Project ID:

For ATGC Facility use only:

Submission Date and time:

Advanced Technology Genomics Core

Nanopore Sequencing Service Request Form

Instructions: Fill out 2 pages of the Nanopore Sequencing service request form. Please fill out one form per sequencing application. Please email the form along with a gel picture, sample purity, and concentration to NanoporeSubmissions@mdanderson.org.

Contact Information:

Principal Investigator Name: | Department:

User Name: | User Email:

Sample source: | Reference gemome:

Is this continuation of a previous project? | Previous Core Project ID:

Project Title:

Sample Type:

- Genomic DNA
- Amplicon DNA
- Plasmid DNA
- ds-cDNA
- Single Cell ds-cDNA sequencing

Sequencing Application:

- *N50 of 5 to 10 kb long read whole genome sequencing
- *N50 of 10 to 30 kb long read whole genome sequencing
- *N50 of > 30 kb long read whole genome sequencing
- *N50 > 50 kb Ultra Long read whole genome sequencing
- Targeted sequencing (Adaptive sampling)
- Full-Length Transcripts sequencing (ds-cDNA sequencing)
- Single Cell ds-cDNA sequencing

* See page 3

The selection of a sequencing application determines the kit used for library preparation. It is not a guarantee of output sequence length.

Sample Information

Samples should be submitted in 1.5ml Eppendorf tubes. The name of the sample submitted on the tube should match the name of the sample you have entered on this form.

No. of samples submitted: | **No. of Flow cell:**

Sample 1.	Qubit Conc ng/ul	OD260/280	260/230
Sample 2.	Qubit Conc ng/ul	OD260/280	260/230
Sample 3.	Qubit Conc ng/ul	OD260/280	260/230
Sample 4.	Qubit Conc ng/ul	OD260/280	260/230

Sample 5.	Qubit Conc ng/ul	OD260/280	260/230
Sample 6.	Qubit Conc ng/ul	OD260/280	260/230

If No. of samples submitted is>6: please email us an Excel sheet.

Data Analysis

Bioinformatician Email: Bioinformatician Name:

ATGC will provide sequencing data in "fastq files" format.

Billing Information

Billing Contact Name: Billing Contact Email:

Note:
To split service charges between two accounts, please provide 'Account 2' information. If service charges are to be split between 3 or more accounts, please provide additional account information in the 'Additional Account Information' section below.

Account 1:		Account 2:	
Dept ID (6 digits):		Dept ID (6 digits):	
Fund Group (2 digits):		Fund Group (2 digits):	
Fund (6 digits)		Fund (6 digits)	
Fund Type (2 digits)		Fund Type (2 digits)	
PCBU (5 letters)		PCBU (5 letters)	
Project (6 digits)		Project (6 digits)	
Activity (4 digits)		Activity (4 digits)	
Expiration Date:		Expiration Date:	
Amount/Percentage to be Billed:		Amount/Percentage to be Billed:	

Additional Account Information:

Dept Administrator or Authorized Financial designee. Print the Name and Sign.

Project Description/Custom Requests

THE UNIVERSITY OF TEXAS
MD Anderson Cancer Center
Making Cancer History®

Submission Requirements:

- Purity as measured using Nanodrop - OD 260/280 of 1.8-2 and OD 260/230 of 2.0-2.2.
- Sample submission requirements are shown in the table below. We require the use of a fluorescence method to measure sample concentration.

Application	Sample Type	Quantity	Volume	Buffer	MW
*N50 of 5 to 10 kb long read whole genome sequencing	Genomic DNA	6ug	100ul	10mM Tris pH 8.0	>50kb
*N50 of 10 to 30 kb long read whole genome sequencing	Genomic DNA	30ug	100ul	10mM Tris pH 8.0	>50kb
*N50 of > 30 kb long read whole genome sequencing	Genomic DNA	60ug	100ul	10mM Tris pH 8.0	>100kb
*N50 > 50 kb Ultra Long read whole genome sequencing	Genomic DNA	60ug	100ul	10mM Tris pH 8.0	>100kb
Targeted sequencing (Adaptive sampling)	Genomic DNA	6ug	100ul	10mM Tris pH 8.0	>50kb
Full-Length Transcripts Sequencing	ds-cDNA	500ng	100ul	10mM Tris pH 8.0	Average Fragment size: ~2 kb
Single Cell ds-cDNA sequencing	Single Cell ds-cDNA sequencing	12ng	15ul	10mM Tris pH 8.0	Average Fragment size: ~2 kb

- HMW DNA Average fragment size, as measured by pulse-field, or low percentage agarose gel analysis.
- The DNA needs to be dissolved in 10mM TRIS (PH 8.0) or Qiagen EB Buffer.
- No detergents or surfactants in the buffer.
- While we will target your selected read length, the actual N50 will vary based on sample qualities.
- In a full flow-cell run, the output is only an estimate and cannot be guaranteed.

Please Note: It is important that input DNA has been checked for quality before submitting to ATGC. Low molecular weight, incorrectly quantified, and/or contaminated DNA (e.g. salt, EDTA, protein, organic solvents, RNA) can have a significant impact on downstream processes and ultimately, your sequencing runs.

*The N50 is related to the median and mean length of a set of sequences. Its value represents the length of the shortest read in the group of longest sequences that together represent (at least) 50% of the nucleotides in the set of sequences.