

UH Seq-N-Edit Core (SNEC)

Sample Submission Guidelines

Sample Submission

To ship samples to SNEC:

UH Seq-N-Edit Core

4008 SERC

University of Houston

3517 Cullen Blvd

Houston, Texas 77204

Contact: Sujash Chatterjee or Yinhong Pan,

Email: UHsequencing@gmail.com

Phone: (713) 743-9291

To bring samples in person please come to 4008 SERC from 10:00am to 5:00pm, Monday through Friday. If you need to drop off samples outside of this time, please email UHsequencing@gmail.com or call 713-743-9291 to confirm someone will be there. Please number your samples for easy reference. If you have done any QC on your samples e-mail or print a copy of the results, even if we will also be doing QC.

Sample Pick Up

SNEC is not able to store samples or libraries for more than three months. Please arrange to pick up any leftover samples and libraries within that time frame, or they will be discarded.

Sample Volume & Concentration

For library prep, sequencing and related services the manufacturer's requirements are listed below.

For QC only (no library prep/sequencing) provide the following volume minimum:
Please submit the QC request form (digital copy).

Bioanalyzer:	2uL
Nanodrop:	2uL
Qubit:	2uL (2-3uL for very low ChIP samples)
qPCR:	3uL

For library preparation

Please submit the sequencing request form.

Unless otherwise specified, samples are pooled equimolar.

All RNA must be DNA-free

Exome-seq library prep

TruSeq Exome Library Prep Kit	500 ng – 1ug, > 20ng/uL, target size 45Mb
SureSelect Human All Exon V6	500 ng - 3ug, target size 60Mb

RNAseq library prep

TruSeq Stranded Total RNA Library	500 ng– 2ug, >50ng/uL, RIN > 8
SureSelect Strand Specific RNA-Seq kit	500 ng– 2ug, >50ng/uL, RIN > 8

microRNAseq library prep

NEBNext Multiplex Small RNA Library Prep Set	500 ng - 2ug, >50ng/uL, RIN > 7
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Other Library prep Please contact us with projects for more details.

Whole Genome Sequencing (WGS)

ChIPseq

**ATACseq
16s Library Preparation
For Sequencing on NextSeq 500**

Sample Requirements:

Prepared Libraries:	Minimum 10ul @ 4nM or 20uL @ 2nM
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Required information: submission form (digital copy)

Sequencing Parameters:	Single Read or Paired End + length (ie 75SR, 75PE, etc.) + number of flow cells
Sample Sheet:	Sample names and barcode information (digital copy)

2% PhiX spike-in to eukaryotic libraries and 10% PhiX spike-in to prokaryotic libraries for necessary diversity (please specify if requirements differ).

We highly recommend library QC by SNEC prior to sequencing, which includes BioAnalyzer and Qubit (depending on library type and whether pooling is done by you or us – See QC volume requirements)

Flow Cell Choices

Mid output (130M reads)	150 cycle kit
	300 cycle kit
High output (400M reads)	75 cycle kit
	150 cycle kit
	300 cycle kit

Other Services

ddPCR: Sample requirements depend on the scope and protocol; please contact us to discuss your project.