

# HR Next Generation Sequencing Service

## Contact Information

Principal Investigator:

Department:

User Name:

User Email:

## Project Information

Project Title:

Are these Xenograft

Sample Source:

Reference Genome:

Is this continuation of a previous project? Yes  No

## Sample Type:

- |                                      |  |  |                                    |
|--------------------------------------|--|--|------------------------------------|
| <input type="checkbox"/> ChIP DNA    | <input type="checkbox"/> Circulating DNA   | <input type="checkbox"/> Genomic DNA     | <input type="checkbox"/> Total RNA |
| <input type="checkbox"/> FFPE DNA    | <input type="checkbox"/> Plasmid DNA       | <input type="checkbox"/> Circulating RNA | <input type="checkbox"/> FFPE RNA  |
| <input type="checkbox"/> PCR Product | <input type="checkbox"/> Premade Libraries | <input type="checkbox"/> RIP RNA         | <input type="checkbox"/> Exosome   |

## Sequencing Application:

### DNA Seq Application

- Amplicon-seq  
 \*ChIP-seq  
 Whole Genome

### Capture Seq

- Clinical Exome-seq (Agilent)  
 Exome-seq (Agilent)  
 Exome-seq (Twist)  
 T200.1 Panel  
 Targeted-seq (User supplied probes)  
 TwinStrand Duplex Sequencing

### RNA Seq Application

- microRNA-Seq  
 Ultra Low Input mRNA-seq

### Strand Specific

- Stranded mRNA-seq Stranded  
 Total RNA-seq RNA  
 Twist Access  
 Ultra Low Input Total RNA seq

\*ChIP-Seq Only: May we shear your samples to an appropriate size range?  Yes  No

### Single Cell

- 10x Genomics  Tapestri  Single Cell  
 Other

Must specify application

## Sample submission note:

1. Samples should be submitted in 1.5ml Eppendorf tubes.
2. If you use your own label, please place the label on the 1.5ml tube vertically or horizontally around the bottom 2/3 of the tube. Please Keep the top 1/3 of the tube free for core lab use.

No. of tubes submitted (samples or library pools):

No. of Lane or Run

**Sequencing Instrument**

**Flow Cell and Default Run Format**

- SP**  SP-500 (250nt PE)  \*SP-500 Xp (250nt PE)  SP-300 (150nt PE)  SP-300 Xp (150nt PE)  
 SP-200 (100nt PE)  SP-200 Xp (100nt PE)  SP-100 (50nt PE)  SP-100 Xp (50nt PE)
- 
- S1**  S1-300 (150nt PE)  S1-300 Xp (150nt PE)  S1-200 (100nt PE)  
 S1-200 Xp (100nt PE)  S1-100 (50nt PE)  S1-100 Xp (50nt PE)
- 
- S2**  S2-300 (150nt PE)  S2-300 Xp (150nt PE)  S2-200 (100nt PE)  
 S2-200 Xp (100nt PE)  S2-100 (50nt PE)  S2-100 Xp (50nt PE)
- 
- S4**  S4-300 (150nt PE)  S4-300 Xp (150nt PE)  S4-200 (100nt PE)  S4-200 Xp (100nt PE)

**NovaSeq Xp flow cell Note:** the Xp workflow divides the flow cell into 2 (SP-Xp, S1-Xp, S2-Xp) or 4 (S4-Xp) lanes. If selecting Xp, please indicate the number of lanes requested. \*SP-500 XP(requires 2 lane submission)

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- NextSeq500**  MID 150 (75nt PE)  MID 300 (150nt PE)  
 High 75 (75nt SR)  High 150 (75nt PE)

- 
- iSeq**  300 (150nt PE)

- 
- MiSeq**  V3-150 (75nt PE)  V3-600 (300nt PE)  V2-300 (150nt PE)  V2-500 (250nt PE)  Nano

- 
- NovaSeq X**  1.5B-100(50nt PE)  1.5B-200(100nt PE)  1.5B-300(150nt PE)  
 10B-100(50nt PE)  10B-200(100nt PE)  10B-300(150nt PE)  
 25B-300(150nt PE)

**Note:** NovaSeq X requests are in lane format. The 1.5B flow cell has 2 lanes. The 10B and 25b flow cells have 8 lanes.

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**Run Format:** Read1  Read2  Index1  Index2

1. You prepared libraries, premade libraries, required to fill out Run Format.
2. If the run is different from the default Run Format, please specify it in the Run Format.

**Custom Sequencing Primer Use:** Are you using a custom primer for sequencing?  Yes  No

If yes was selected, please continue to answer the next two questions.

1. Do you want us to spike in PhIX and mix the custom primer with Illumina primers?  Yes  No

2. The custom primer Conc write here

**Custom Index Primer Use:** Are you using a custom index primer for sequencing?  Yes  No

The custom index primer Conc write here