

Local Run Manager

PCR Amplicon Analysis Module v2

Release Notes

PCR AMPLICON ANALYSIS MODULE v2.1

Introduction

These Release Notes detail notable items for the Local Run Manager PCR Amplicon Analysis Module v2.1 release.

Please note that the PCR Amplicon Analysis Module v2.1 requires Local Run Manager Framework v3.0 or higher and is not compatible with Local Run Manager Framework v2.4 or lower.

For more information on module version compatibility per instrument platform, refer to Local Run Manager Module Selector (<https://customprotocolselector.illumina.com/selectors/LRM-module-selector/Content/Source/FrontPages/LRM-module-selector.htm>).

For more information about this analysis module and how to use it, refer to the Local Run Manager PCR Amplicon Analysis Module Workflow Guide, available from the Local Run Manager Support Page, Documentation & Literature (https://sapac.support.illumina.com/sequencing/sequencing_software/local-run-manager.html).

NEW FEATURES:

- Updated the following Library Prep Kit with new Index Kits & existing Index Kits and removed End-of-Life Index Kits:

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

	<p>Ilmn DNA-RNA UD Indexes SetA Tagmentation (New)</p> <p>Ilmn DNA-RNA UD Indexes SetB Tagmentation (New)</p> <p>Ilmn DNA-RNA UD Indexes SetC Tagmentation (New)</p> <p>Ilmn DNA-RNA UD Indexes SetD Tagmentation (New)</p> <p>Ilmn DNA-RNA UD Indexes SetABCD Tagmentation(New)</p> <p>Nextera XT Index Kit - 24 Indexes 96 Samples</p> <p>Nextera XT Index Kit v2 Set A</p> <p>Nextera XT Index Kit v2 Set B</p> <p>Nextera XT Index Kit v2 Set C</p> <p>Nextera XT Index Kit v2 Set D</p> <p>Nextera XT Index Kit v2 Set A B C D</p> <p>IDT-Ilmn DNA-RNA UD Indexes SetA Tagmentation (New)</p> <p>IDT-Ilmn DNA-RNA UD Indexes SetB Tagmentation (New)</p> <p>IDT-Ilmn DNA-RNA UD Indexes SetC Tagmentation</p> <p>IDT-Ilmn DNA-RNA UD Indexes SetD Tagmentation</p> <p>IDT-Ilmn DNA-RNA UD Indexes SetABCD Tagmentation (New)</p> <p>IDT-ILMN Nextera DNA UD Indexes Set A - 96 Indexes (Removed)</p> <p>IDT-ILMN Nextera DNA UD Indexes Set B - 96 Indexes (Removed)</p> <p>IDT-ILMN Nextera DNA UD Indexes Set C - 96 Indexes (Removed)</p> <p>IDT-ILMN Nextera DNA UD Indexes Set D - 96 Indexes (Removed)</p> <p>IDT-ILMN Nextera DNA UD Indexes Set A B C D - 384 Indexes (Removed)</p>
--	--

- Removed the following End-Of-Life Library Prep Kit and the associated Index Kits:

Library Prep Kit	Index Kits
Nextera Mate Pair	Nextera Mate Pair

- All settings will be written in lower case in the generated output sample sheet.

DEFECT REPAIRS:

- Fixed the discrepancy of the FASTQ data generation.
- Fixed the issue where Analysis ended with "Histogram cannot be empty" error. There will be some changes to the 'Depth of Coverage in Targeted Regions' graphs in the aggregated report and per sample reports as part of this fix.
- Fixed issue where Custom Primers don't update in the Local Run Manager run if they are updated in the Control Software.
- Fixed issue where Adapter trimming settings do not save on LRM UI.
- Fixed issue where tooltip icons are missing for each Module-Specific settings on LRM 4.2(with Chromium v114.0.5735.199).

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 issue include formatting, ensure headers are specified, ensure workflow field is exactly as Local Run Manager interface display, etc.
- During module update, library prep kit and index kit that were no longer supported still persist.
- Workflow does not support human hg38 genome due to a known issue related to the configuration of the hg38 build of the human genome.
- 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.

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.
- Following analysis software are integrated in the PCR Amplicon Analysis Module.
 - BuildFASTQ v2.5.44.6 is used for BCL to FASTQ conversion
 - BWA-MEM v0.7.7-isis and BWA BackTrack-Legacy v0.6.1 are used for alignment
 - GATK v1.6-23-gf0210b3 is used for variant calling
 - MARS is used for annotation

PCR AMPLICON ANALYSIS MODULE v2.0

Introduction

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

Please note that the PCR Amplicon Analysis Module v2.0 requires Local Run Manager Framework v3.0 or higher and is not compatible with Local Run Manager Framework v2.4 or lower.

For more information on module version compatibility per instrument platform, refer to Local Run Manager Module Selector (<https://customprotocolselector.illumina.com/selectors/LRM-module-selector/Content/Source/FrontPages/LRM-module-selector.htm>).

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

(https://sapac.support.illumina.com/sequencing/sequencing_software/local-run-manager.html).

NEW FEATURES:

- Illumina Library Prep Kits (LPK) and Index Adapter Kits (IAK) are decoupled.
 - Users are 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.
 - Renamed Library Prep Kit Nextera DNA Flex as Illumina DNA Prep and updated corresponding Index Kits.

Library Prep Kit	Index Kits
Illumina DNA Prep	Nextera DNA CD Indexes - 24 Indexes Tubed
	Nextera DNA CD Indexes - 96 Indexes Plated
	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 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

- Added two Index Kits to Nextera XT Library Prep Kit.
 - IDT-Ilmn DNA-RNA UD Indexes SetC Tagmentation
 - IDT-Ilmn DNA-RNA UD Indexes SetD Tagmentation
- Added Custom Primers use warning when applicable on the interface.
- Removed Show Index Name/Sequence option when the Library Prep Kit is set to Custom.
- Compatibility check with Local Run Manager Framework v3.0 only.
- Windows 10 integration updates.

DEFECT REPAIRS:

- When the user selects certain library prep kits, like Nextera DNA (renamed as illumina DNA Prep), the I7 and I5 index fields are now marked as required fields.
- Fixed issue where Samples Output Sheet and Results page were at an incorrect order.

KNOWN ISSUES:

- When importing sample sheet into the MiSeq Control Software (MCS), 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.
- During Module update, library prep kits that were no longer supported still persist.
- Workflow does not support human hg38 genome due to a known issue related to the configuration of the hg38 build of the human genome.
- Custom Primers don't update in the Local Run Manager run if they are updated in the Control Software.
- If the Local Run Manager Analysis Service is restarted, this could cause a running analysis to crash. Analysis can be requeued if this happens.

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.
- Following analysis software are integrated in the Assembly Analysis Module.
 - BuildFASTQ v2.5.0.0 is used for BCL to FASTQ conversion
 - BWA-MEM v0.7.7-isis and BWA BackTrack-Legacy v0.6.1 are used for alignment
 - GATK v1.6-23-gf0210b3 is used for variant calling
 - MARS is used for annotation

PREVIOUS RELEASE NOTES

PCR AMPLICON ANALYSIS MODULE v1.0

Introduction

These Release Notes detail notable items for the Local Run Manager PCR Amplicon Analysis Module v1.0 release.

Please note that the PCR Amplicon 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 PCR Amplicon 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

NEW FEATURES:

- Initial Release

DEFECT REPAIRS:

- N/A

KNOWN ISSUES:

- Workflow does not support human hg38 genome due to a known issue related to the configuration of the hg38 build of the human genome.
- When the user selects certain library prep kits, like Nextera DNA, the I7 and I5 index fields will not be marked as required fields.
- Custom Primers don't update in the Local Run Manager run if they are updated in the Control Software.
- 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.