

Sample Submission Ticket

SOLiD Sequencing

Investigator Information:

Your Name: _____ Today's Date: _____
PI/Lab: _____ Phone Number: _____
Email Contact: _____@umassmed.edu
Speed Type: _____ PI Signature*: _____
(original signature required)

Sample Information: One ticket is required for each sample submitted.

Sample Name: _____ (min amount is 20ul at 10nm) Insert Size: _____
Volume: _____ Concentration: _____ How was this determined? _____

Is your Sample Bar-Coded or Multiplex? Circle one below

- NO it is not barcoded or multiplex and I want LOTS of reads and run all to myself
YES it is coded and I want to share the run, see below

BarCode Info for this sample ... ONLY ONE PER SAMPLE, Please indicate which

RNA Set, Number: _____
Or
DNA Multiplex Set, Number: _____

Are there adapters, linkers, or any non-random, non-genomic or non-transcriptome sequences in your library? If so, please describe:

What is your read-length? 35 or 50 bases (Circle one, this does NOT include the barcode)

Reference seq for validation? _____ Not sure? Then what species is it? _____

How much depth do you want? Briefly, a single sample can be run on an entire slide/field or the field can be split into smaller portions by the use of barcodes. To do this the Barcodes must be balanced. The multiplex barcodes can be run in shares of 4 or 8. The RNA barcodes need at least 5 for balance. If you choose "NO! I WANT THE WHOLE THING" then you will get a single run with just your library. If you have barcodes or are multiplexing, then here is where you tell us if you are planning to run with other samples from your group or if you are submitting to the queue and waiting for suitable running partner(s).

A "share" of the flow cell is 1/8 of the surface: how many shares do you want for this sample? _____ (e.g. if you have four matched samples, run them at 2 shares each; or run 8 at one share each; the size of a share will vary with library quality and instrument specs. Currently one share is 30-50 million seeded beads and you can expect 15-30 million reads, this number is expected to increase with the next upgrade.)

Sample Drop Off Information: Samples should be dropped off at the Core Lab (2 Biotech, lab 207) during business hours. Please give them directly to a staff member for login. It helps to email ahead to let us know when you are coming, nemo@umassmed.edu

Data Information: The results from Deep Sequencing analysis are routinely deposited in a pick up directory on the high performance cluster HPCC. You (or someone in your group) must have an account on one of these machines. Who will be receiving the data from this analysis? Please list their name and email here: _____

Data will be available from the pick up area for 2 weeks from the completion of the pipeline analysis. Please contact us immediately if there is any required re-analysis. If you request special analyses or extra genomes, there may be an additional fee.