

# **Local Run Manager**

## **16S Metagenomics Analysis Module**

### **v2.0**

### **Release Notes**

## Introduction

These Release Notes detail notable items for the Local Run Manager 16S Metagenomics Analysis Module v2.0 release.

Please note that the 16S Metagenomics Analysis Module v2.0 requires Local Run Manager Framework v3.0 or higher and is not compatible with Local Run Manager Framework v2.0 or lower. For more information on module version compatibility per instrument platform, refer to [Local Run Manager Module Selector](#).

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.

### NEW FEATURES:

- Illumina Library Prep Kits (LPK) and Index Adapter Kits (IAK) are decoupled.
  - Users now able to choose both the LPK and IAK options from Local Run Manager interface.
  - Sample sheet export from Local Run Manager will now include the Index Kits field on a separate line from the Library Prep Kits.
  - Added support for custom Library Prep Kits and Index Kits.
  - Added UMI Anchor Kit toggle for applicable Index Kits.
  - Added separate directories for Illumina Library Prep Kits and Index Kits.
- Updated Library Prep Kit names with corresponding Index Adapter Kits.

old name	new name
Nextera DNA Flex	Illumina DNA Prep

Library Prep Kits	Index Kits
Illumina DNA Prep	IDT-Ilmn DNA-RNA UD Indexes SetA Tagmentation
	IDT-Ilmn DNA-RNA UD Indexes SetB Tagmentation
	IDT-Ilmn DNA-RNA UD Indexes SetC Tagmentation
	IDT-Ilmn DNA-RNA UD Indexes SetD Tagmentation
	IDT-Ilmn DNA-RNA UD Indexes SetABCD Tagmentation
	IDT-ILMN Nextera DNA UD Indexes Set C - 96 Indexes
	IDT-ILMN Nextera DNA UD Indexes Set D - 96 Indexes
	IDT-ILMN Nextera DNA UD Indexes Set A B C D - 384 Indexes
	Nextera DNA CD Indexes - 24 Indexes Tubed
	Nextera DNA CD Indexes - 96 Indexes Plated

- Added two Index Kits (IDT-Ilmn DNA-RNA UD Indexes SetC and Set D Tagmentation) in Nextera XT Library Prep Kit

Prep Kit	Nextera XT

<b>Index Kits</b>	Nextera XT Index Kit - 24 Indexes 96 Samples
	Nextera XT v2 Index Kit Set A
	Nextera XT v2 Index Kit Set B
	Nextera XT v2 Index Kit Set C
	Nextera XT v2 Index Kit Set D
	Nextera XT v2 Index Kit Set A B C D
	IDT-ILMN Nextera DNA UD Indexes Set A - 96 Indexes
	IDT-ILMN Nextera DNA UD Indexes Set B - 96 Indexes
	IDT-ILMN Nextera DNA UD Indexes Set C - 96 Indexes
	IDT-ILMN Nextera DNA UD Indexes Set D - 96 Indexes
	IDT-ILMN Nextera DNA UD Indexes Set A B C D - 384 Indexes
	IDT-Ilmn DNA-RNA UD Indexes SetC Tagmentation
	IDT-Ilmn DNA-RNA UD Indexes SetD Tagmentation

**DEFECT REPAIRS:**

- When the user selects certain library prep kits, like Nextera DNA, the I7 and I5 index fields are now marked as required fields.

**KNOWN ISSUES:**

- When importing sample sheet onto the MiSeq Control SW, unclear error message might be displayed. Check sample sheet if error is seen.
  - Common issues include formatting, ensure headers are specified, ensure Workflow field is exactly as Local Run Manager interface displays, etc.
- Sample table grid are not aligned with the Sample Number column as higher sample numbers are added.
- During Module update, library prep kit that were no longer supported still persist. To update Library Prep Kit list, follow below steps.
  - Uninstall previous module (if any)
  - Uninstall current module
  - Uninstall all components of LRM including Postgres

- Re-install LRM
  - Re-install current module
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- If the Local Run Manager Analysis Service is restarted during analysis, this could cause a running analysis to crash. Analysis can be requeued if this happens.
  - 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 forward orientation. Local Run Manager will automatically reverse complement the i5 indexes when writing the sample sheet used for analysis in the NextSeq, iSeq and MiniSeq. Local Run Manager will not reverse complement i5 indexes in the MiSeq.

# PREVIOUS RELEASE NOTES

## 16S METAGENOMICS ANALYSIS MODULE v1.0

### 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.