

# Universal Analysis Software v2.5.0\_20220811.201258Z

## Release Notes

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## Introduction

These release notes describe changes to components of the Universal Analysis Software v2.5.0\_20220811.201258Z and known issues. If you are updating from a version prior to 2.4.20211.013.235212Z, review the release notes for previous version for information on the changes introduced in that release. See the applicable guides for instructions on using the software.

## Universal Analysis Software v2.5.0\_20220811.201258Z

### New Features

The following features are added across all ForenSeq kits:

- Added global feature to select and bookmark samples across all ForenSeq kits
- Enabled high level data summary across all ForenSeq kits
- Added new categories, sorting and filtering capabilities for all ForenSeq kits
- Updated main navigation rail to include universal search and support access to all Projects, Runs, and Samples across all ForenSeq kits
- Added new bulk download feature to enable download of multiple sample reports simultaneously across all ForenSeq kits
- Added ability to create custom project reports and individual reports that automatically download and zip from the Sample List page, across all ForenSeq kits.
- Added ability to copy samples or easily create a new project to move samples from project to project.

The following features are added for the ForenSeq Imagen Kit:

- Two assay types and their Analysis methods

- -ForenSeq Imagen assay and ForenSeq Imagen Analysis Method to support phenotypic estimations
- -ForenSeq Imagen Geo assay and ForenSeq Imagen Geo Analysis Method to support phenotypic and biogeographic ancestry estimations

The following features are added for the ForenSeq MainstAY SE kit:

- Assay type with its Analysis Method
  - ForenSeq MainstAY SE assay and ForenSeq MainstAY SE Analysis Method

The following features are added

## Defect Repairs

The following bug fixes and repairs were introduced for ForenSeq mtDNA kits:

- Updated EMPOP report from the mtDNA Whole Genome analysis for position 3107 previously reported as a deletion.
- Updated EMPOP report for no coverage positions from mtDNA Whole Genome analysis, previously reported as “N”, to enable EMPOP compatibility.
- Updated variant calling to be consistent with SWGDAM Interpretation Guidelines for Mitochondrial DNA Analysis by Forensic DNA Testing Laboratories –includes realignment of 16189del and 310del
- Updated the NUMT (nuclear mtDNA insertions) filter to reduce possibility of filtering actual calls.
- Updated Trimming rules
  - Updated conditions for checking the presence of upstream and downstream primers.
  - Added trimming rule (during primer trimming step) in position 1490 and 8442 due to higher error rate in some samples.
- Updated alignment adjustment around ‘T’ in 303-315 and 16184-16193 C-stretches and to be consistent with SWGDAM Interpretation Guidelines for Mitochondrial DNA Analysis.

## Known Defects

- None

## Additional Notes

- None

## Version History

Version	Date	Description of Change
A	Aug 2022	Initial Release