sequencingcenter

John Wayne Cancer Institute
Providence Saint John's Health Center

Sample Submission Form

Date:		**Email:**	
Name:		**Phone:**	
Principle Investigator:			

Internal Use Only

Dr. Hoon Approval:		**Total Estimated Cost:**	

Read Length:	☐ 1 x 75bp ☐ 2 x 75bp ☐ 2 x 100bp ☐ 2 x 150bp	**Read Type:**	☐ Single read ☐ Paired-end reads
Library Type:	☐ Whole Human Genome ☐ RNA-seq (mRNA) ☐ ChIP-seq ☐ Human Exome ☐ Methyl-seq ☐ HTG EdgeSeq miRNA-seq ☐ ATAC-seq ☐ Other:		
Index Type:	☐ Single Index ☐ Dual Index		
Sequencing Platform:	☐ Illumina NextSeq 550 High-Output Mode ☐ Illumina NextSeq 550 Mid-Output Mode ☐ Illumina MiSeq		
Sample Type	☐ Cell line ☐ PBL ☐ Plasma ☐ Serum ☐ Other: ☐ FFPE ☐ Frozen Tissue ☐ cfDNA ☐ Urine		

Project Information	**Project Title:** **Objective** (include if the sequencing is for discovery, validation, manuscript, collaborative study with external group, etc. Please note, discovery will require deeper sequencing and will incur a higher cost): **Total anticipated sample size for sequencing:** **Expected outcomes and next steps after sequencing:** **Timeline** (abstract, publication, or grant submission deadline):		
Bioinformatics	**Type of analysis required** (expression profiling, mutation screening, gene fusions, etc.):		
Number of Samples Submitted:		**Residual Samples:**	☐ Discard ☐ 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 **≥ 15 µl**; Sample concentration ≥ 100 ng/ µl; Quantity appropriate for assay.
    - Exome Sequencing: ≥ 300 ng of genomic DNA from cell line, PBL, frozen tissue, FFPE, or saliva.
    - RNA-seq: ≥ 200 ng of RNA from FFPE or other degraded source; ≥ 1.5 µg of RNA from cell line, PBL, frozen tissue, or other high quality source.
    - Please contact Kevin Tran (kevin.tran@providence.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 ≥ 1Kbp on the Bioanalyzer or TapeStation. Please attach or email the traces and/or gel image for each sample to Kevin Tran (kevin.tran@providence.org)
- RNA quality should be determined by RIN number or DV200 by Agilent Bioanalyzer or TapeStation.
    - RIN ≥ 7.0 for RNA from cell line, PBL, frozen tissue, or other high quality source.
    - DV200 ≥ 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.
    - 1.6-3.0 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 Kevin Tran (kevin.tran@providence.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

Signature:	
Date:	

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Comments and issues:

Checklist:

☐ Supplied a minimum of 100ng/ul in 15ul.

☐ Completed and submitted the Sample Submission Spreadsheet (xlsx).

☐ Each sample has a unique ID.