

Setting up sparQ Library Prep Kit in Illumina Experiment Manager

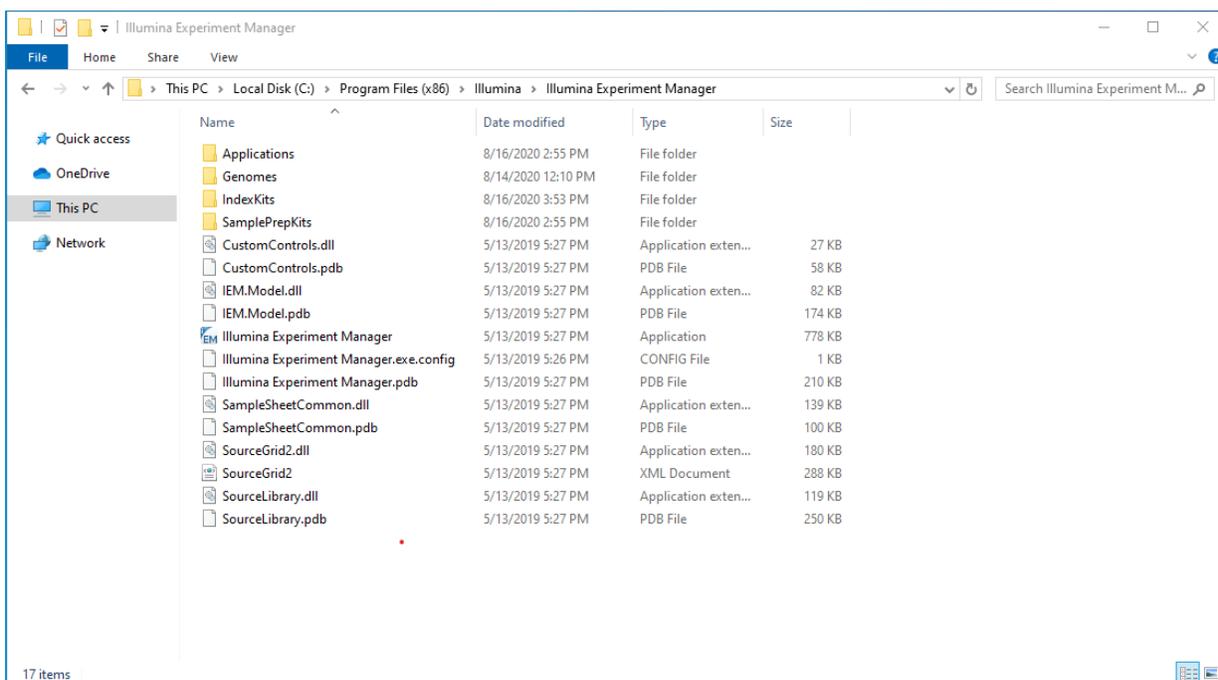
Illumina Experiment Manager (IEM) software is a useful tool for creating sample sheets for setup of Illumina® sequencing runs and data analysis.

IEM software can be downloaded for free on the Illumina homepage.

This protocol will guide you through how to add the sparQ UDI Adapters into the IEM for sample sheet setup.

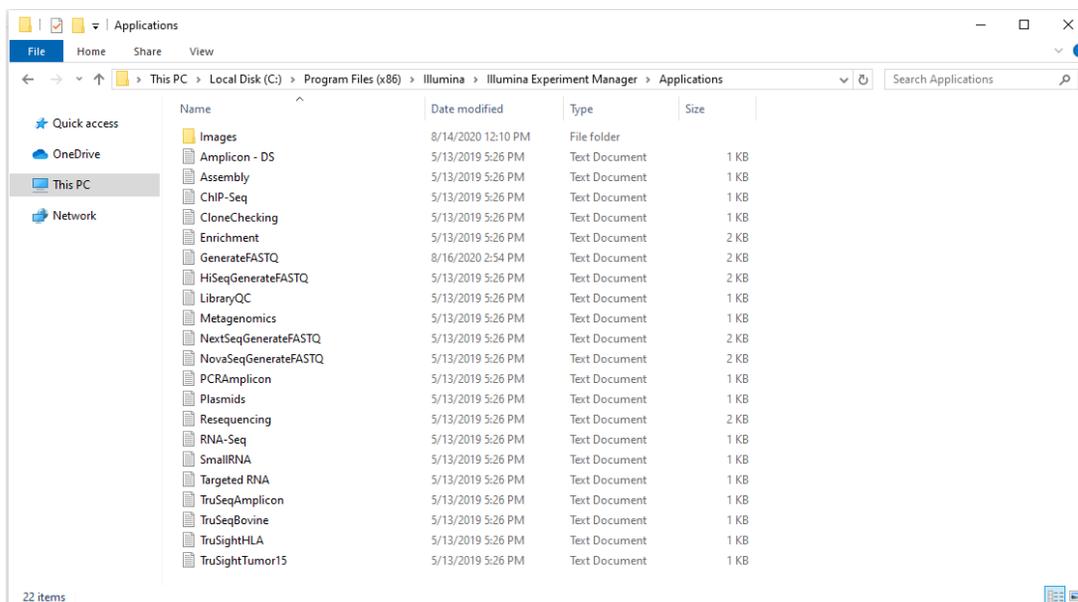
1. Determine which version of the IEM software you have downloaded.
The files' folder names will correspond to the IEM software version they are compatible with. You can locate the version of IEM software on top of the first screen.
2. Download the appropriate .txt files from the corresponding folder from the Quantabio website (<https://www.quantabio.com/products/sparq-fraglibrary-prep> or <https://www.quantabio.com/products/sparq-library-prep>).

Within program files find the Illumina folder, navigate to:
"Illumina\Illumina Experiment Manager\SamplePrepKits".



3. Select the file "sparQ Library Prep Kit" and paste it into this folder.
4. Within program files find the Illumina folder, navigate to:
"Illumina\Illumina Experiment Manager\IndexKits".
5. Select the file "sparQ Unique Dual Indices 96 Set A.txt" and paste it into this folder.

6. Add the kit to the applications you would like it to be present in.
7. In program files, navigate to:
 - “Illumina\Illumina Experiment Manager\Applications”.



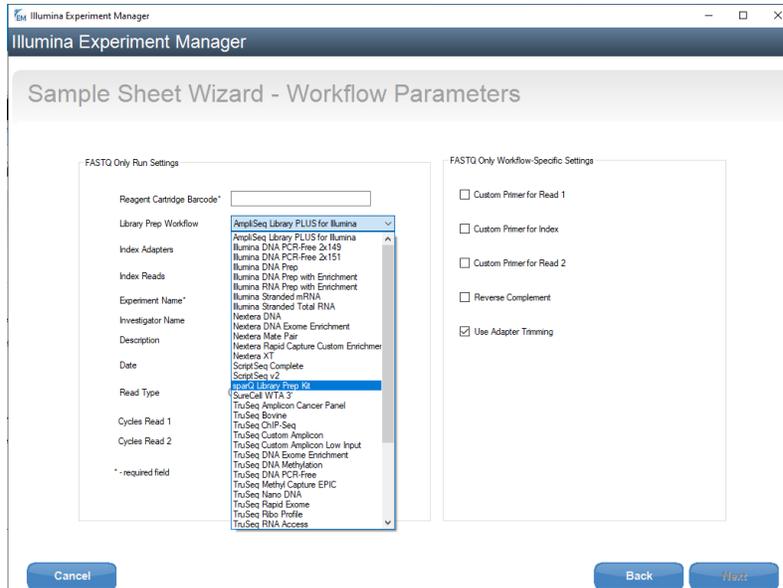
8. Select the correct application that you would like these indexes to populate in.
9. Open the file and locate the [Compatible Sample Prep Kits] section.
 - a. Add the following text to this section:
 - sparQ Library Prep Kit

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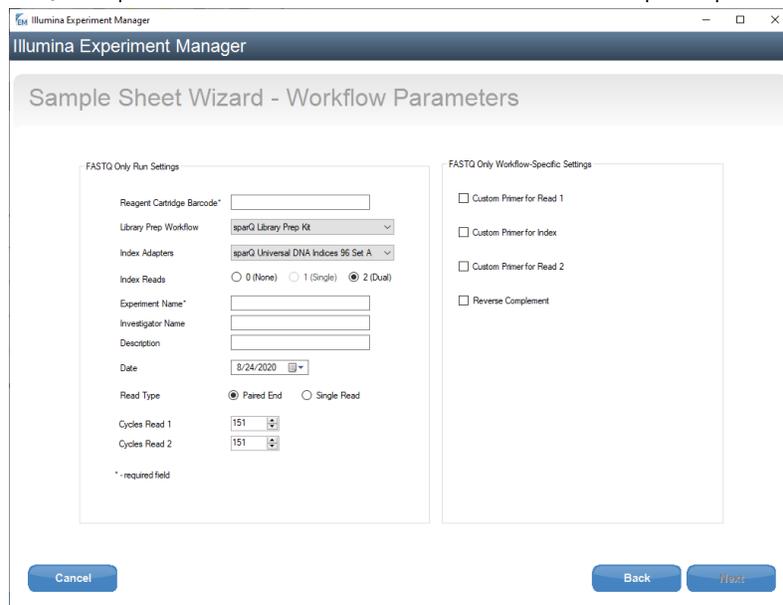
GenerateFASTQ - Notepad
File Edit Format View Help
[Version]
1
[Workflow Name]
GenerateFASTQ
[Display Name]
FASTQ Only
[Category]
Other

[Compatible Sample Prep Kits]
sparQ Library Prep Kit
TruSeq DNA PCR-Free
TruSeq Nano DNA
TruSeq Synthetic Long-Read DNA
TruSeq Bovine
Nextera DNA
Nextera DNA Flex
Nextera Mate Pair
Nextera Rapid Capture Custom Enrichment
TruSeq DNA Exome Enrichment
TruSeq Rapid Exome
TruSight Enrichment
Nextera XT
TruSeq Custom Amplicon
TruSeq Custom Amplicon Low Input
TruSeq Amplicon Cancer Panel
TruSight Tumor 26 genes
TruSight Tumor 15 genes
TruSight Myeloid
TruSeq ChIP-Seq
TruSeq DNA Methylation
TruSeq Methyl Capture EPIC
TruSeq RNA Access
TruSeq RNA v2
TruSeq Stranded mRNA
TruSeq Stranded Total RNA
TruSeq Targeted RNA Expression
TruSeq Small RNA
TruSeq Ribo Profile
ScriptSeq Complete
ScriptSeq v2
SureCell WTA 3'
TruSeq RNA Exome Enrichment
Nextera DNA Exome Enrichment
Ampliseq Library PLUS for Illumina
Nextera Flex for Enrichment
[Workflow-Specific Parameters]
Label Type LabelInSampleSheet TrueVal FalseVal DefaultVal Required DisplayAsCol
Reverse Complement BOOL ReverseComplement 1 0 FALSE FALSE FALSE
  
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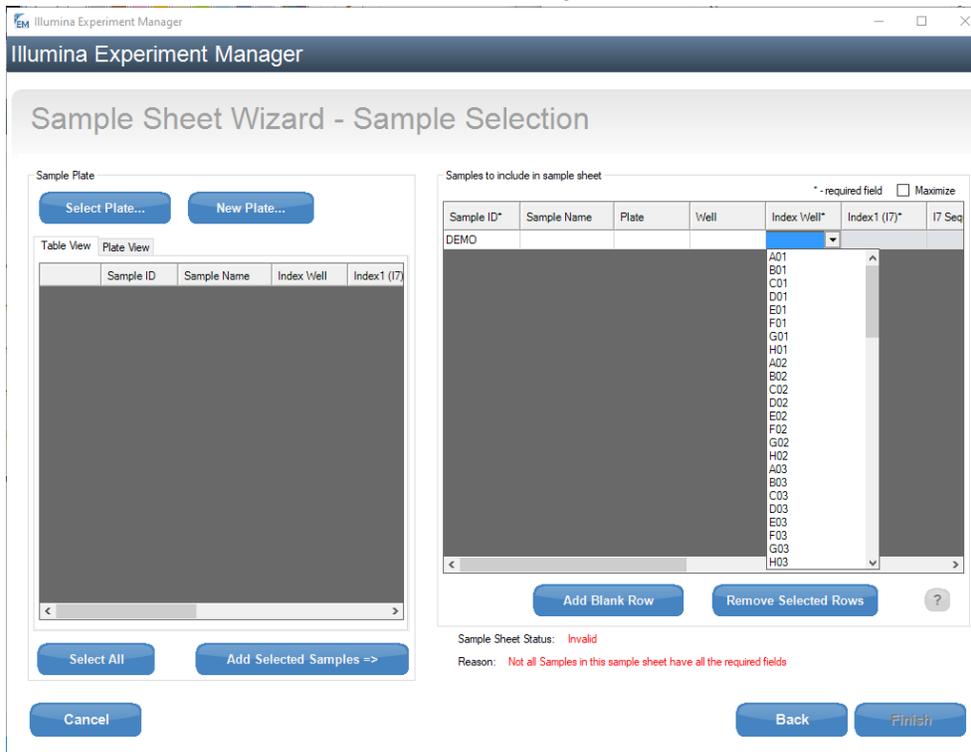
10. Save and close this file
 - a. User account must have admin privileges to save files in this format.
 - b. If user account does not have admin privileges save the .txt file in a separate location. Copy, paste and replace the file into the Illumina subfolders.
11. Close any open instance of IEM software.
Opening a new instance of IEM software is required for the changes to take place.
12. Navigate through the IEM software screens until reaching the Sample Sheet Wizard.
 - a. Find “sparQ Library prep kit” in the Library Prep Workflow pulldown menu.



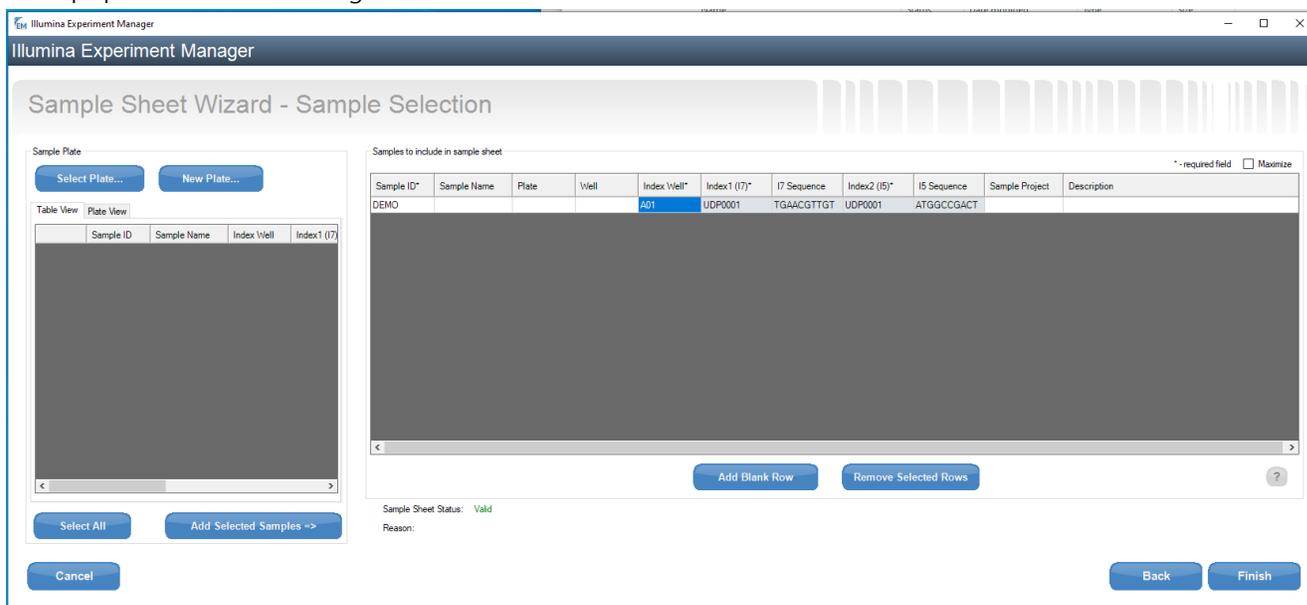
- b. Find “sparQ Unique Dual Indices 96 Set A” from Index Adapters pulldown menu.



13. After selection each barcode index will auto generate for the selected index adapter.



14. The sample sheet setup should be identical now to setting up any other library prep kit. Indexes will auto populate after selecting the well location of each index.



15. The sample sheet can now be populated per sample. Auto conversion to the correct barcode for analysis will be done by the IEM software for the Nextseq, HiSeqX, HiSeq3000 and HiSeq4000 platforms. Adapter trimming will also be accurate during fastQ generation.