

HTSF FASTseq Sample Expectations Form

UNC HTSF FAST_SEQ Sample Expectations Form

HTSF Contact: Tara Skelley and Amy Perou

Investigator:

Submitter:

Project: FAST_SEQ

FAST_SEQ Platform: MiSEQ

UNC HTSF requires a release form for all requests for FAST_SEQ sample runs. Below are the conditions for sample acceptance at HTSF and the expectations the study should have for sequencing results. The form needs to be signed by both PI and submitter prior to submission. Each submitter from a lab group will need to sign a form for samples to be accepted. A submitter only needs to turn in the form once, forms will be kept on file for reference.

Study will request run with 48hr minimum prior drop off

1-Study must contact the HTSF and confirm availability of open FAST_SEQ lanes

*Contact Tara or Amy via email, at least 48hr ahead of planned run time, to confirm availability for the week. HTSF opens lanes one calendar week at a time.

*HTSF will confirm availability within 24hr of run time.

- 1-HTSF will confirm HTSF FAST_SEQ Sample Expectation form is on file for submitter
- 2- A date and time for drop off will be confirmed with the study
- 3- A FAST_SEQ manifest will be sent to project
- 4- A FAST_SEQ Sample Expectation Form will be sent, if not on file

2-Study must fill out and return the following 3 documents to the HTSF, via email, 24hr prior to run time:

1-FAST_SEQ manifest

*FAST_SEQ manifest must be completed (blue highlighted fields) with PI name, Submitter name, Funding Information, Sample IDs, MiSEQ seq details and data return email

*HTSF staff will submit manifest on the study's behalf and return a confirmed manifest to submitter with confirmation of drop off date available

2-MiSEQ sample sheet

*MiSeq Sample sheet will be completed with Sample IDs, the corresponding indexes and the run requirements.

*Sample ID's should contain only alphanumeric characters. Spaces (and special characters) are not allowed by Illumina software and will be replaced with an underscore, if present

* If you have questions on filling out sample sheet, contact us beforehand

*HTSF will load the sample sheet when run is ready to load

3-FAST_SEQ Sample Expectation form (if not on file)

ONCE ALL PAPERWORK HAS BEEN FILED WITH HTSF STAFF, YOUR RUN IS RESERVED

FAST_SEQ Queue: multiple studies can request time for FAST_SEQ runs. The first study to submit the FAST_SEQ manifest and MiSEQ sample sheet will be assigned the open run slot

Any lab will be allowed one FAST_SEQ lane per week based on sequencer availability. Additional lanes can be

requested, but are not guaranteed to be accepted.

Study will supply:

In a large Ziplock bag labeled with PI name, Submitter Name, Batch # (found on confirmed manifest)

1- Illumina kits needed for run

*Thawed MiSEQ kit of appropriate size

* Appropriate Flowcell Package

2- **Fully prepared sample in ready to load state** labeled with Sample Name, PI Name, and batch #

*Denatured sample that is diluted to appropriate loading concentration

FOR BEST RESULTS:

1- use 10N NaOH stock

2- on day of submission, prepare 0.2N dilution for use

* Study is responsible for adding PHiX at required % for the run

* HTSF will store sample at 4°C until ready to run

3- Primer requirements:

*Standard Illumina Primers are in the kit you supply

* Primer needed for run if Custom. – indicate Custom (Col. Z) and primer name in SPECIAL NEEDS field on manifest

*HTSF can supply “Old Nextera Primers” – indicate Custom (Col. Z) and primer name in SPECIAL NEEDS field on manifest

4- A copy of the confirmed manifest

*Study will bring sample package to HTSF (Genome Sciences Building, room 1153) and place in 4°C fridge

*Study will complete drop off application, HTSF will check in the samples and notify staff of arrival.

Sequencing Expectations:

1. Study supplies the kits: Kits purchased by the study are not covered by the HTSF Illumina maintenance contract. We will engage with Illumina Tech support in case of a run failure on study’s behalf. If Illumina tech support does not provide a replacement kit and/or determines that the run failure is not because of hardware/reagents then the study will be responsible for purchase of a new kit and HTSF fees.
2. Study is responsible for all sample QA/QC and sample preparation. **HTSF will not run QA/QC or prepare samples**
3. HTSF does not guarantee the run success or quality of the data from a FAST_SEQ run
4. If a study fails to submit samples at the reserved time, the HTSF may offer the run slot to another study. However, if no other study is available to take the run slot, there will be a charge for the lost run time.

I understand the recommendations made by UNC HTSF, as well as the potential risks of proceeding with FAST_SEQ sequencing. I still wish to proceed with study prepared sample submission and sequencing. By signing below, I am indicating that I understand that I will still be responsible for the full price of services requested regardless of sequencing success and/or sequence quality.

Principle Investigator Signature

Date

Study Submitter Signature

Date

Please return this form to:

Tara Skelley -- tskelley@email.unc.edu

Amy Perou -- amyperou@med.unc.edu