

# **Illumina Experiment Manager (IEM) Software v1.15**

## **Release Notes**

*For MiSeq, NextSeq, HiSeq, and NovaSeq Systems*

**08-JAN-2018**

## Introduction

These Release Notes detail the key changes to Illumina Experiment Manager (IEM) between the specific versions listed in the table below:

<b>Software Application</b>	<b>Prior Version</b>	<b>New Version</b>
<i>Illumina Experiment Manager</i>	1.14	1.15

If you are upgrading from a version before v1.13, review any previous release notes for features and bug fixes introduced in addition to the changes outlined below.

During installation, previous versions of IEM will automatically be uninstalled. However, if you are upgrading from version 1.13 or earlier, then IEM must be uninstalled manually. Click **Start Menu, Control Panel**, and then **Programs and Features** to uninstall any prior version of IEM before proceeding with installation.

### IMPROVEMENTS:

- Added support for the following library prep kits:

<b>Instrument</b>	<b>Application</b>	<b>Added Library Prep Workflow</b>	<b>Added Index Adapters</b>
MiSeq	FASTQ Only	AmpliSeq Library PLUS for Illumina (96)	AmpliSeq Library PLUS for Illumina (96)
NextSeq/MiniSeq	NextSeq FASTQ Only	AmpliSeq Library PLUS for Illumina (96)	AmpliSeq Library PLUS for Illumina (96)
HiSeq	HiSeq FASTQ Only	AmpliSeq Library PLUS for Illumina (96)	AmpliSeq Library PLUS for Illumina (96)
NovaSeq	NovaSeq FASTQ Only	AmpliSeq Library PLUS for Illumina (96)	AmpliSeq Library PLUS for Illumina (96)

### DEFECT REPAIRS:

- Fixed an issue where editing a NovaSeq Sample Sheet with the "NovaSeq Xp workflow" option enabled would assign all samples to Lane 1. Samples are now all assigned to the correct lane as specified in the original Sample Sheet.
- Fixed an issue where values for the "GenomeFolder" column would not be displayed when editing a Sample Sheet that contained that column. Values for "GenomeFolder" are now displayed when editing Sample Sheets.
- Fixed an issue where an "Index Out of Range" error would occur when importing a Sample Plate file that did not contain a sample in well A01. Sample Plate files that do not contain a sample in well A01 can now be imported without issues.

**KNOWN ISSUES:**

- The “Variant Quality Cutoff” setting does not get populated with the correct value when editing a Sample Sheet that contains the “VariantFilterQualityCutoff” setting.
- The “NovaSeq XP workflow” checkbox becomes unchecked whenever a “Library Prep Workflow” is selected
- The appearance of the software’s user interface may be distorted when the Windows operating system display settings are configured to use enlarged font sizes. To remedy this, change the Windows font size display settings to 100%.

**OTHER:**

- Removed support for the the following index adapters:

<b>Compatible Library Prep Workflow</b>	<b>Removed Index Adapters</b>
Nextera DNA Flex	<ul style="list-style-type: none"> <li>• Nextera DNA Single Indexes (24 indexes, plated)</li> </ul>
TruSeq RNA Exome Enrichment	<ul style="list-style-type: none"> <li>• IDT-ILMN TruSeq RNA UD Indexes (24 Indexes)</li> <li>• IDT-ILMN TruSeq RNA UD Indexes (96 Indexes)</li> <li>• TruSeq RNA CD Indexes (96 Indexes)</li> </ul>

- Changed the default number of Cycles Read 1 and Cycles Read 2 for “Nextera Mate Pair” to 151 (was previously 101).
- The default folder path for the “Genome Repository” is now set within the installation location of the IEM software. The “Genome Repository” folder path can still be changed by going into the “Settings” screen.