

# FORENSEQ UNIVERSAL ANALYSIS SOFTWARE V2.1 RELEASE NOTES

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## Introduction

These release notes describe changes to ForenSeq™ Universal Analysis Software v2.1 and known issues. If you are updating from a version prior to ForenSeq Universal Analysis Software v2.1, review the release notes for ForenSeq Universal Analysis Software v2.0 for information on the changes introduced in that release. See the applicable guides for instructions on using the software.

## ForenSeq Universal Analysis Software v2.1

### New Features

- Ability to conduct the following tasks:
  - Analyze ForenSeq mtDNA Whole Genome libraries
  - Track system and user events for runs, projects, and sample analysis results
  - Comment on tracked system and user events
  - View tracked system and user events in reports
  - Collapse the project sidebar
  - Navigate the mitochondrial genome (mtGenome) using the up and down keyboard buttons
- Call percentages calculated to five significant figures
- Call percentages rendered to three significant figures only

### Defect Repairs

- Sample report header for negative amplification control and reagent blank samples reads as “Call”
- HL60 reference genome supports heteroplasmy at the following positions:
  - 1490: T or Y
  - 2445: T or Y
  - 4821: G or R
  - 5149: C or Y
  - 12071: T or Y

- Analysis icons in project sidebar sync with the sample analysis result

## Known Defects

- None

## Additional Notes

- None

## Version History

Version	Date	Description of Change
A	August 2020	Initial release