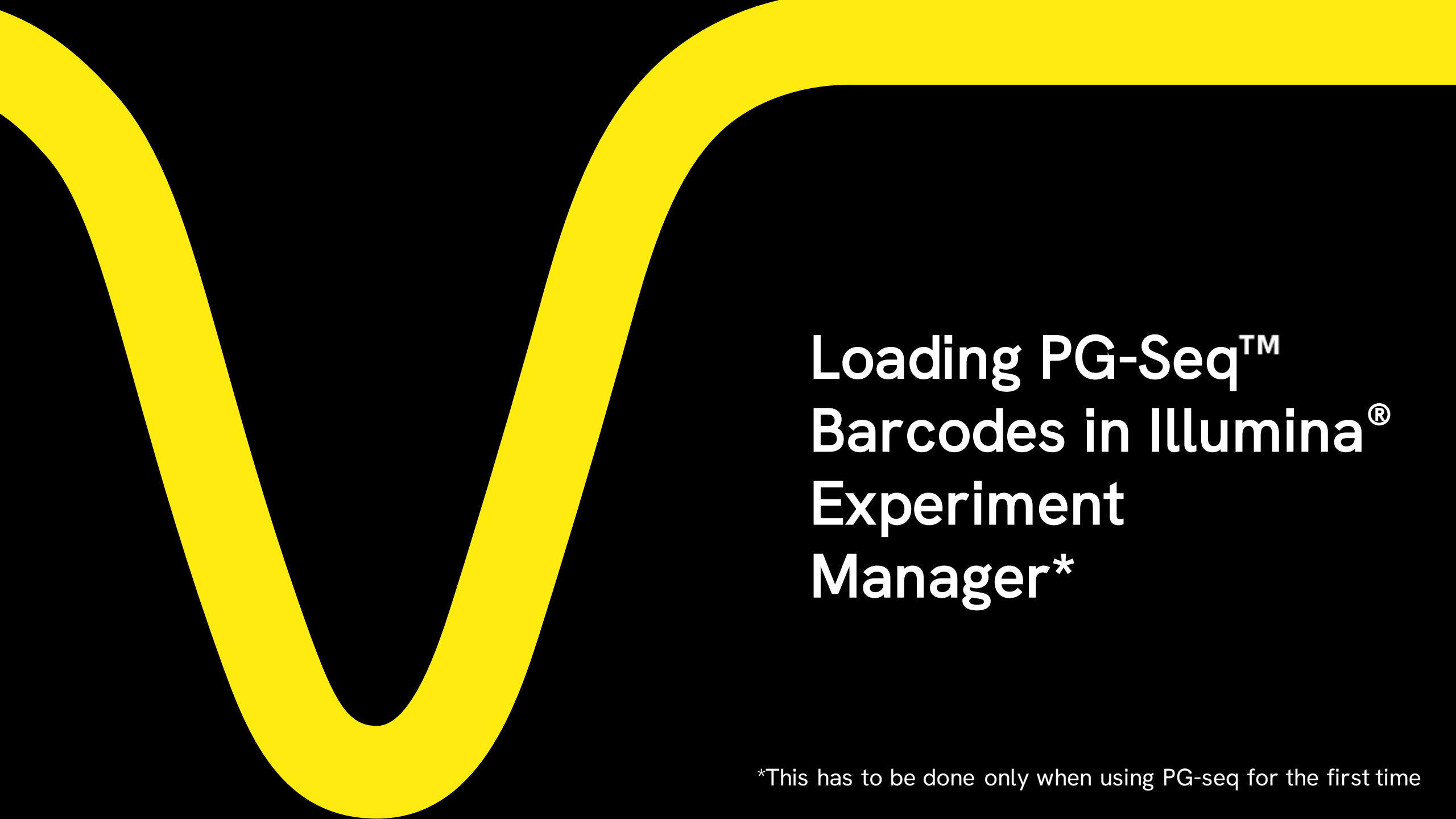


# SampleSheet Generation for PG-Seq™ Rapid v2 kit

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\*

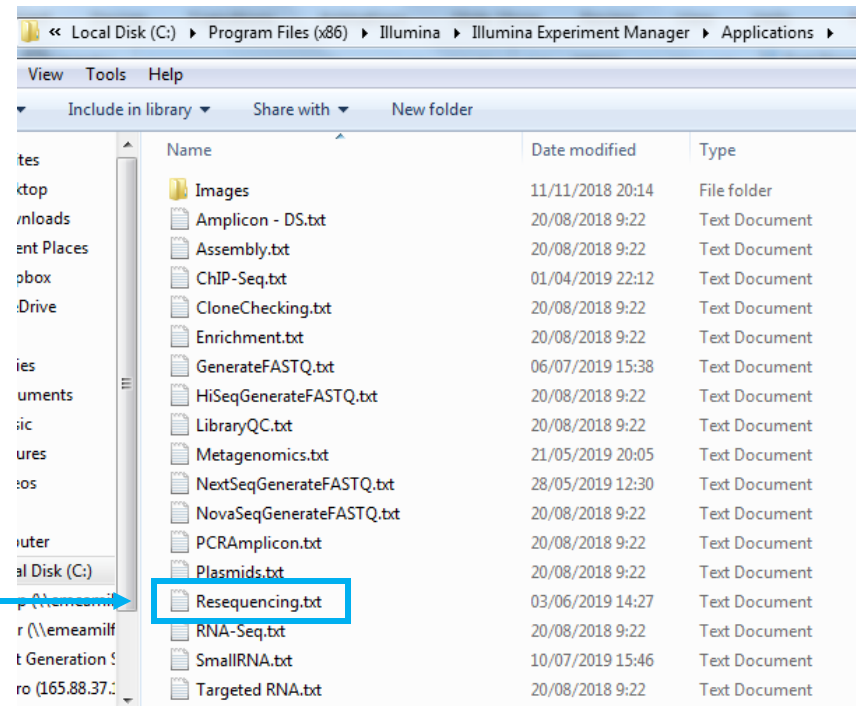
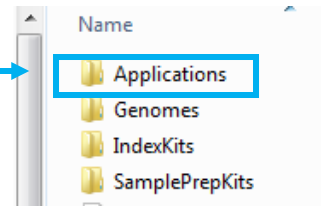
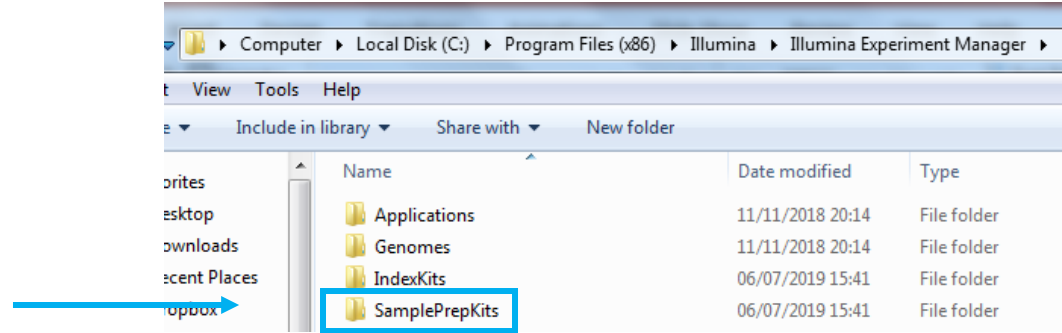
\*This has to be done only when using PG-seq for the first time

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

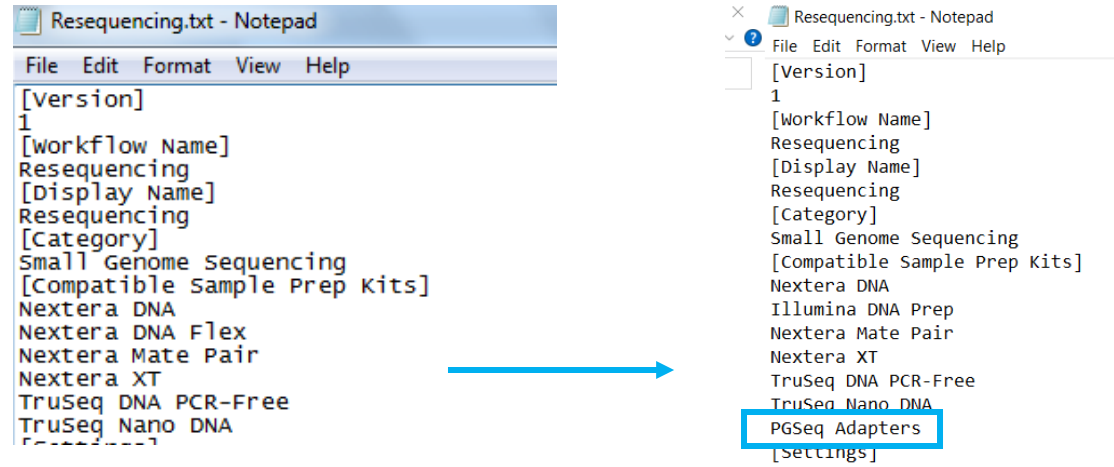
2. In the "SamplePrepKits" folder paste the PGSeq Adapters.txt file

3. Go to "Applications" folder

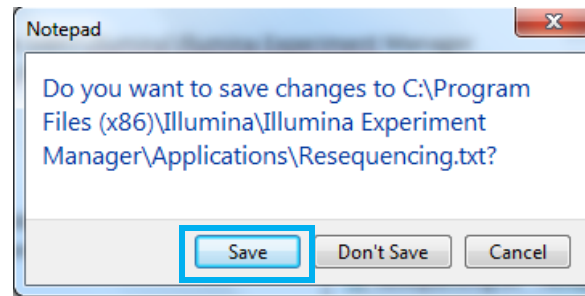
4. Within this folder open the Resequencing.txt file




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



6. Save changes

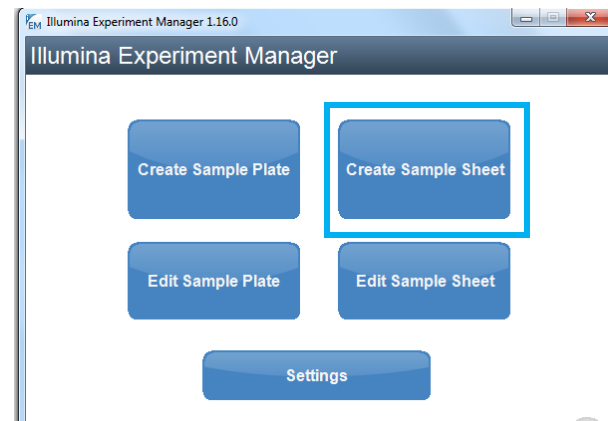


A thick, bright yellow wavy line starts from the left edge of the frame, curves down into a deep valley, and then curves back up towards the top right corner, ending in a horizontal bar that spans the width of the image.

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).

## 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

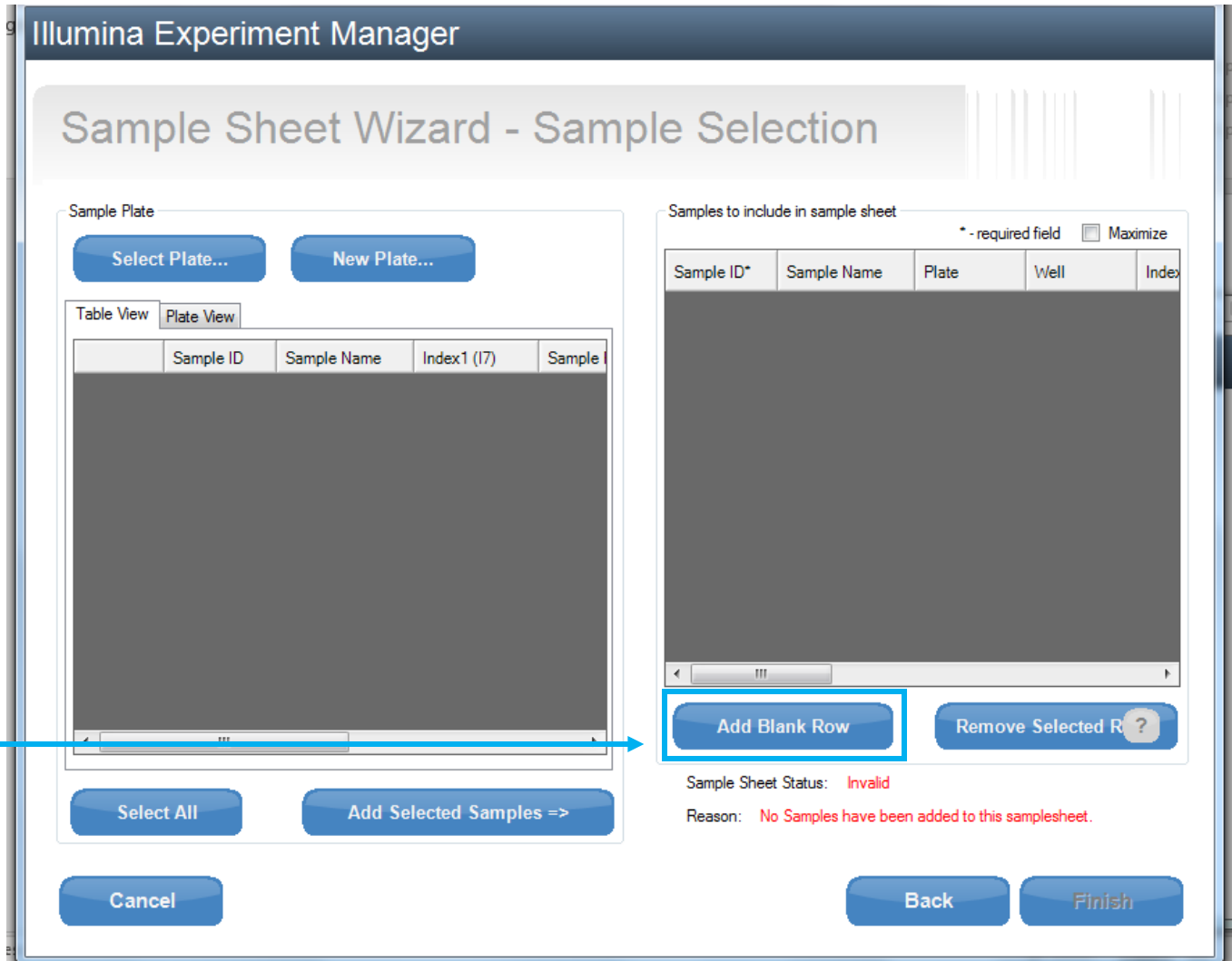
Reverse Complement

Indel Realignment GATK

Variant Quality Filter

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	

Add Blank Row Remove

Sample Sheet Status: **Invalid**  
Reason: Not all Samples in this sample sheet have all the required f

Finish

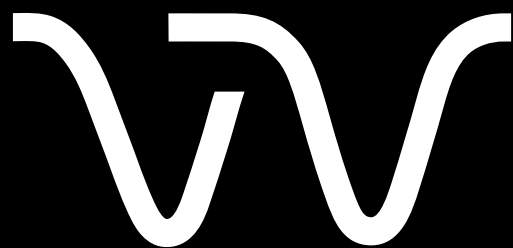
11. Write Sample Name

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

13. In the Genome Folder field, select *Homo\_sapiens* genome for all samples

Sample ID*	Sample Name	Plate	Well	Index1 (I7)*	I7 Sequence	Genome Folder*
01				A01	ATCTAGCCGG	Homo_sapiens\UCSC\hg19\Sequence\WholeGenomeFasta
02				B01	TATCTTCTCCT	Homo_sapiens\UCSC\hg19\Sequence\WholeGenomeFasta
03				C01	TAGATGCCGT	Homo_sapiens\UCSC\hg19\Sequence\WholeGenomeFasta
						Arabidopsis_thaliana\NCBI\build9.1\Sequence\WholeGenomeFasta
						Bos_taurus\Ensembl\UMD3.1\Sequence\WholeGenomeFasta
						Escherichia_coli_K_12_DH10B\NCBI\2008-03-17\Sequence\WholeGenomeFasta
						Homo_sapiens\UCSC\hg19\Sequence\WholeGenomeFasta
						Mus_musculus\UCSC\mm9\Sequence\WholeGenomeFasta
						PhiX\Illumina\RTA\Sequence\WholeGenomeFasta
						Rattus_norvegicus\UCSC\rn4\Sequence\WholeGenomeFasta
						Saccharomyces_cerevisiae\UCSC\sacCer2\Sequence\WholeGenomeFasta
						Staphylococcus_aureus_NCTC_8325\NCBI\2006-02-13





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