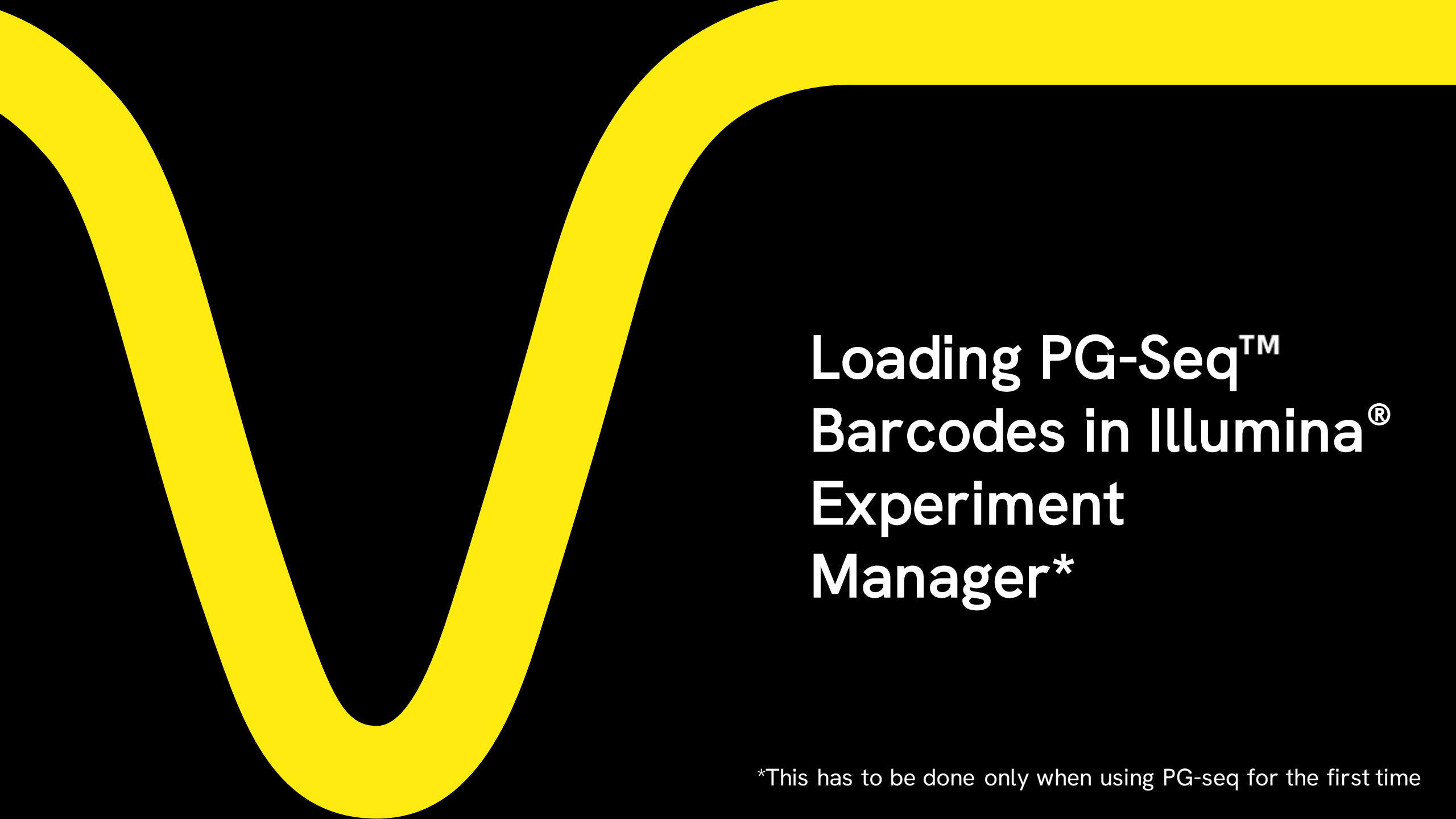


SampleSheet Generation for PG-Seq™ Rapid v2 kit

revvity

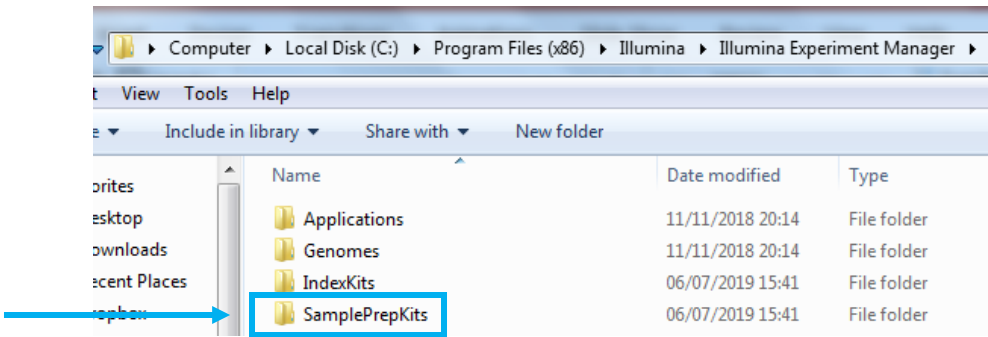
Revvity does not endorse or make recommendations with respect to research, medication, or treatments. All information presented is for informational purposes only and is not intended as medical advice. For country specific recommendations, please consult your local health care professionals.



Loading PG-Seq™ Barcodes in Illumina® Experiment Manager*

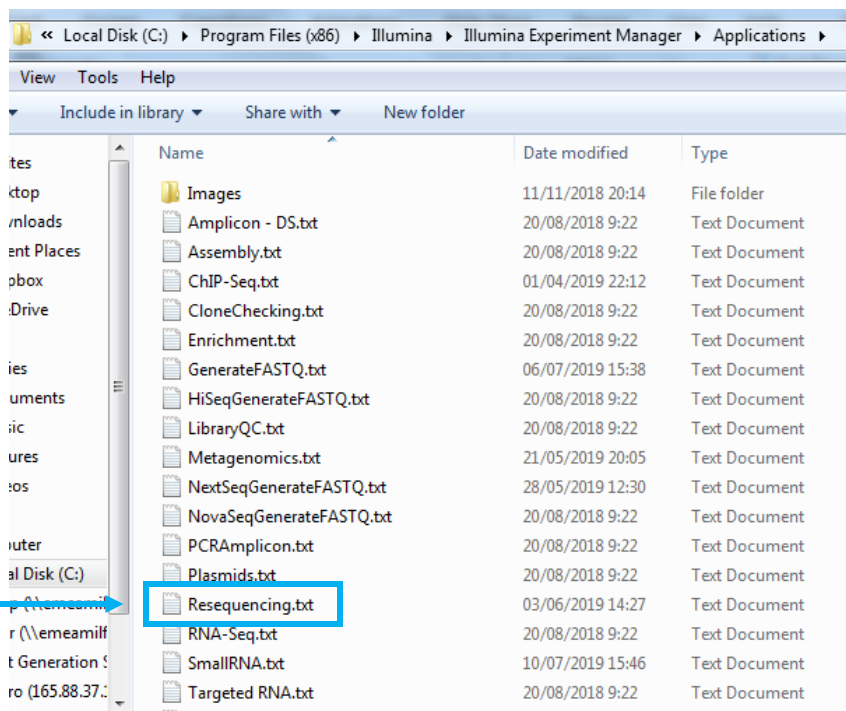
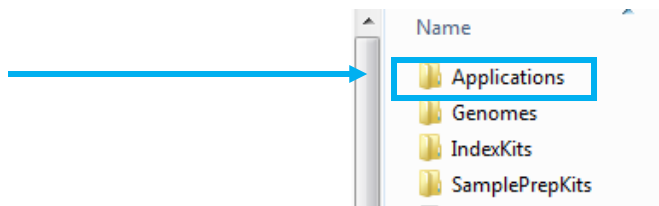
*This has to be done only when using PG-seq for the first time

1. Go to C:\Program Files (x86)\Illumina\Illumina Experiment Manager



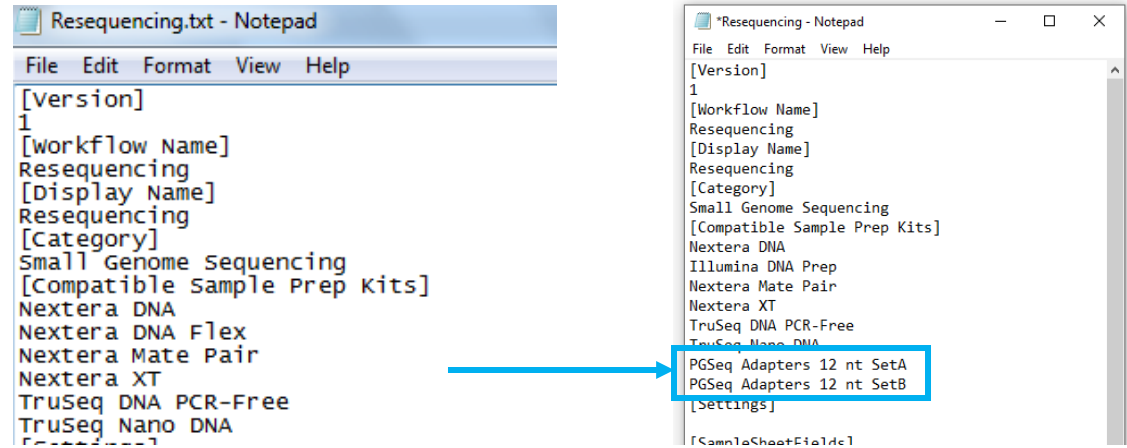
2. In the "SamplePrepKits" folder paste the PGSeq Adapters 12 nt SetA.txt and PGSeq Adapters 12 nt SetB.txt files

3. Go to "Applications" folder

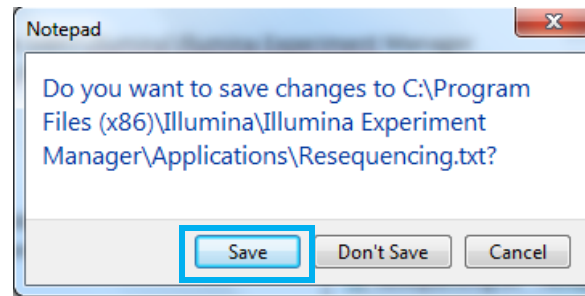



4. Within this folder open the Resequencing.txt file

5. In the list of kits that appears add the txt files relevant to you



6. Save changes

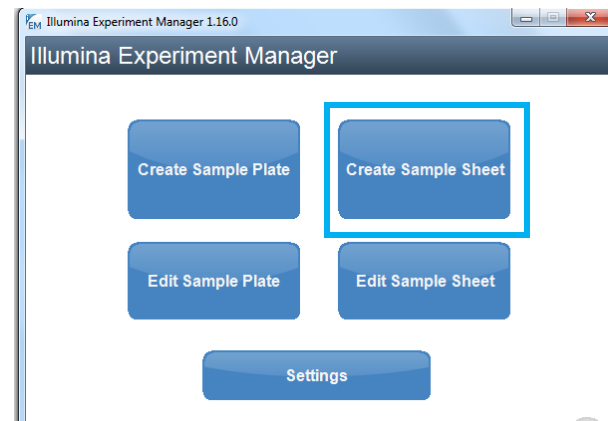


A thick, bright yellow wavy line starts from the left edge of the frame, curves down into a deep valley, and then curves back up towards the top right corner, ending in a horizontal bar that spans the width of the image.

Creating a
SampleSheet for PG-
Seq™ Barcodes

1. Open Illumina® Experiment Manager Software

2. Select *Create Sample Sheet*



3. In the new screen that appears, select *MiSeq*



4. Press *Next*



Sample Sheet Wizard - MiSeq Appli

Select Category

5. Select "Small Genome Sequencing"



Targeted
Resequencing



Small Genome
Sequencing



RNA
Sequencing



Other

6. Select "Resequencing"



Resequencing



Plasmids



Assembly

7. Select "Next"



Cancel

Back

Next

8. Make sure screen looks EXACTLY like this (putting corresponding Reagent cartridge barcode and experiment name). Select the right Set according to the barcodes used

Set A → Barcodes 1-96
Set B → Barcodes 97-192

Illumina Experiment Manager

Sample Sheet Wizard - Workflow Parameters

Resequencing Run Settings

Reagent Cartridge Barcode*

Library Prep Workflow

Index Adapters

Index Reads 0 (None) 1 (Single) 2 (Dual)

Experiment Name*

Investigator Name

Description

Date

Read Type Paired End Single Read

Cycles Read 1

* - required field

Resequencing Workflow-Specific Settings

Custom Primer for Read 1

Custom Primer for Index

Custom Primer for Read 2

Use Somatic Variant Caller

Flag PCR Duplicates

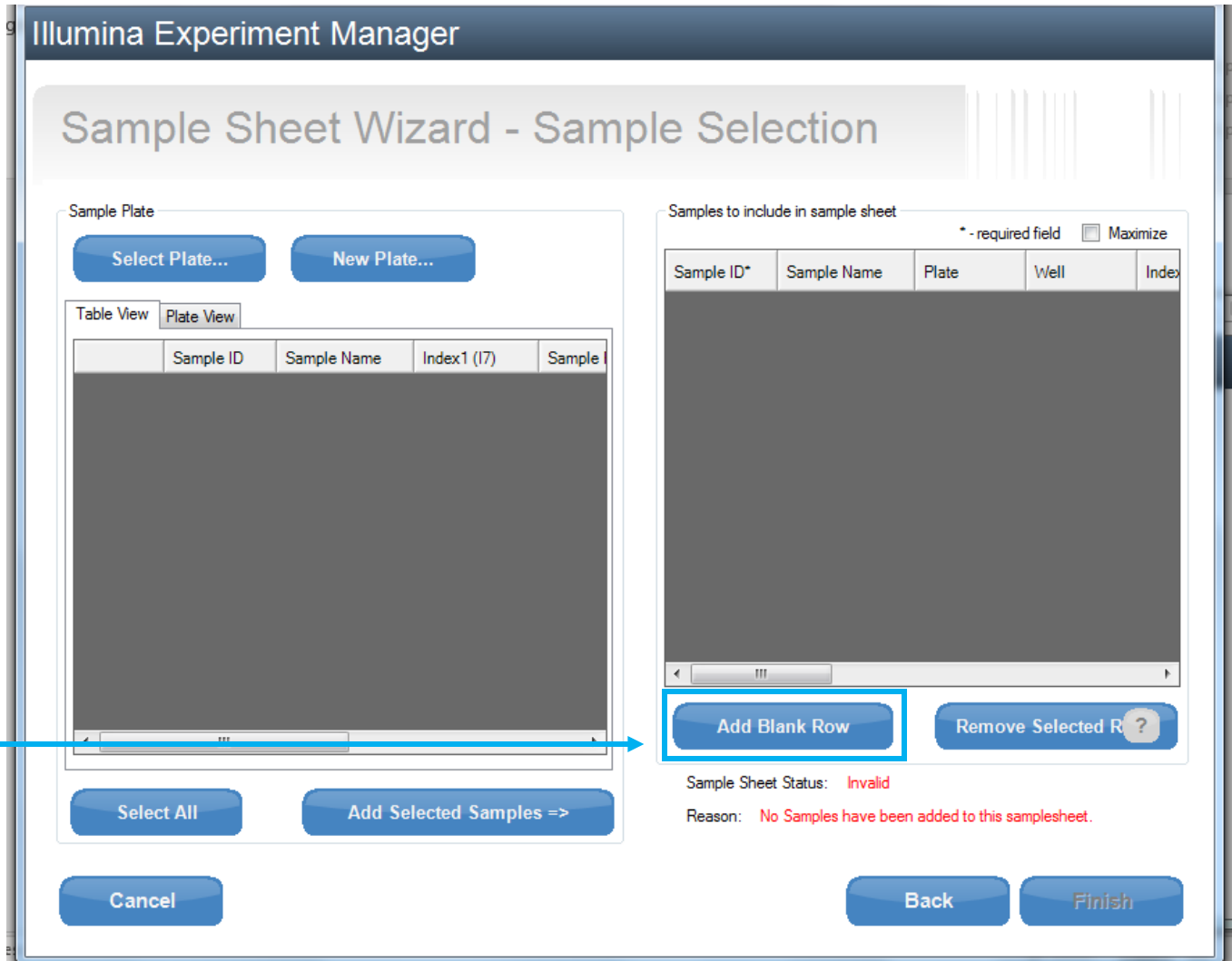
Reverse Complement

Indel Realignment GATK

Variant Quality Filter

Cancel Back Next

9. Press Next



10. In the screen that appears, add one row per sample you want to analyze, using the button "Add Blank Row"



Illumina Experiment Manager

Sample Sheet Wizard - Sample Selection

Sample Plate

Select Plate... New Plate...

Table View **Plate View**

| Sample ID | Sample Name | Index1 (I7) | Sample |
|-----------|-------------|-------------|--------|
| | | | |
| | | | |
| | | | |

Select All Add Selected Samples =>

Cancel

Samples to include in sample sheet

* - required field Maximize

| Sample ID* | Sample Name | Plate | Well | Index1 (I7)* | I7 Sequence |
|------------|-------------|-------|------|--------------|-------------|
| 01 | | | | A01 | |
| 02 | | | | B01 | |
| 03 | | | | C01 | |
| | | | | D01 | |
| | | | | E01 | |
| | | | | F01 | |
| | | | | G01 | |
| | | | | H01 | |
| | | | | A02 | |
| | | | | B02 | |
| | | | | C02 | |
| | | | | D02 | |
| | | | | E02 | |
| | | | | F02 | |
| | | | | G02 | |
| | | | | H02 | |
| | | | | A03 | |
| | | | | B03 | |
| | | | | C03 | |
| | | | | D03 | |
| | | | | E03 | |

Add Blank Row Remove

Sample Sheet Status: **Invalid**

Reason: **Not all Samples in this sample sheet have all the required fields**

Finish

11. Write Sample Name

12. Select the index used for each sample from the list

13. In the Genome Folder field, select *Homo_sapiens* genome for all samples

Samples to include in sample sheet

* - required field Maximize

| Sample Name | Plate | Well | Index1 (I7)* | I7 Sequence | Genome Folder* |
|-------------|-------|------|--------------|-------------|-------------------|
| | | | A01 | GGCCGGCTAG | Homo_sapiens\UCS0 |
| | | | B01 | AAGGAAGAGA | |
| | | | C01 | GGACGGCATC | |

Sample Sheet Wizard - Sample Selection

Sample Plate

Select Plate... New Plate...

Table View Plate View

| Sample ID | Sample Name | Index1 (I7) | Sample |
|-----------|-------------|-------------|--------|
|-----------|-------------|-------------|--------|

Select All Add Selected Samples =>

Samples to include in sample sheet * - required field Maximize

| Index1 (I7)* | I7 Sequence | Genome Folder* | Sample |
|--------------|-------------|---|--------|
| A01 | GGCCGGCTAG | Homo_sapiens/UCSC/hg19/Sequence/WholeGenome | |
| B01 | AAGGAAGAGA | Homo_sapiens/UCSC/hg19/Sequence/WholeGenome | |
| C01 | GGACGGCATC | Homo_sapiens/UCSC/hg19/Sequence/WholeGenome | |

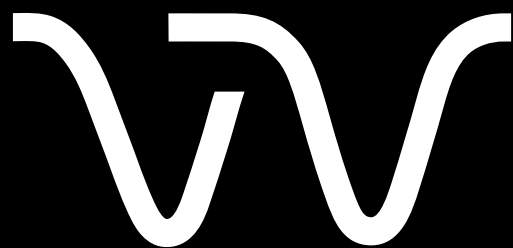
Add Blank Row Remove Selected Rows ?

Sample Sheet Status: Valid
Reason:

Cancel Back Finish

14. Press "Finish"

15. Save the sample sheet



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