University of North Carolina at Chapel Hill

High Throughput Sequencing Facility - 1

Form associated with:
Service Project HTSF--CJ-[CID] at High Throughput Sequencing Facility - 1
Owner: Corbin Jones (Jones, Corbin (UNC) Lab)

HTSF Nanopore Submission Form DNA

* **I will be submitting DNA for:**

- ○ Ligation Sequencing (SQK-LSK114)
- ○ Ligation Sequencing with Barcoding (SQK-NBD114.96)
- ○ Rapid Sequencing (SQK-RAD114)
- ○ Rapid Sequencing with Barcoding (SQK-RBK114.24)

* **Type of Sample**

- ☐ High Molecular Weight DNA / gDNA
- ☐ Fragmented DNA
- ☐ PCR Amplicons
- ☐ cDNA

* **Do these samples contain human DNA? (required)**

- ○ Yes
- ○ No

Sample Buffer:

- ☐ EB
- ☐ Nuclease-Free Water

* **Sample Information:**

Sample Name	Volume (µL)	Qubit Conc. (ng/µL)	Nanodrop Conc. (ng/µL)	A_{260}/A_{280} ratio	A_{260}/A_{230} ratio

* **Flow Cell Selection:**

- ☐ MinION Flow Cell
- ☐ PromethION Flow Cell

Approx. Transcriptome Size

Approx. Coverage Needed

Estimated number of Flow Cells

Additional Comments / Special Needs

Bioinformatics and Data Delivery

I would like my data to be basecalled using:
- ☐ HAC (High Accuracy - Usually sufficient for most applications)
- ☐ SUP (Super-High Accuracy - Computing intensive and may add 1-2 weeks to data delivery)
- ☐ Methylation

File Format:
- ☐ FASTQ / BAM
- ☐ POD5 (only necessary if you wish to do basecalling on your own)

Data Delivery Notification email addresses:

How would you like to retrieve your data from HTSF?
- ☐ Deliver my data to ITS Research Computing storage (/proj)
- ☐ Provide me with a URL to download my data via the web
- ☐ Pre-arranged data delivery method for this project
- ☐ Other

Note: For Bioinformatics Analysis and Consulting (Assembly, Custom Solutions, etc.) – Please contact the Bioinformatics and Analytics Research Collaborative (BARC) – may be subject to extra costs.