

# **Local Run Manager**

## **Resequencing Analysis Module v2.0**

### **Release Notes**

## Introduction

These Release Notes detail notable items for the Local Run Manager Resequencing Analysis Module v2.0 release.

Please note that the Resequencing Analysis Module v2.0 requires Local Run Manager Framework v2.0.0 or higher and is not compatible with Local Run Manager Framework v1.3.1 or lower.

For more information about this analysis module and how to use it, refer to the Local Run Manager Resequencing Analysis Module Workflow Guide, available from the Illumina Local Run Manager Support Page, Documentation & Literature.

[http://support.illumina.com/sequencing/sequencing\\_software/local-run-manager/documentation.html](http://support.illumina.com/sequencing/sequencing_software/local-run-manager/documentation.html)

### NEW FEATURES:

- Added support for processing datasets generated from iSeq 100, MiniSeq, MiSeq, and NextSeq 550 sequencing systems.
- Added support for importing and exporting Sample Sheet files on the Run Setup page.
- Added support for the following Library Prep Kits:
  - IDT-ILMN TruSeq DNA-RNA UD Indexes 24 Indexes
  - IDT-ILMN TruSeq DNA-RNA UD Indexes 96 Indexes
  - Nextera DNA CD Indexes – 24 Indexes Tubed
  - Nextera DNA CD Indexes – 96 Indexes Plated
  - Nextera DNA (formerly Nextera)
  - TruSeq DNA-RNA CD Indexes 96 Indexes (formerly TruSeq HT)
  - TruSeq DNA-RNA Single Indexes Set A&B (formerly TruSeq LT)
- Added support for entering custom index sequences directly on the Run Setup page.
- Added support for the following special characters to be used as part of the “Run Name” and “Run Description” on the Run Setup page:

` ~ ! @ # \$ % - \_ { }

Increased the maximum number of samples on the Run Setup page to 1536.

### DEFECT REPAIRS:

- None

### KNOWN ISSUES:

- Special characters `~!@#%\_-\_{} will be allowed in the Sample Description when you enter it in the LRM UI, but will throw an error when you try to save the run.
- Custom primers don't update in the Local Run Manager run if they are updated in the Control Software.

- If a genome in the Genome Repository has one or more subfolders with a .fa file, you will see multiple occurrences of the same genome in the genome dropdown.
- When the user selects certain library prep kits, like Nextera DNA, the I7 and I5 index fields will not be marked as required fields.
- If the Local Run Manager Analysis Service is restarted, this could cause a running analysis to crash.

**OTHER:**

- When using a custom kit, you must always enter your i5 indexes in the MiSeq or forward orientation. Local Run Manager will automatically reverse complement the indexes when writing the sample sheet used for analysis.