

# sequencingcenter

John Wayne Cancer Institute  
Providence Saint John's Health Center

## Sample Submission Form

<b>Institution:</b>	
<b>Date:</b>	
<b>Name:</b>	
<b>Email:</b>	
<b>Phone:</b>	

Internal Use Only

<b>Approval:</b>		<b>Total Cost:</b>	
<b>Date Received:</b>		<b>P.O.#:</b>	

<b>Read Length:</b>		<b>Read Type:</b>	<input type="checkbox"/> Single read <input type="checkbox"/> Paired-end reads
<b>Library Type:</b>	<input type="checkbox"/> Whole Human Genome <input type="checkbox"/> Human Exome <input type="checkbox"/> RNA-seq (mRNA) <input type="checkbox"/> HTG EdgeSeq miRNA-seq <input type="checkbox"/> ChIP-seq <input type="checkbox"/> Methyl-seq <input type="checkbox"/> Other:		
<b>Index Type:</b>	<input type="checkbox"/> Single Index <input type="checkbox"/> Dual Index		
<b>Sequencing Platform:</b>	<input type="checkbox"/> Illumina HiSeq 2500 High-Output Mode <input type="checkbox"/> Illumina HiSeq 2500 Rapid Mode <input type="checkbox"/> Illumina MiSeq		
<b>Project Objective:</b>			
<b>Number of Samples Submitted:</b>		<b>Residual Samples:</b>	<input type="checkbox"/> Discard <input type="checkbox"/> Return (additional shipping charges may apply)

### **Submission Information:**

- An incomplete Submission Form, Services Agreement Form, or Sample Submission Sheet will result in a delay with your order.
- The submitter is responsible for the samples submitted to the Sequencing Center including all necessary consent, HIPAA compliance, and any applicable specimen regulations.
- Unless otherwise arranged, leftover samples will be discarded 3 weeks after the sequencing data is delivered. The sample can also be shipped back to you for an additional shipping fee.
- Unless otherwise arranged, your sequencing data will be stored for 3 months after the sequencing data is delivered. Thereafter your sequencing data will be deleted from our system and will not be recoverable.

### **Sample Requirements and Standard Sequencing Run Parameters:**

- Library preparation and sequencing data quality is highly dependent on the starting sample quality and quantity. It is the submitter's responsibility to ensure that the samples submitted are high quality, accurately quantified, and sufficient for library preparation.
- Samples must be suspended in EB (Tris-Cl 10 mM, pH 8.5) or 1X TE buffer; Volume  $\geq 15 \mu\text{l}$ ; Sample concentration  $\geq 10 \text{ ng}/\mu\text{l}$ ; Quantity appropriate for assay.
  - Exome Sequencing:  $\geq 300 \text{ ng}$  of genomic DNA from cell line, PBL, frozen tissue, FFPE, or saliva.
  - RNA-seq:  $\geq 200 \text{ ng}$  of RNA from FFPE or other degraded source;  $\geq 1.5 \mu\text{g}$  of RNA from cell line, PBL, frozen tissue, or other high quality source.
  - Please contact Sandy Hsu ([hsut@jwci.org](mailto:hsut@jwci.org)) for additional sample input requirements of other library types.
- **Sample concentration should be measured by Qubit, PicoGreen, or RiboGreen.** Nanodrop is not an accurate method for measuring sample concentration.
- DNA quality and integrity should be measured by Agilent Bioanalyzer, TapeStation, or on agarose gel with a high molecular weight ladder. High quality, intact, genomic DNA (from cell line, PBL, frozen tissue, or saliva) will appear as one distinct band with no smearing below 20 Kbp. DNA from FFPE should show a single distinct peak  $\geq 1\text{Kbp}$  on the Bioanalyzer or TapeStation. Please attach or email the traces and/or gel image for each sample to Sandy Hsu ([hsut@jwci.org](mailto:hsut@jwci.org)).
- RNA quality should be determined by RIN number or DV200 by Agilent Bioanalyzer or TapeStation.
  - RIN  $\geq 7.0$  for RNA from cell line, PBL, frozen tissue, or other high quality source.
  - DV200  $\geq 30\%$  for RNA from FFPE or other degraded sources.
- DNA and RNA samples should be free of protein contamination and other particulates such as melanin.
- Samples should be contained in a 0.5 mL or 1.5 mL tube with the lid secured with parafilm.  
**Please clearly label each sample tube with the following:**

- SampleID (for individual samples) on the cap and side of each tube; SampleID should match the SampleID provided in the Sample Submission Sheet.
- Date and institution or PI initials on the side of each tube.
- Unless otherwise arranged, the standard sequencing run parameters are the following:
  - 5-10% PhiX spike-in.
  - 6-10 pM loading concentration depending on library type and quality. Molarity will be estimated using a combination of TapeStation trace and Qubit.

**Sample Shipping Instructions:**

John Wayne Cancer Institute  
 2200 Santa Monica Blvd.  
 Rm 128 Sequencing Center  
 Santa Monica, CA 90404  
 Attn: Sequencing Center

- Please email shipment tracking information to Sandy Hsu (hsut@jwci.org).
- Samples should be shipped on enough dry ice to keep the samples frozen upon arrival at JWCI.

**I have read and understand the above submission information and requirements**

<b>Signature:</b>	
<b>Date:</b>	

[illegible]

\* SampleID format may not exceed 15 characters or contain the following illegal characters (spaces ? ( ) [ ] / \ = + < > : ; " ' , \* ^ | & .)