

Customer-prepared Library Sample Submission Form

Institution	
Date	
Requestor Name	
Email	
Phone	

Internal Use Only

P.O.#:	
Date Received:	

Read Length:		Read Type:	<input type="checkbox"/> Single read <input type="checkbox"/> Paired-end reads	
Library Type:	<input type="checkbox"/> Whole Human Genome <input type="checkbox"/> Human Exome <input type="checkbox"/> RNA-seq <input type="checkbox"/> Other:		Sequencing Loading Concentration (pM):	
Index Type:	<input type="checkbox"/> Single Index <input type="checkbox"/> Dual Index			
Sequencing Platform:	<input type="checkbox"/> Illumina HiSeq 2500 High-Output Mode <input type="checkbox"/> Illumina HiSeq 2500 Rapid Mode <input type="checkbox"/> Illumina MiSeq			
Total Number of Samples Submitted:				

Submission Information:

- An incomplete Submission Form, Services Agreement Form, or Sample Index 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 samples 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.

Library Requirements and Standard Sequencing Run Parameters:

- It is the submitter's responsibility to ensure that the custom libraries are high quality and prepared accurately. We cannot guarantee sequencing results from customer-prepared libraries.
- Libraries must be suspended in EB (Tris-Cl 10 mM, pH 8.5) or 1X TE buffer; Molarity ≥ 4.0 nM; Volume ≥ 20 μ l for individual samples and volume ≥ 35 μ l for pooled samples.
- Libraries 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 libraries) **or** PoolID (for pooled libraries) on the cap and side of each tube
- Date and institution or PI initials on the side of each tube
- Library size should be measured by Agilent Bioanalyzer or TapeStation. Please attach or email the traces for each sample or pool to Sandy Hsu (hsut@jwci.org)
- Library molarity should be calculated from library size (see above) and concentration measured by Qubit, PicoGreen, or the KAPA Library Quantification qPCR Kit. Nanodrop is not an accurate method for measuring library concentration.
- 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.
 - Demultiplexing with the provided Sample Index Sheet.

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).
- Libraries 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

Signature:	
Date:	

Customer-prepared Libraries

[illegible]

*If samples are being submitted in a prepared pool, enter the PoolID only and use the sample index sheet for assigning SampleID to each sample in the pool. The PoolID or SampleID may not exceed 15 characters or contain the following illegal characters (spaces ? () [] / \ = + < > : ; " ' , * ^ | & .)