



How to use Roche Adapter/Primer sequencing indexes (barcodes) with Illumina® Experiment Manager (IEM)

v9.0

Technical Support

January 2022

What is Illumina[®] Experiment Manager (IEM)?

https://support.illumina.com/sequencing/sequencing_software/experiment_manager/downloads.html

- IEM is a desktop tool that enables the user to assemble a sample sheet in comma-separated values (CSV) file format that is used by the Illumina sequencer software to initiate a sequencing run.
 - The Illumina sequencer can also be initiated without a sample sheet.
- The information in the sample sheet include sample names and sequencing indexes (barcodes) associated with each sample.
- By default, Roche library prep kits (KAPA & AVENIO Edge reagents) and Roche sequencing indexes are not included in IEM. To conveniently access these kits in IEM, the default IEM file installation must be modified.

Installing Roche library prep kits

Tested with IEM version 1.19.1

1. Locate the installation path for IEM v1.19.1 on your computer. Generally, the default location is [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager](#). For custom installations the corresponding folders must be used. Administrator privileges may be needed to copy files into these folders.
2. Navigate to [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager\SamplePrepKits](#). This folder contains all of the pre-installed Illumina library prep kits (in separate text files for each kit).
3. Back up the directory [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager\SamplePrepKits](#) to a local folder.
4. Six custom KAPA SamplePrepKits files (KAPA HTP_LTP Library Prep Kit, KAPA HyperPrep, KAPA HyperPlus, KAPA EvoPlus, KAPA Stranded RNA-Seq Kit and KAPA RNA HyperPrep) and two custom AVENIO Edge SamplePrepKits files (AVENIO Edge DNA HyperPrep and AVENIO Edge DNA HyperPlus) are provided with these instructions in a folder entitled [SamplePrepKits](#). These text files contain a list of KAPA Adapter kits and AVENIO Edge Primer kits that are compatible with the KAPA library prep kits and AVENIO Edge DNA library prep kits, respectively, in the correct format.

Installing Roche library prep kits (cont.)

Tested with IEM version 1.19.1

5. Copy the appropriate custom SamplePrepKits files from the [SamplePrepKits](#) folder to [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager\SamplePrepKits](#). You may require Administrator rights as IEM has write protections in place on its files.
6. IEM can now read the contents of this file.

Name	Date modified	Type	Size
 KAPA EvoPlus	11/19/2021 3:12 PM	Text Document	1 KB
 KAPA HTP_LTP Library Prep Kit	9/6/2021 5:37 PM	Text Document	1 KB
 KAPA HyperPlus	9/6/2021 5:37 PM	Text Document	1 KB
 KAPA HyperPrep	9/6/2021 5:37 PM	Text Document	1 KB
 KAPA RNA HyperPrep	9/6/2021 5:37 PM	Text Document	1 KB
 KAPA Stranded RNA-Seq Kit	9/6/2021 5:38 PM	Text Document	1 KB

Name	Date modified	Type	Size
 AVENIO Edge DNA HyperPlus	1/5/2022 1:16 PM	Text Document	1 KB
 AVENIO Edge DNA HyperPrep	1/5/2022 1:16 PM	Text Document	1 KB

NEXT: copy appropriate custom IndexKits

Installing Roche index sequences

Tested with IEM version 1.19.1

1. Navigate to `C:\Program Files (x86)\Illumina\Illumina Experiment Manager\IndexKits`. This folder contains all of the pre-installed Illumina index sets (in separate text files for each index type).
2. Back up the directory `C:\Program Files (x86)\Illumina\Illumina Experiment Manager\IndexKits` to a local folder.
3. Custom IndexKits files (e.g. KAPA UDI Adapters.txt or AVENIO Edge UDI Primer Mixes_1 - 96.txt) are provided with these instructions in a folder entitled **IndexKits**. These text files contain the entire list of 8-nucleotide index sequences in the correct format.

Name	Date modified	Type	Size
KAPA DI Adapters	5/16/2017		
KAPA UDI Adapters	1/25/2019 2:00 PM	Text Document	8 KB
KAPA UDI Primer Mixes_1 - 96	8/12/2020 12:02 PM	Text Document	9 KB
KAPA UDI Primer Mixes_1 - 384	9/6/2021 10:25 AM	Text Document	1 KB
KAPA UDI Primer Mixes_97 - 192	9/6/2021 10:16 AM	Text Document	9 KB
KAPA UDI Primer Mixes_193 - 288	9/6/2021 10:16 AM	Text Document	9 KB
KAPA UDI Primer Mixes_289 - 384	9/6/2021 10:16 AM	Text Document	9 KB
AVENIO Edge UDI Primer Mixes_1 - 96	1/5/2022 1:16 PM	Text Document	9 KB

Installing Roche index sequences (cont.)

Tested with IEM version 1.19.1

4. Copy the appropriate custom IndexKits files from the **IndexKits** folder to [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager\IndexKits](C:\Program Files (x86)\Illumina\Illumina Experiment Manager\IndexKits). You may require Administrator rights as IEM has write protections in place on its files.
5. IEM can now read the contents of this file.

NEXT: edit or copy appropriate FASTQ application files

Installing/Modifying FASTQ & Other Applications

Tested with IEM version 1.19.1

1. Navigate to the [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager\Applications](#) folder.
2. Back up the directory [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager\Applications](#) to a local folder.
3. The custom KAPA & AVENIO Edge [SamplePrepKits](#) file must be registered with each appropriate FASTQ application (or other application) depending on the sequencer to be utilized.

Name	Date modified	Type	Size
ChIP-Seq	1/4/2022 2:44 PM	Text Document	1 KB
Enrichment	1/4/2022 2:44 PM	Text Document	2 KB
GenerateFASTQ	11/19/2021 3:13 PM	Text Document	2 KB
HiSeqGenerateFASTQ	11/19/2021 3:13 PM	Text Document	2 KB
LibraryQC	1/4/2022 2:44 PM	Text Document	2 KB
Metagenomics	1/4/2022 2:45 PM	Text Document	1 KB
NextSeqGenerateFASTQ	11/19/2021 3:13 PM	Text Document	2 KB
NovaSeqGenerateFASTQ	11/19/2021 3:13 PM	Text Document	2 KB
PCRAmplicon	1/4/2022 2:45 PM	Text Document	1 KB
Resequencing	11/19/2021 3:13 PM	Text Document	2 KB
RNA-Seq	1/4/2022 2:45 PM	Text Document	1 KB
Targeted RNA	1/4/2022 2:43 PM	Text Document	1 KB

Installing/Modifying FASTQ & Other Applications (cont.)

Tested with IEM version 1.19.1

4. Each sequencer will have a “GenerateFASTQ” text file in the **Applications** folder (e.g., the NextSeq instrument will have a “NextSeqGenerateFASTQ” text file).
 - a. *NextSeq instrument: NextSeqGenerateFASTQ*
 - b. *NovaSeq instrument: NovaSeqGenerateFASTQ*
 - c. *HiSeq instrument: HiSeqGenerateFASTQ*
 - d. *Other: GenerateFASTQ*
5. Copy the custom “GenerateFASTQ” text files from the **Applications** folder to **C:\Program Files (x86)\Illumina\Illumina Experiment Manager\Applications**. You may require Administrator rights as IEM has write protections in place on its files.
6. IEM can now read the contents of this file.
7. Restart IEM and create a new sample sheet. Once a Roche library prep kit is selected, all applicable Roche Adapters should now be available from the dropdown list.

Installing/Modifying FASTQ & Other Applications (cont.)

Tested with IEM version 1.19.1

- **Alternatively**, if your specific application does not have a custom text file available, open the relevant text file directly from the [C:\Program Files \(x86\)\Illumina\Illumina Experiment Manager\Applications](C:\Program Files (x86)\Illumina\Illumina Experiment Manager\Applications) folder using a text editor such as Notepad on Windows. You may require Administrator rights as IEM has write protections in place on its files.
- To add the KAPA/AVENIO Edge SamplePrepKits to a specific application, find the [\[Compatible Sample Prep Kits\]](#) line and write the name of the custom SamplePrepKits file (KAPA HTP_LTP Library Prep Kit, KAPA HyperPrep, KAPA HyperPlus, KAPA EvoPlus, KAPA Stranded RNA-Seq Kit, KAPA RNA HyperPrep, AVENIO Edge DNA HyperPrep or AVENIO Edge DNA HyperPlus) directly after this line. Do not remove the other Illumina Sample Prep Kits listed.
- Take care to avoid typographical errors.
- Restart the IEM and create a new sample sheet. Once a Roche library prep kit is selected, all applicable Roche Adapters should now be available from the dropdown list.

Version History

Version	Changes
v1.0	First version.
v2.0	KAPA UDI Adapters added.
v3.0	Instructions updated after IEM version update.
v4.0	Fix typographical errors. Convert to PDF. Made publicly available.
v5.0	Added UDI Primer Mixes. Included Local Run Manager folder.
V6.0 (January 2021)	Updated all 5 “GenerateFASTQ” text files in the Applications folder to be compatible with v1.19.1 of IEM.
V7.0 (September 2021)	Added KAPA UDI Primer Mixes 97 – 384
V8.0 (December 2021)	Added EvoPlus Kits
V9.0 (January 2022)	Added additional sequencing Applications & AVENIO Edge appropriate custom files. Renamed folder to Roche Sequencing Adapters_IEM_v9. Removed Local Run Manager folder.

KAPA and AVENIO Edge reagents are for Research Use Only. Not for use in diagnostic procedures.
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