Universal Analysis Software v2.4.20211013.235212Z Release Notes

Table of Contents

Introduction

These release notes describe the ForenSeq™ Universal Analysis Software v2.4.20211013.235212Z and known issues. If you are updating from a version prior to Universal Analysis Software, review the release notes for ForenSeq Universal Analysis Software v2.3 for information on the changes introduced in that release. See the applicable guides for instructions on using the software.

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New Features

- Updated stutter filter in the analysis method to include n-2 and n+1 stutter as separate filters, from n-1

- Ability to perform the following task: create a flanking region report

- Updated Dark Mode for all analysis modules to support color deficiency accessibility

- Updated Icons for Run Status and added new status for Analysis Status for all analysis modules (errored, waiting to be analyzed, analyzing) as well as analysis start time and method

- Updated icons for the Detected QC flag and added a new Not Detected QC flag for ForenSeq MainstAY and ForenSeq Kintelligence samples

- Added instructions for creating Flanking Regions report and the report format for ForenSeq MainstAY analysis module

- Updated project report to include allele calls for homozygous loci and ascending order for heterozygous loci

- Added ability to find SW version number in system settings for all analysis modules

- Updated calculation for total Alleles in MainstAY sample summary, for female samples

- Updated quality flags to trigger when Y loci are detected in female samples, or any loci are detected in Negative Template Controls for MainstAY samples in MainstAY projects

- Updated loci coverage view for MainstAY analysis module such that green indicates a locus with no QC indicators, orange indicates a locus with at least one QC indicator and gray indicates locus dropout

- Updated loci coverage plots to display range of amplicon sizes to allow sorting based on increasing amplicon locus length range and /or alphabetically by name

- STR ordered by chromosome in ForenSeq MainstAY reports

- Change the term 'Gender' to 'Biological Sex' in the UI and reports

- Updated the Sample Type from ForenSeq Positive Amplification Control to NA24385 for ForenSeq MainstAY and ForenSeq Kintelligence, and HL60 for ForenSeq mtDNA Control Region and ForenSeq mtDNA Whole Genome

Defect Repairs

- SNPs in flanking regions appeared as separate alleles in the histogram view, this has been changed to exhibit only variants within the repeat region as separate alleles

- Adjust threshold such that alleles with >10 reads are displayed on the sample results page

- Updated ability to remove loci from a new analysis method.

Known Defects

- None

Additional Notes

- None

Version History

Version	Date	Description of Change
C	Mar 2023	Update
B	Oct 2021	Update
A	May 2021	Initial release