Applied Biosystems™ GeneMapper™ *ID-X* Software version 1.7: New features and validation

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INTRODUCTION

Applied Biosystems™ GeneMapper™ *ID-X* Software v1.7 continues the proven legacy of trusted analysis algorithms while adding new functionality and expanding compatibility. GeneMapper *ID-X* Software v1.7 supports data analysis from the Applied Bioystems™ SeqStudio™ Flex Genetic Analyzer for Human Identification as well as legacy CE instrumentation going back to the ABI PRISM™ 310 Genetic Analyzer and includes support for Microsoft™ Windows™ 11. New features bring improvements to analysts' abilities to compare and annotate DNA profiles within the GeneMapper *ID-X* Software v1.7. Additionally, new analysis options exist to provide additional levels of customization for stutter and locus level thresholds as well as the ability to identify and filter or annotate pull up. The validation and verification results are included from the completed evaluation to the SWGDAM guidelines and DAB Quality Assurance Standards (QAS).

NEW FEATURES

Database
- PostgreSQL®
- Database dashboard
- Automated & On-demand backups

Analysis
- Allele-Specific Stutter
- Additive Stutter
- Marker-Specific Analytical Threshold
- Pull Up Filter
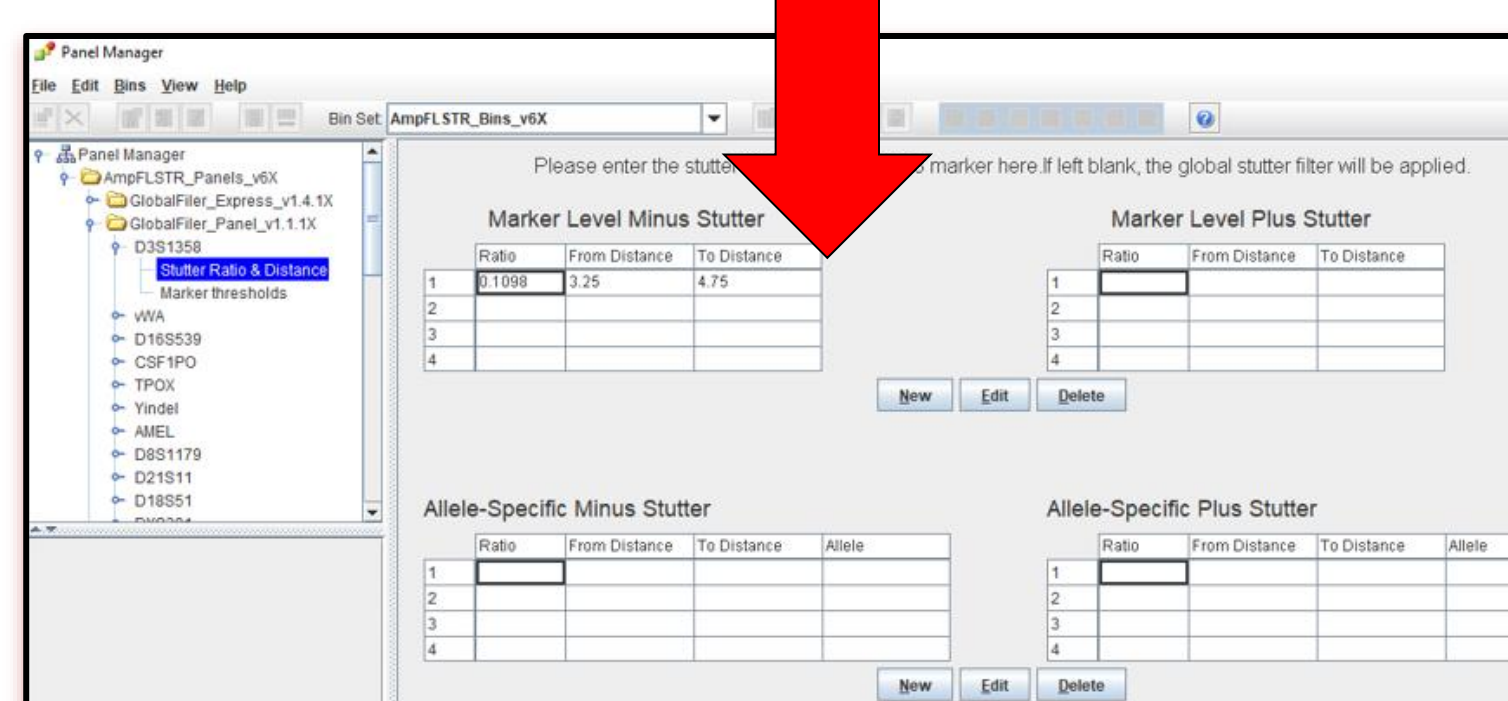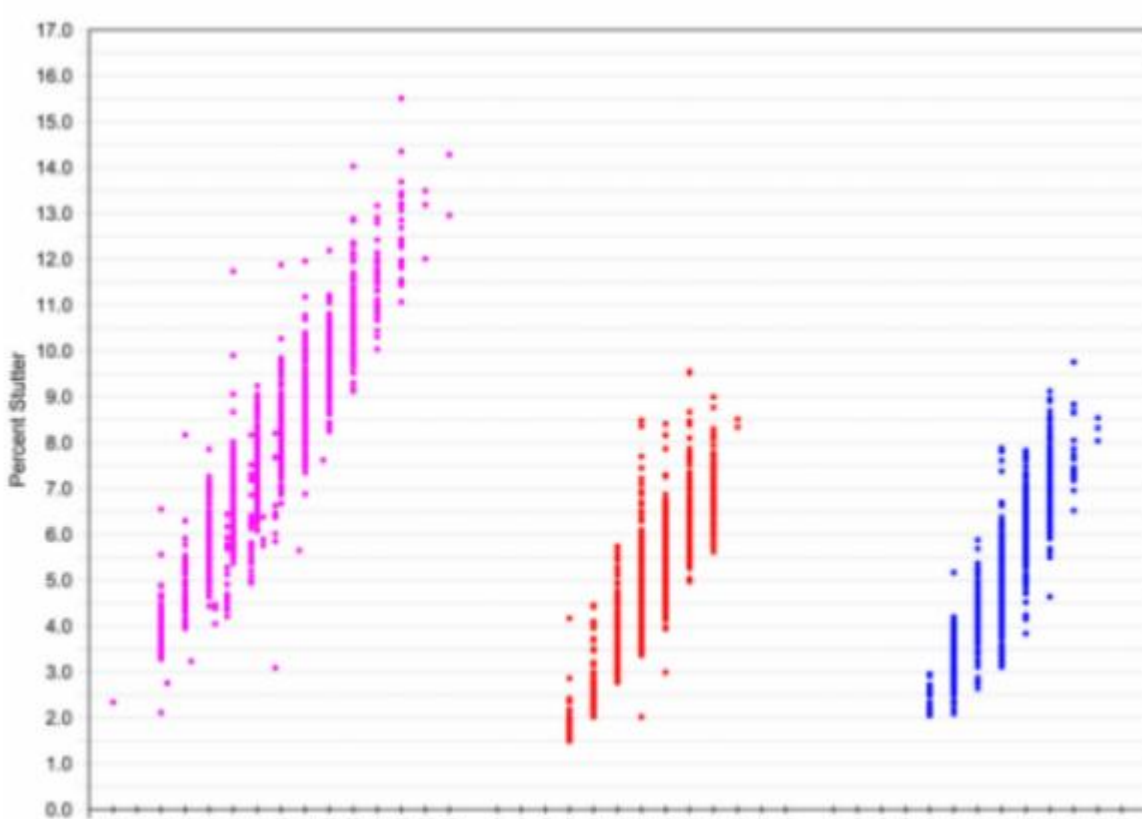- Analysis Settings import

User Interface
- Multi-project support
- Multi-plot view
- Electropherogram notes
- Profile Comparison improvements
- Auto-save
- Printing improvements
- Analysis Settings on Plot view
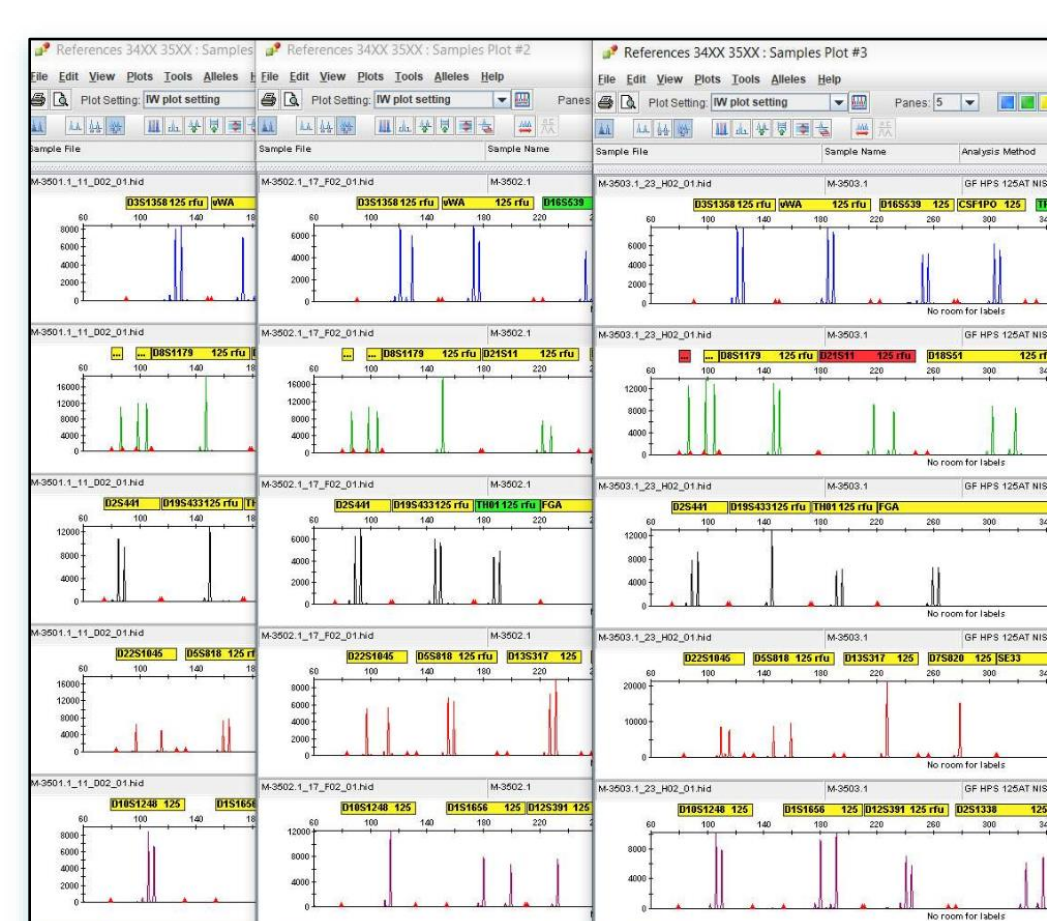
Compatibility
- Windows™10 and Windows™ 11 compatible
- Java 64 bit
- CE core series:
  - SeqStudio Flex Genetic Analyzers
  - 3500/xL Genetic Analyzers
 - SeqStudio™ Genetic Analyzer
- RapidHIT™ ID System
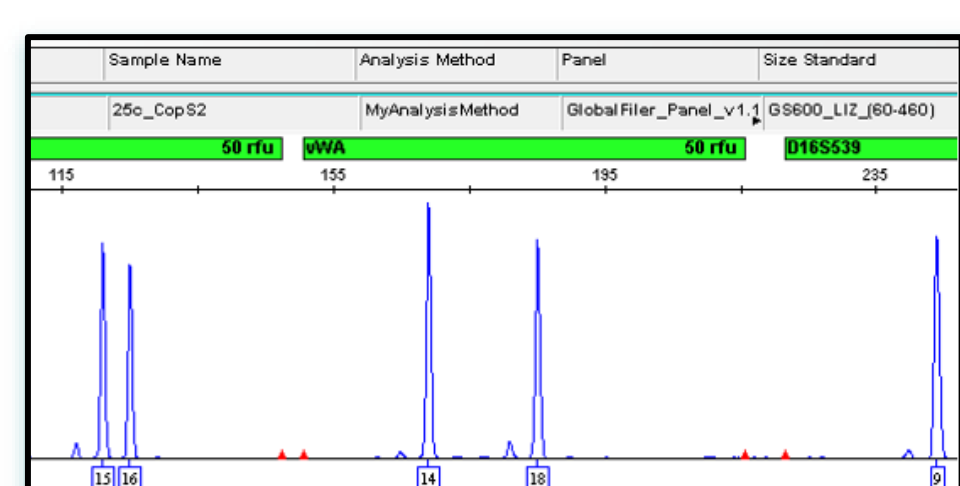
At-a-Glance Analysis Settings in Plot View. Analysis Method, Panel, Size Standard, and Analytical Threshold are now available in the plot for ease of reference.

Multi-plot view. Multiple sample plots can be opened simultaneously allowing for easy analysis and comparison of results
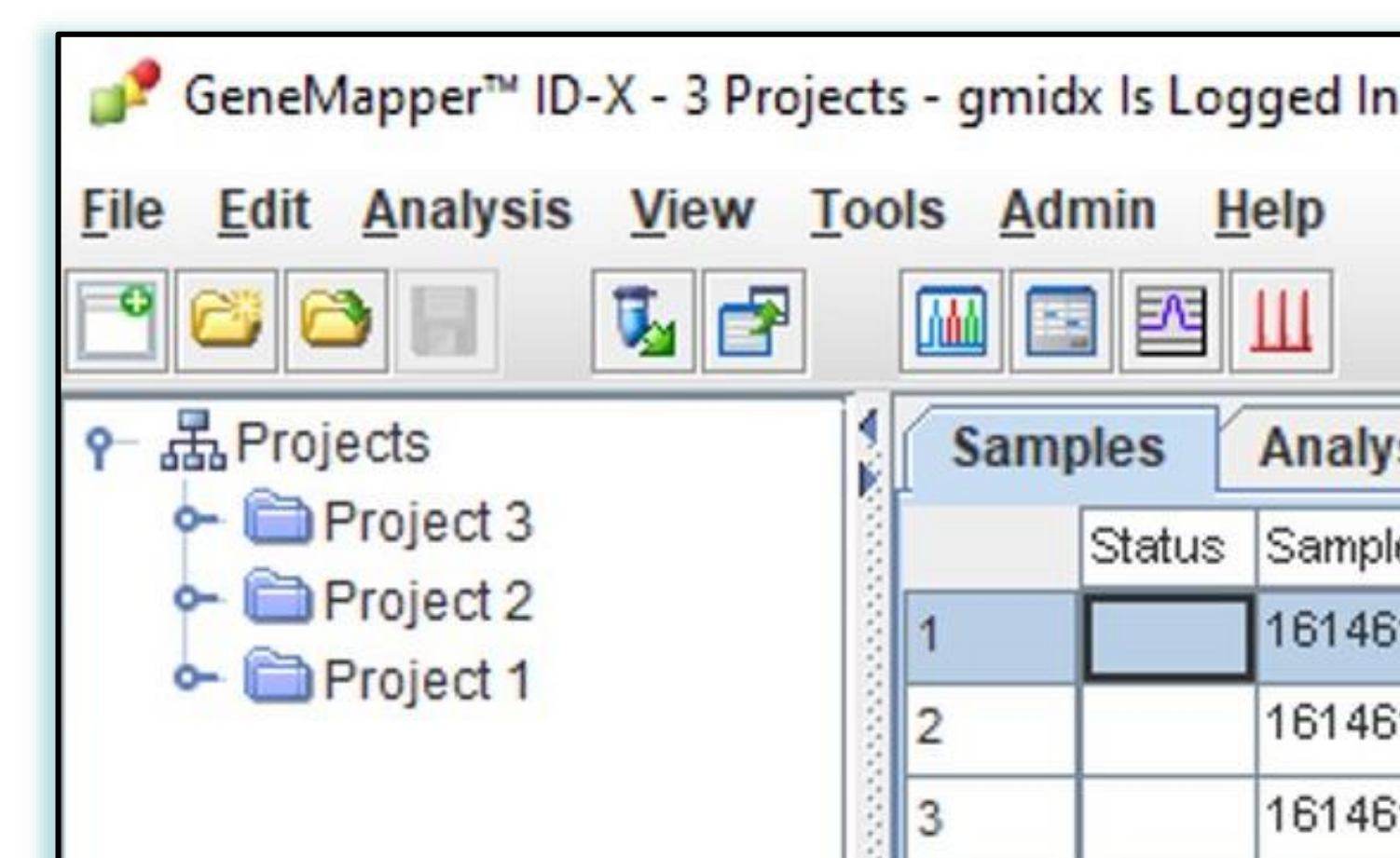

Allele-specific stutter can be added in Panel Manager and automatically filtered, saving analyst time and allowing for close modelling of real-world stutter behavior.
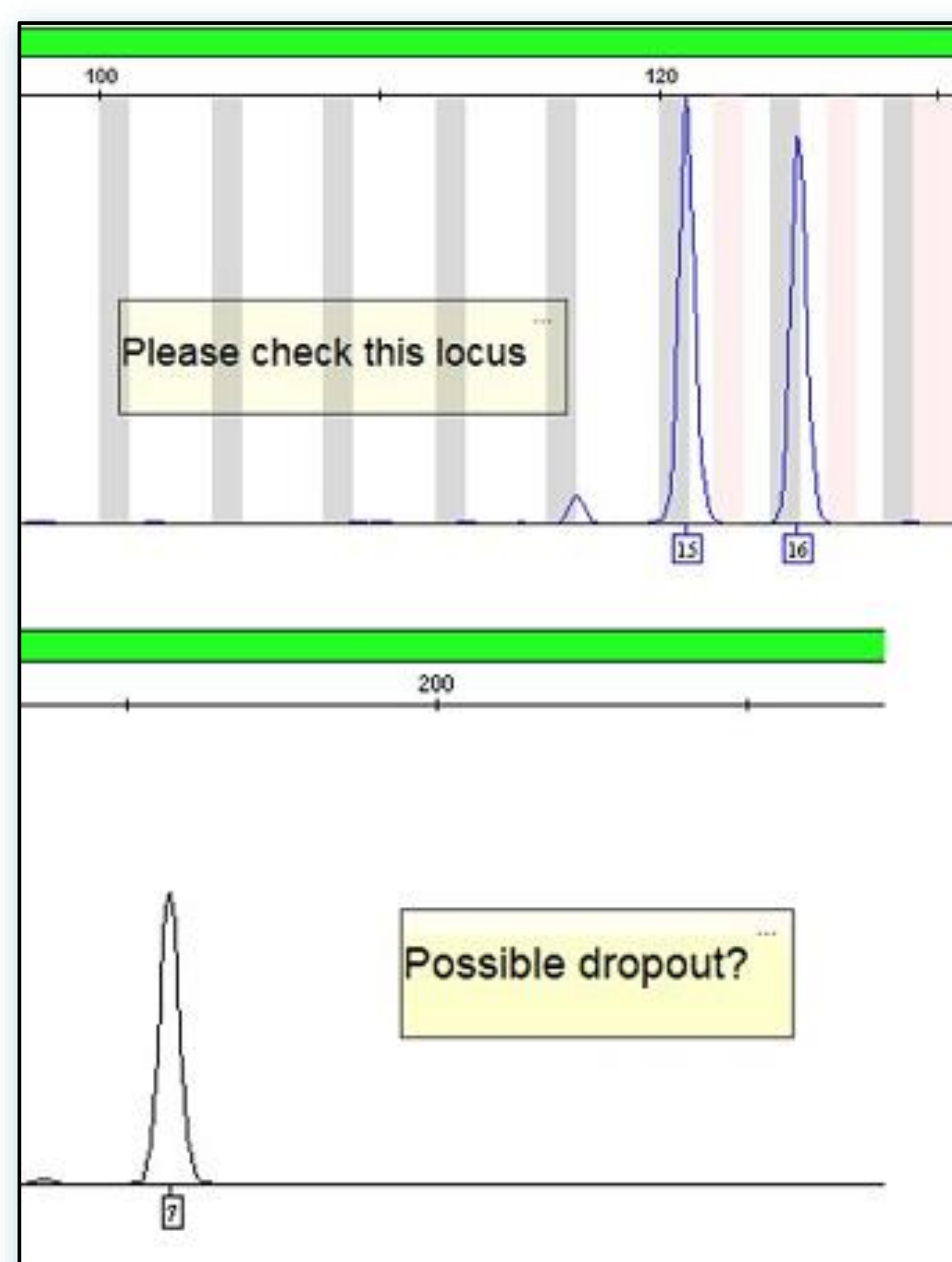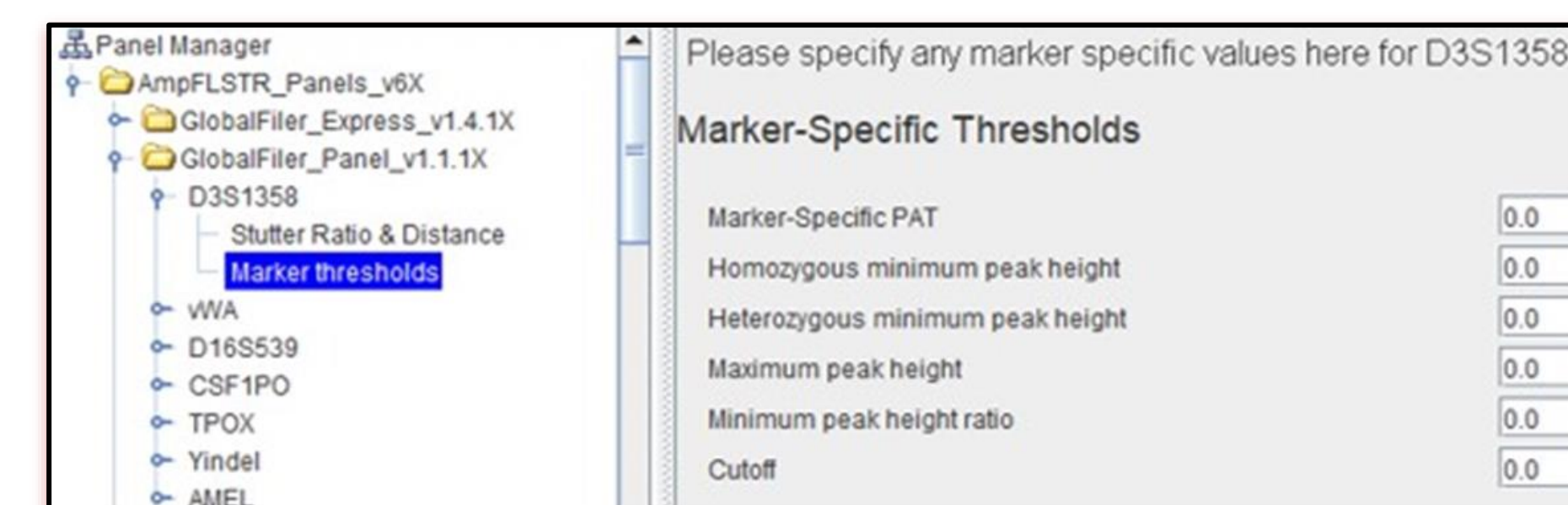

Notes can be electronically added to any electropherogram to record analyst comments and observations. Notes appear, both, on screen and in print form and can be audited.

Multi-project Support & expanded Profile Comparison allows for multiple projects to be opened at once and includes the ability to compare profiles across any open project.

Marker-Specific Thresholds can be applied in Panel Manager and enabled in Analysis Methods.

MATERIAL AND METHODS

Verification and validation of GeneMapper *ID-X* v1.7 (GMID-X) were performed according to SWGDAM Validation Guidelines for DNA Analysis Methods (SWGDAM, December 2016) and the FBI Quality Assurance Standards (QAS, July 2020).

Four models of computer were used for verification, with 16-32 GB RAM and Windows 10 and Windows 11 OS.

Instrument compatibility of GeneMapper *ID-X* v1.7 was tested with the following instruments:
- SeqStudio™ Flex Series Genetic Analyzer
- SeqStudio™ Genetic Analyzer
- Applied Biosystems™ 3730 Genetic Analyzer
- Applied Biosystems™ 3500 / 3500xL Genetic Analyzer
- Applied Biosystems™ 3130 / 3130xl Genetic Analyzer
- ABI PRISM™ 3100-Avant™ / 3100 Genetic Analyzer
- 310 Genetic Analyzer

The following tests were performed:
- Backwards compatibility of projects and settings from GeneMapper *ID-X* v1.1 to v1.6 with v1.7
- Sizing and genotyping concordance – peak sizes, heights, data points and allele calls compared between GeneMapper *ID-X* Software v1.6 and v1.7
- Functional testing of all new features in GeneMapper *ID-X* Software v1.7

RESULTS

GeneMapper *ID-X* Software v1.7 can open, read, and re-analyze project and settings files from GeneMapper *ID-X* Software v1.1 through v1.6.

3,146 samples and >160,000 genotypes from multiple chemistries were analyzed in GeneMapper *ID-X* Software v1.6 and v1.7. The v1.6 data was analyzed with v6X panels and bins; the v1.7 data was analyzed with v7X panels and bins. There was 100% concordance of peak sizes, heights, data points, and allele calls between data.

94 samples from Applied Biosystems™ GlobalFiler™ IQC PCR Amplification Kit, run on the 3500xL instrument, were analyzed with GeneMapper *ID-X* Software v1.7 on Windows 10 OS and GeneMapper *ID-X* Software v1.7 on Windows 11 OS. There was 100% concordance of peak sizes, heights, data points, and allele calls between data analyzed with GeneMapper *ID-X* Software v1.7 on Windows 10 OS and GeneMapper *ID-X* Software v1.7 on Windows 11 OS.

All new functionality worked as expected in testing, with correct results given in all test cases.

CONCLUSION

GeneMapper *ID-X* Software v1.7 can be used to process sample files generated on all HID CE instruments, including the new SeqStudio Flex, and with all PCR amplification kits. The same results for sizing, genotyping, profile comparison, and mixture analysis were obtained using GeneMapper *ID-X* Software v1.6 and v1.7. All new features and updates to GeneMapper *ID-X* Software v1.7 were successfully and correctly implemented without deleterious effects on other software functionality.

Innovative features were integrated to allow for easier use and streamline sample processing.

For more information visit: thermofisher.com/gmidx

Learn more about GeneMapper *ID-X* v1.7 here:

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