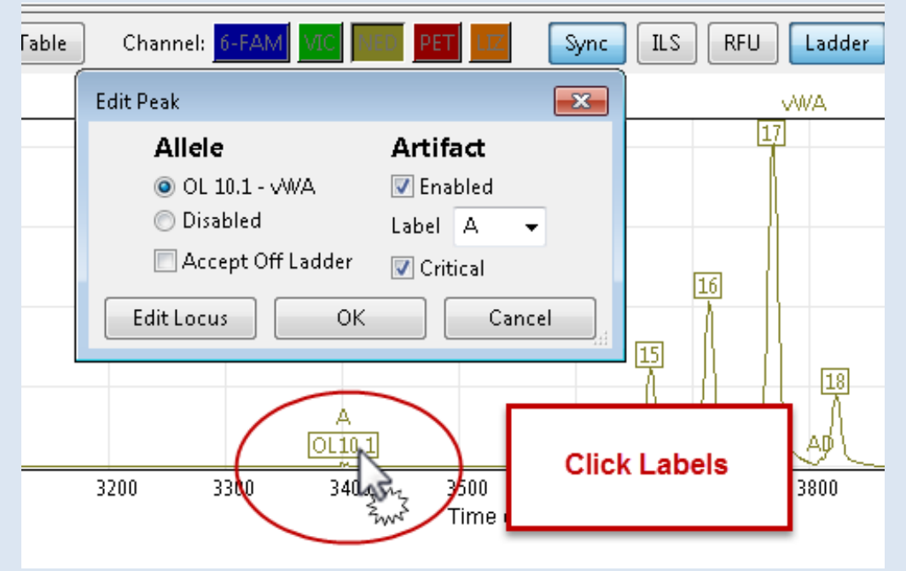
Pull-up Analysis in Mixtures



2 Person mixture 3 Person mixture ≥3 Person mixture

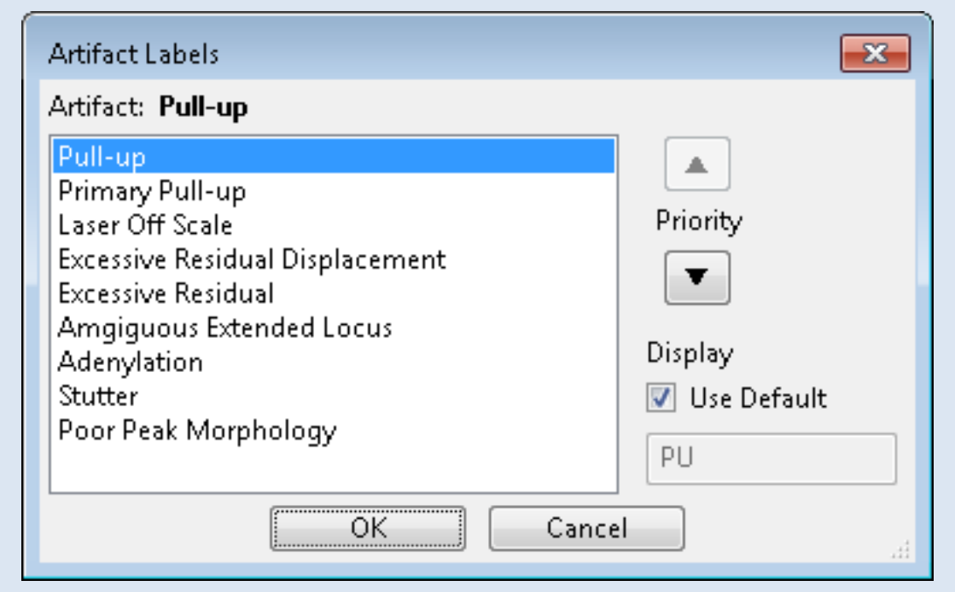
Automated pull-up and artifact determination facilitates efficient and accurate mixture analysis.

More Osiris Improvements

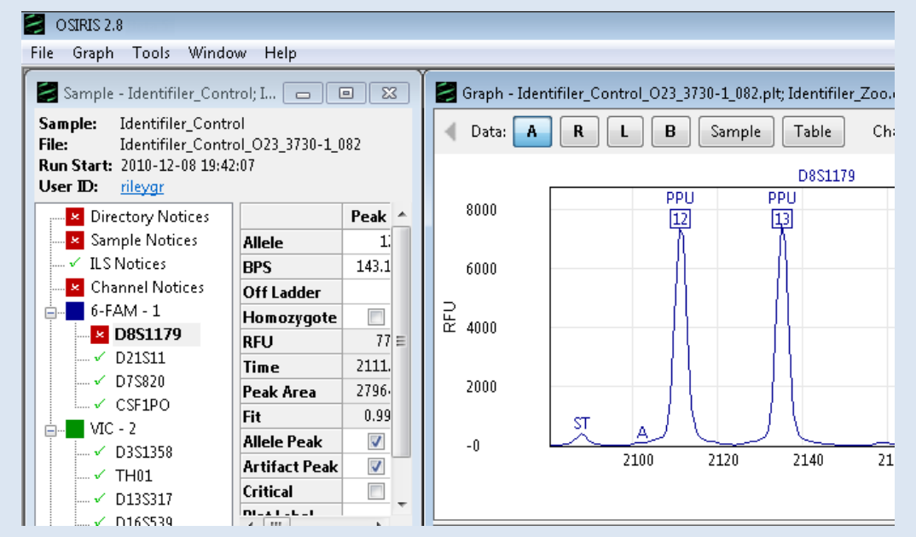


Click to edit

Click to edit alleles & artifacts in the Graph View. Change labels, add custom labels.

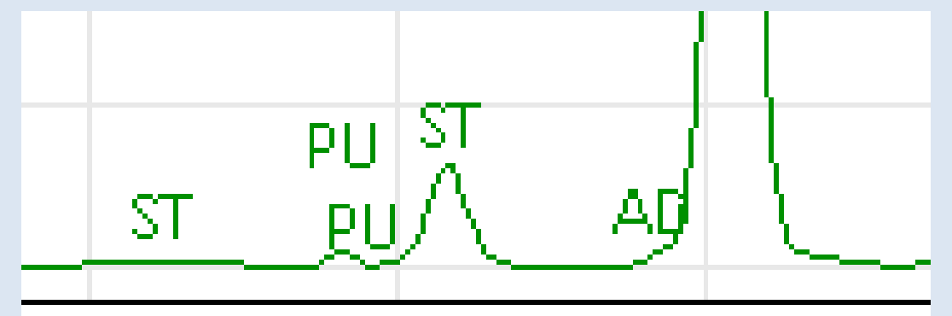


User-defined artifact labels and label priority



Sample notices table

Scroll through and zoom to loci in the Sample notices table in the Graph View.



Artifact-specific labels

OSIRIS Software

- Open source
- Validated as an expert system
- Cross-platform
  - PC (XP/Win7/8/10)
  - Mac OS10.8-10.10
- Displays
  - Stacked graph
  - Table
- Quality analysis
- Reanalysis prediction
- Flexible User configuration
- Flexible export
  - Table, LIMS, graphical
- Configured for most kits
- Files in both .hid and .fsa format
- Rapid analysis
  - < 30 s/96 samples

Using OSIRIS

OSIRIS is a freely available download on the Osiris web page :
http://www.ncbi.nlm.nih.gov/projects/SNP/osiris/

The Osiris User's Guide is on the homepage and in the program (F1) with a tutorial. The download includes demonstration data from various kits.

Open Source Collaboration

OSIRIS source code is on the GitHub repository.
We invite new collaborators to join the Osiris community to help improve Osiris.

For questions or requests, please contact:
forensics@ncbi.nlm.nih.gov

For announcements about Osiris releases and tips, subscribe to the Osiris announcement list from our homepage or:
http://www.ncbi.nlm.nih.gov/mailman/listinfo/forensics-announce

Email a question. Osiris Home page.

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