Sample Submission Ticket

Investigator Information:
Your Name: ___________________________ Today’s Date: __________
PI/Lab: ___________________________ Phone Number: ___________________________
Email Contact: ___________________________ umassmed.edu
Speed Type: ___________________________ PI Signature*: ___________________________
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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.

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