Local Run Manager Resequencing Analysis Module Release Notes
Document Number: 1000000009021, Ver. 03
Release Date: 26-JAN-2021

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Local Run Manager

Resequencing Analysis Module v3.0

Release Notes

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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 <u>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</u>. 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 Resequencing 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-Ilmn DNA-RNA UD Indexes SetA Tagmentation - ILMN PCR-Free	IDT-Ilmn DNA-RNA UD Indexes SetA Tagmentation - ILMN PCR-Free
	IDT-Ilmn DNA-RNA UD Indexes SetB Tagmentation - ILMN PCR-Free	IDT-Ilmn DNA-RNA UD Indexes SetB Tagmentation - ILMN PCR-Free
	IDT-Ilmn DNA-RNA UD Indexes SetC Tagmentation - ILMN PCR-Free	IDT-Ilmn DNA-RNA UD Indexes SetC Tagmentation - ILMN PCR-Free
	IDT-Ilmn DNA-RNA UD Indexes SetD Tagmentation - ILMN PCR-Free	IDT-Ilmn 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

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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 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

- 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.
- Fixed Resequencing GATK error where Input string was formatted incorrectly.

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.
    - o 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 number are added.

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- Analysis terminated with error message of unable to merge temporary Tribble output file. Starling aligner is recommended until issue is fixed.

- 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

- Recommended to not utilize commas and parantheses for Library Prep Kit and Index Kit name as it causes Index Kit selection to be disabled.

- Version of GATK Variant Caller version in reported as N/A.

- 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 occurances 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.

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PREVIOUS RELEASE NOTES

RESEQUENCING MODULE v2.0

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:

    o IDT-ILMN TruSeq DNA-RNA UD Indexes 24 Indexes

    o IDT-ILMN TruSeq DNA-RNA UD Indexes 96 Indexes

    o Nextera DNA CD Indexes – 24 Indexes Tubed

    o Nextera DNA CD Indexes – 96 Indexes Plated

    o Nextera DNA (formerly Nextera)

    o TruSeq DNA-RNA CD Indexes 96 Indexes (formerly TruSeq HT)

    o 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:
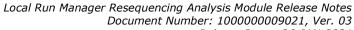
    ` ~ ! @ # $ % - _ { }

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 occurances 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.

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OTHER:

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