Illumina® SeqLab

Release Notes

BaseSpace® Clarity LIMS X Edition v2.5

Hamilton Methods v2.0.1

December 2016

Introduction

These release notes provide an overview of the key updates to components of Illumina SeqLab since the initial release containing BaseSpace Clarity LIMS X Edition v1.6.5 and Hamilton Methods v1.0. The new versions are Clarity LIMS X Edition v2.5 and Hamilton Methods v2.0.1 These versions have been developed, tested and are to be implemented together. They are not backwards compatible with previous versions. These notes encompass the changes for the following v2.0.1 methods: PCR-Free PrePCR Master, PCR-Free PostPCR Master, Nano PrePCR Master, and Nano PostPCR Master.

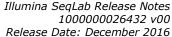# I. BaseSpace Clarity LIMS X Edition v2.5

NEW FEATURES:

- Upgrade from Clarity LIMS v3.5 to v4.2.
- Added Fragment Analyzer (FA) support.
- Updated configuration to support multiple task names on the cBot 2 system.

IMPROVEMENTS:

- UCT/DCT volumes support separate values for Nano and PCR-Free workflows.
- Added a check at the Create PDP Pool step to prevent pooling samples from multiple workflows.
- Support of individual reagent lots added to steps instead of comma-separated lists.
- Enforce column-major-contiguous sample placement at all applicable automated steps.
- Improved the Projects & Samples view in the Clarity LIMS Web Interface.
- Added a Sample Management view and a sample accessioning feature.
- Added User and Client Management to the Clarity LIMS Web Interface.
- Added security improvements to the application infrastructure, including transitioning away from JBoss to Tomcat.
- Added on-the-fly search indexing for samples via elastic search.
- Added Sample Status tracker.
- Added safe stopping point notifications.

BUG FIXES:

- Corrected the calculation for Lanes Remaining during Create Production CST Batch.
- A sample that initially fails at qPCR and then passes after a requeue is no longer requeued after passing.
- Corrected an issue where the requeue counter on a sample was incremented even if Repeat Library Prep was aborted.
- The maximum requeues error message is no longer hard-coded at 4.

- Fixed a bug where timeouts occurred when the entire string of existing reagent lot kits is returned to the Hamilton Microlab STAR (ML STAR).

- Unused database connections in the HCSX API adapter no longer report exceptions at startup.

- Corrected retry interval for Tomcat connection with RabbitMQ.

KNOWN ISSUES:

- Sample failures at Semi-Automated Make LQC do not force failures at Eval qPCR.

- System allows for any FA marker to be used. Workflow is only compatible with the High Sensitivity NGS kit (DNF-474).

II.   Illumina SeqLab Hamilton Methods v2.0.1

NEW FEATURES:

- Updated deck layouts to support the following ML STAR hardware: Covaris Locking Plate Holder Module (96839-01), Molded inserts (96858-01), and Wheaton inserts (96869-01).

- Added Automated Fragment Analyzer (FA) method for SSQC and LQC.

- Added EtOH and RSB reservoir tracking.

- Added support for Covaris 96 microTUBE plate (SKU 520078). Full plates only, no partial plates.

IMPROVEMENTS:

- Changed the elution volume at the end of PCR-Free library prep to 40 µl to improve elution efficiency and reduce sample loss.

- Lowered the qPCR threshold for PCR-Free Library Preps to support 40 µl elution volume.

- Added compatibility for European Hamilton CO-RE head waste location.

- Added CFP plate barcode scanning to reduce user errors.

- Added detection of gripper plate transfer failures.

- Improved onboard barcode scanning.

- Improved qPCR accuracy by using the channel arm for the initial sample transfer during Make qPCR.

- Optimized Make CST (1x and 4x) mixing heights and volumes.

- Added new labware definitions for Make CST (1x and 4x).

- Optimized Make PDP mixed to reduce pooling penalty.

DEFECT REPAIRS:

- Resolved 4x CST failure issue by optimizing pipetting configurations.
- Resolved an issue in Make CFP and others where batches could not be created using > 7 plates.

KNOWN ISSUES:

- There are no known issues with this release.