

Local Run Manager

Generate FASTQ Analysis Module

v3.0.1

Release Notes

Introduction

These Release Notes detail notable items for the Local Run Manager Generate FASTQ Analysis Module v3.0.1 release.

Please note that the Generate FASTQ Analysis Module v3.0.1 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 Generate FASTQ Analysis Module Workflow Guide, available from the [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 aside 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.

Library Prep Kit	Illumina DNA PCR-Free 2x149	Illumina DNA PCR-Free 2x151
Index Kits	IDT-Illmn DNA-RNA UD Indexes SetA Tagmentation - ILMN PCR-Free	IDT-Illmn DNA-RNA UD Indexes SetA Tagmentation - ILMN PCR-Free
	IDT-Illmn DNA-RNA UD Indexes SetB Tagmentation - ILMN PCR-Free	IDT-Illmn DNA-RNA UD Indexes SetB Tagmentation - ILMN PCR-Free
	IDT-Illmn DNA-RNA UD Indexes SetC Tagmentation - ILMN PCR-Free	IDT-Illmn DNA-RNA UD Indexes SetC Tagmentation - ILMN PCR-Free
	IDT-Illmn DNA-RNA UD Indexes SetD Tagmentation - ILMN PCR-Free	IDT-Illmn DNA-RNA UD Indexes SetD Tagmentation - ILMN PCR-Free

old name	new name
Nextera Flex for Enrichment	illumina DNA Prep with Enrichment
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
	illumina DNA Prep with Enrichment
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	

- Added Customer primers use warning when applicable on the interface.
- Removed Show Index Name/Sequence option when the Library Prep Kit is set to Custom.
- Obsoleted SureCell Single Cell RNA 1.0 Library Prep Kit.
- Compatibility check with Local Run Manager Framework v3.0 only.
- Removed html and js folders under the Module directory UI folder.
- Windows 10 integration updates.

DEFECT REPAIRS:

- Fixed issue where Samples Output Sheet and Results page were at an incorrect order.

KNOWN ISSUES:

MiSEQ SUITE v4.0:

- 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 perfectly aligned with the Sample Number column as higher sample number are added.
- Statistics fields are missing in GenerateFastQStatistics.xml file (displaying 0). Recommended to use RunParameters.xml file instead if utilizing GenerateFastQStatistics.xml file.
- During Module update, library prep kit that were no longer supported still persist. To update Library Prep Kit list, follow below steps.
 1. Uninstall previous module (if any)
 2. Uninstall current module
 3. Uninstall all components of LRM including Postgres
 4. Re-install LRM
 5. Re-install current module

PREVIOUS RELEASE NOTES

GENERATE FASTQ MODULE v2.0.1

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
 - TruSeq DNA-RNA CD Indexes 96 Indexes
 - TruSeq DNA-RNA Single Indexes Set A&B
 - Nextera DNA
 - Nextera XT
 - Nextera XT V2
 - Nextera DNA CD Indexes - 24 Indexes Tubed
 - Nextera DNA CD Indexes - 96 Indexes Plated
 - TruSeq Methyl Capture EPIC
 - SureCell WTA 3'
 - SureCell Single Cell RNA 1.0
 - TruSight Tumor 15
 - TruSight Tumor 26
 - Nextera Mate Pair
 - TruSeq Small RNA
 - TruSeq Amplicon
 - AmpliSeq Library PLUS for Illumina (96)
 - TruSeq Targeted RNA Expression
 - Nextera Rapid Capture Enrichment
 - TruSight Enrichment Panels
 - TruSight RNA Fusion
 - TruSight Amplicon Panels
 - TruSeq DNA Methylation
 - TruSeq Ribo Profile
 - ScriptSeq Complete
 - ScriptSeq v2
- 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 from 384 to 1536.

- Digitally signed the module installer to allow installation on Illumina instruments with software restriction policies (SRP) enabled.

DEFECT REPAIRS:

- Fixed an issue where adapters sequences would not be trimmed if a user-created library prep kit was selected on the Run Setup page
- For platforms running RTA version 2.x, copy the IndexMetricsOut.bin file to the output run folder
- For non-MiSeq configurations using custom library prep kit, allow 'N's in the i5 index sequence to be correctly reverse complemented

KNOWN ISSUES:

- None