



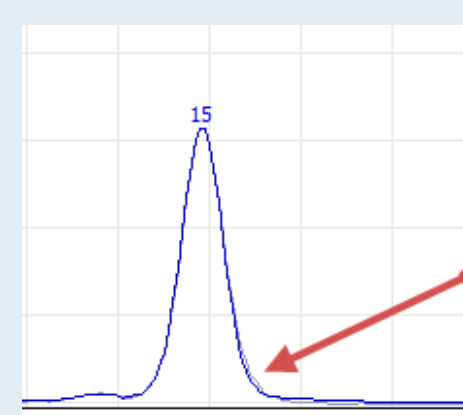
Separating the Wheat from the Chaff: Mathematically Distinguishing Low Level Alleles from Artifacts and Noise with OSIRIS v.2.5

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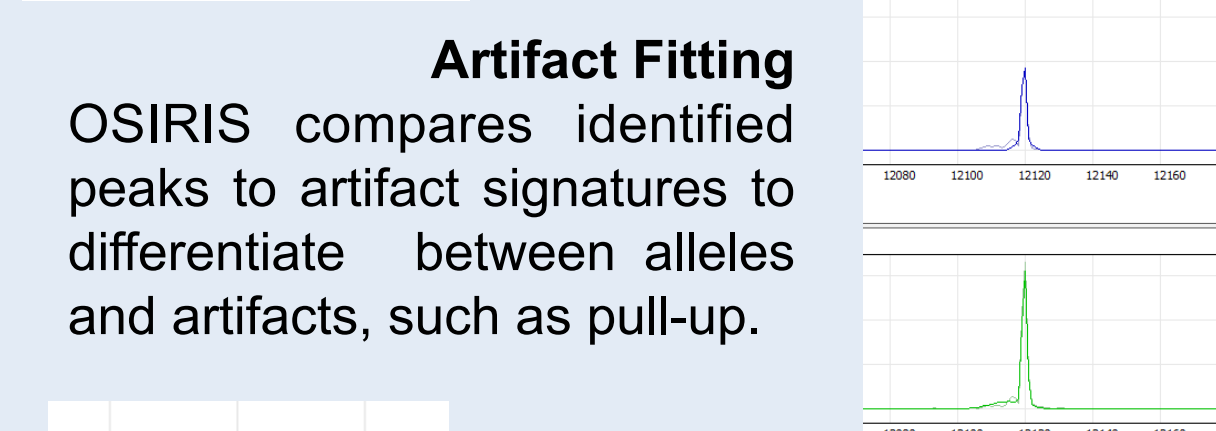


Data analysis

Osiris analyzes data mathematically, compares the curves to peak, artifact, and baseline signatures, assesses sample quality with user criteria.



Peak Fitting
The mathematical curve is dark blue, and the raw data is light blue. Fit is excellent, usually better than 0.999.



Artifact Fitting
OSIRIS compares identified peaks to artifact signatures to differentiate between alleles and artifacts, such as pull-up.

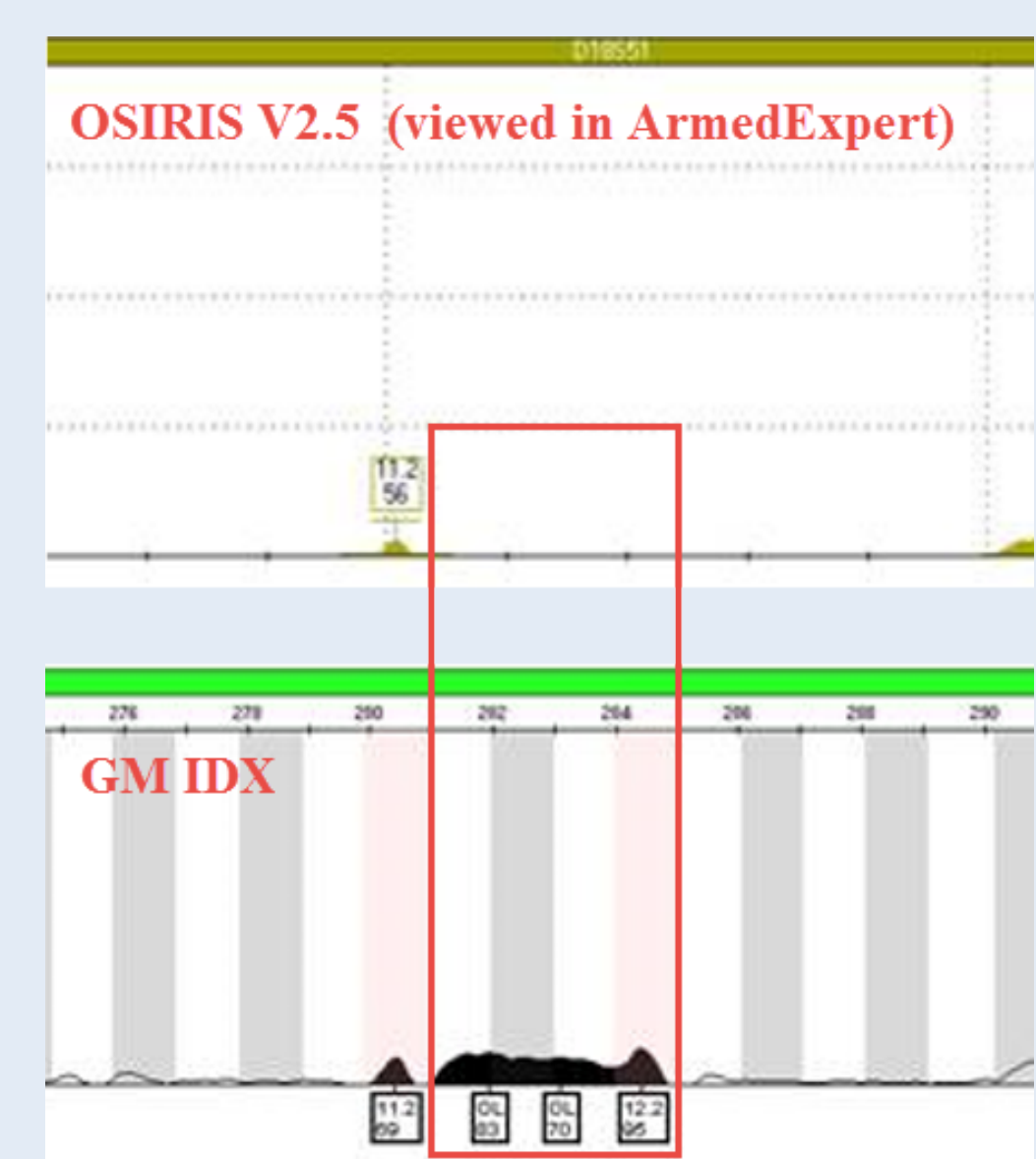
Baseline Fitting
OSIRIS can fit a mathematical curve to an elevated baseline (red arrow), allowing it to be subtracted, giving more accurate peak heights at low analysis thresholds.

Reduce Artifactual Calls



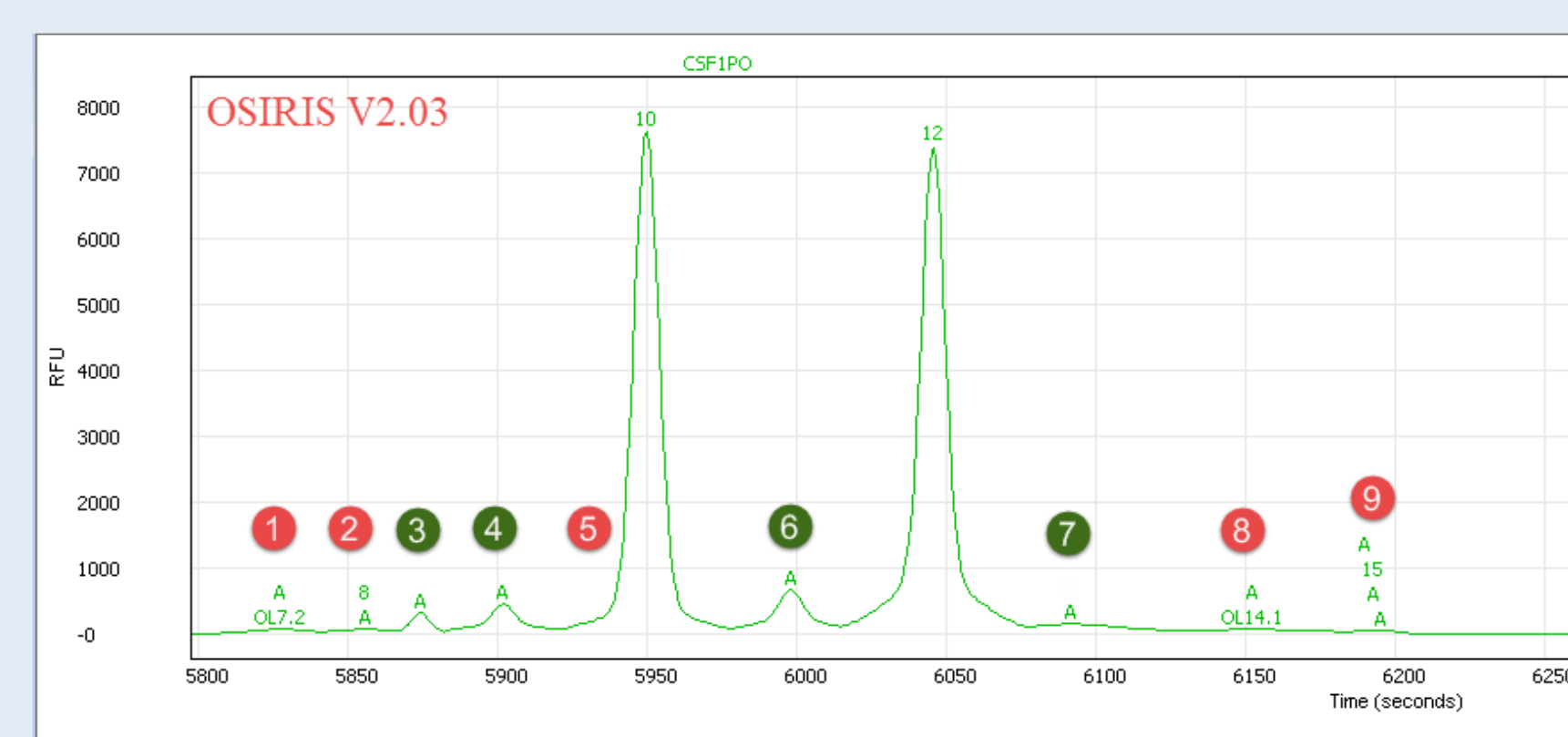
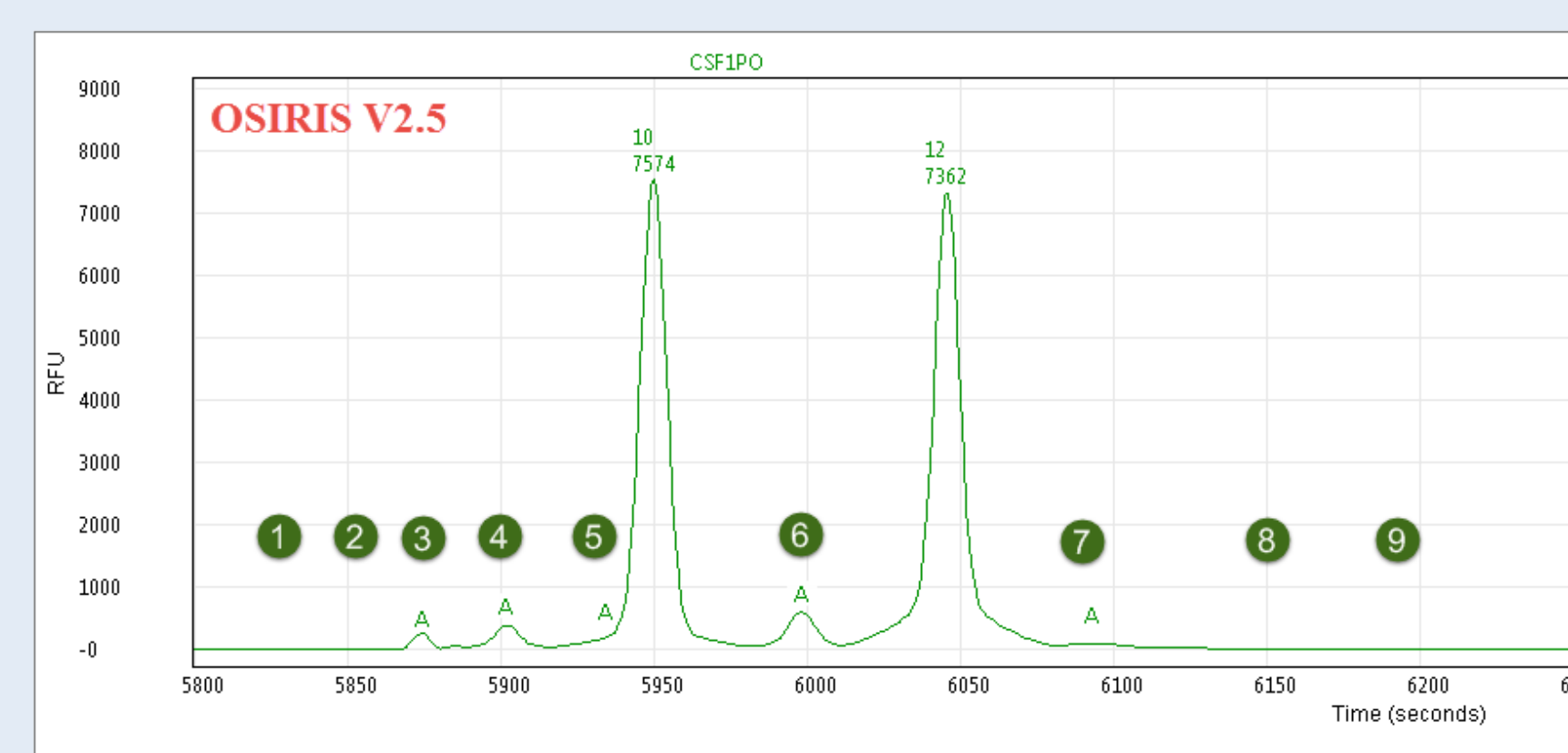
Dynamic normalization corrects baseline and eliminates artifactual allele call (red arrows)

Reduce Baseline Artifacts

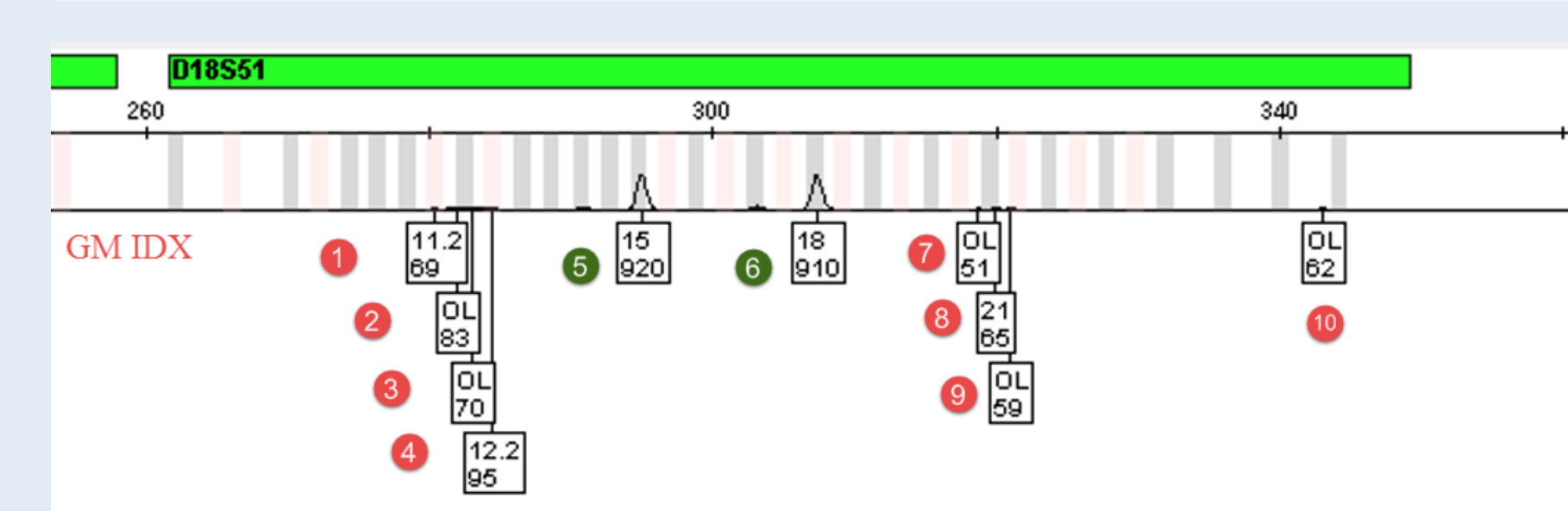
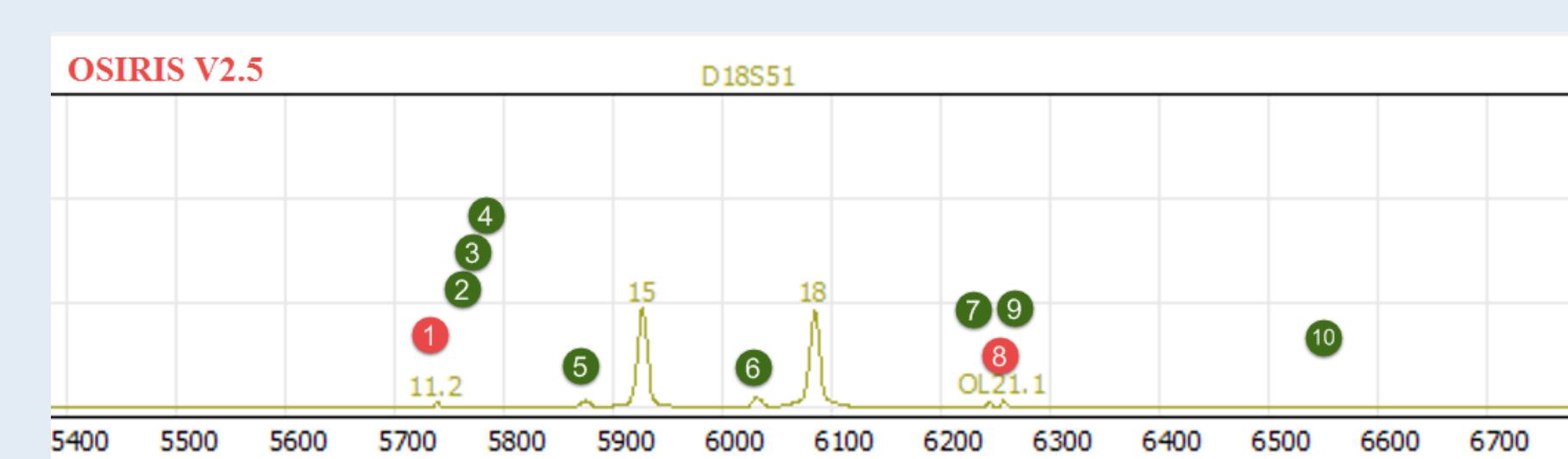


Dynamic normalization prevents artifactual baseline pushup ("table artifact")

Osiris 2.5 Reduces Editing



1. & 2. Eliminated by dynamic normalization
3. Eliminated by pullup detection algorithm
4. Eliminated by stutter filter
5. Eliminated by smart N-1 adenylation filter*
6. Eliminated by additive back/forward stutter filters
7. & 9. Eliminated by dynamic normalization
8. Corrected artifactual call



- 2.-4. Eliminated by dynamic normalization
5. & 6. Eliminated by stutter filter
7. & 9. Eliminated by dynamic normalization
8. Corrected artifactual call

*Osiris' smart adenylation filter works on N-1 shoulders and peaks except when those are in the location of a ladder or user-defined allele. This ensure that minor N-1 alleles get called in mixtures such as TH01 9.3/10

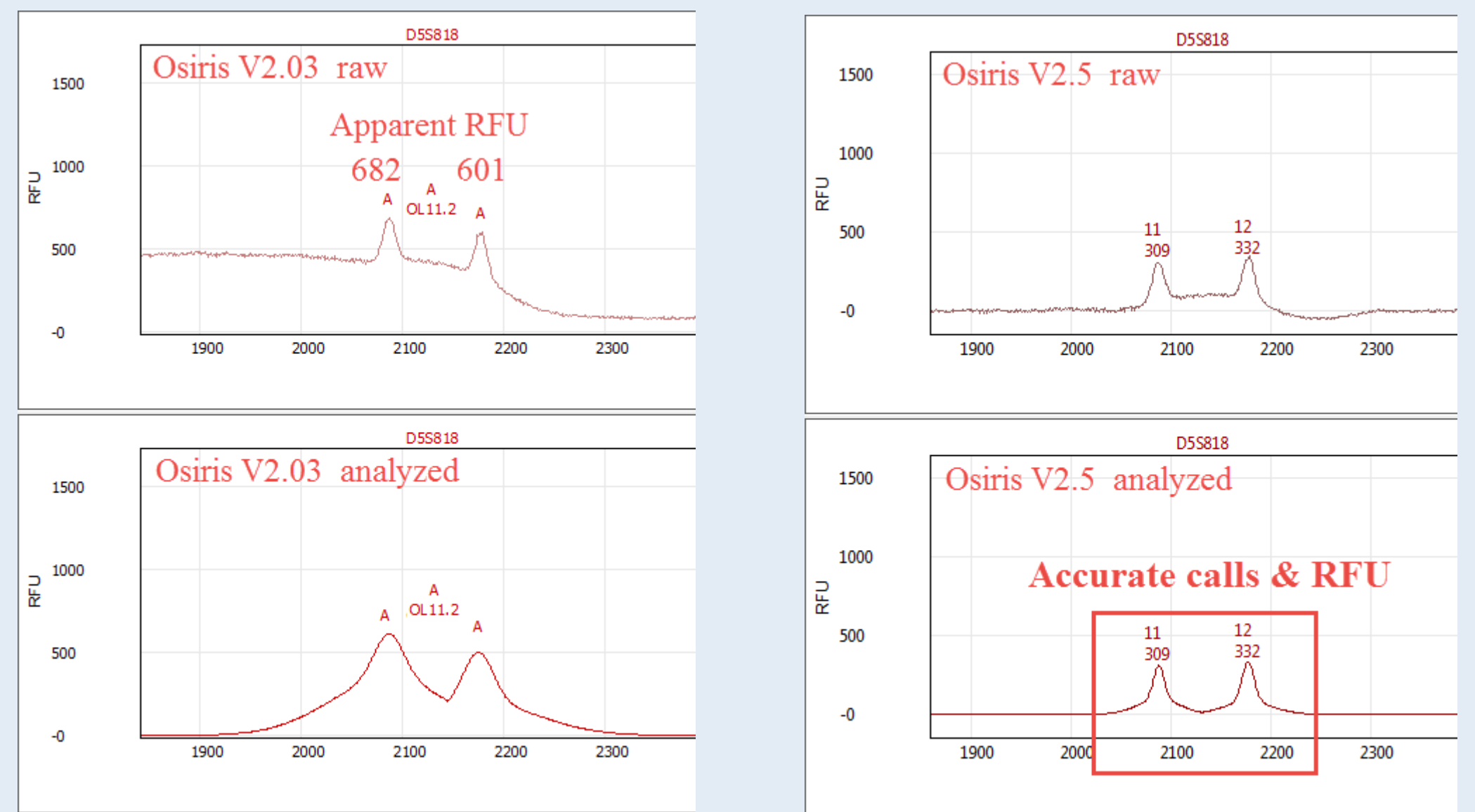
OSIRIS Software

- 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

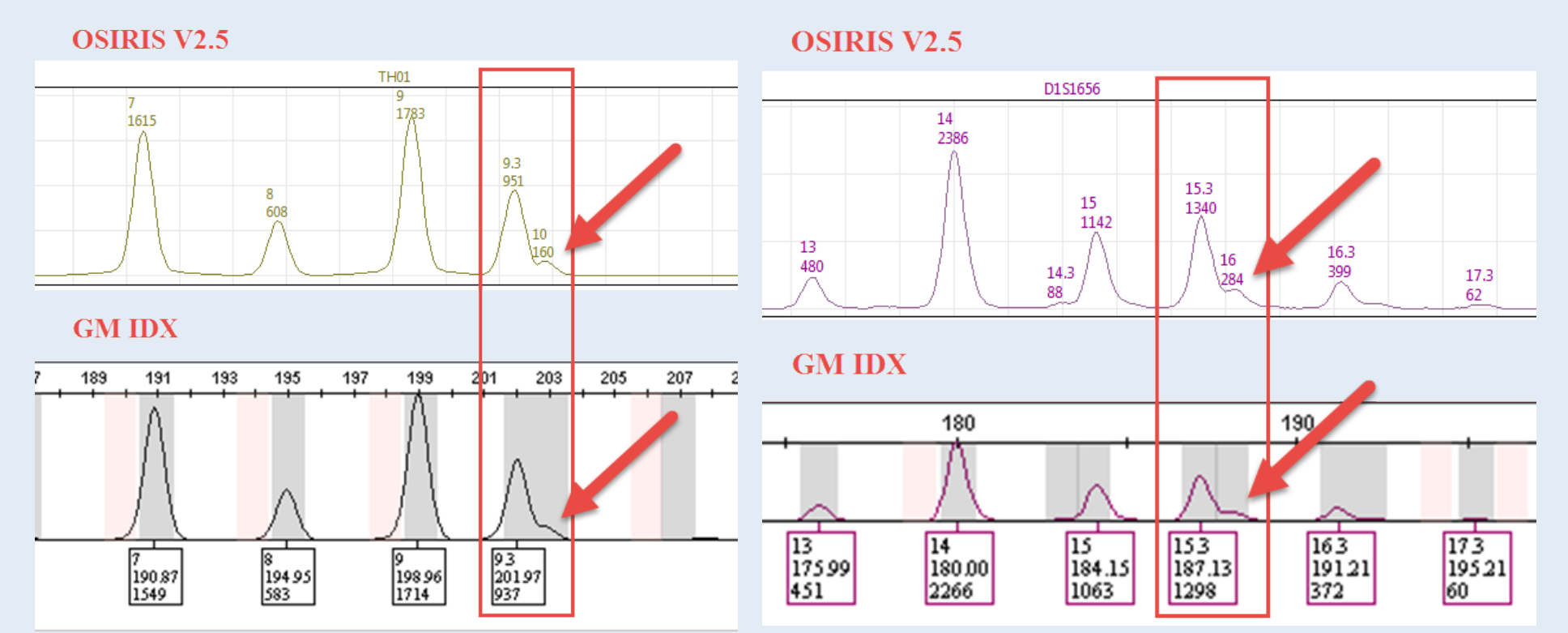
OSIRIS is a freely available download on the Osiris web page :
<http://www.ncbi.nlm.nih.gov/projects/SNP/osiris/>
 The Osiris User's Guide is on the homepage and in the program (F1) with a tutorial. The download includes demonstration data from various kits.
Open Source Collaboration
 OSIRIS source code 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:
<http://www.ncbi.nlm.nih.gov/mailman/listinfo/forensics-announce>

Dynamic Normalization



Corrects calls, artifacts and RFU

Call N-1 and N+1 Alleles



In mixture analysis, Osiris can accurately identify and call minor alleles separated by one nucleotide.

Osiris computes metrics for peak morphology, peak shifting, channel specific baseline noise, and mathematical allele and artifact signatures. Osiris applies these metrics and signatures to discriminate allele peaks from artifacts and noise, allowing users to analyze their data at analytical thresholds well below 50 RFU. Osiris identifies and labels artifacts in a fashion that reduces the number of peaks and loci that require editing, making the analysis process more efficient and accurate.

Osiris Users

- Forensic Casework
- CODIS Indexing
- Clinical Testing
- Cell line verification
- Relationship testing
- Uses**
 - NDIS Approved Expert System
 - Automating Reanalysis
 - Process monitoring
 - Training



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