

# **Local Run Manager**

## **16S Metagenomics Analysis Module**

### **v1.0**

## **Release Notes**

## Introduction

These Release Notes detail notable items for the Local Run Manager 16S Metagenomics Analysis Module v1.0 release.

Please note that the 16S Metagenomics Analysis Module v1.0 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 16S Metagenomics 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:

- Initial Release

### DEFECT REPAIRS:

- N/A

### KNOWN ISSUES:

- When importing a sample sheet into Instrument Control Software with a Custom Taxonomy Database specified in the Settings section, the Module is unable to detect and reject the Sample Sheet when the Custom Taxonomy Database setting has a comma, which is an invalid character for that setting.
- 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 during analysis, this could cause a running analysis to crash.
- Custom Primers don't update in the Local Run Manager run if they are updated in the Control Software.

### 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.