

Deep Sequencing Core Facility @ UMass Medical School

Sample Submission Ticket (for UMass Investigators)

Lab Use Only:

Sample ID# _____

BA File # _____

RunID # _____

Investigator Information

Your Name: _____

Date: _____

PI/Lab: _____

Phone Number: _____

Email Contact: _____

@umassmed.edu

Account to charge: _____ PI Signature: _____ (required)

Sample Information *One ticket for each sample, name on ticket must match name on sample tube*
If you are doing a mixture of libraries either your own barcodes or Illumina bar codes, please turn in the samples in separate tubes, with one ticket and indicate how you want them mixed (1:1, 2:1, etc) here: _____

Sample Name: _____ Median Insert Size: _____

Linker/Adapter set used: **important!** We really need to know this!

READ THE INFO ONLINE IF YOU ARE NOT SURE (www.umassmed.edu/nemo)

_____ IlluminaGDE/DNA _____ TruSeq DNA/RNA/Exome (100 base only)

_____ IlluminaPE _____ Other(describe): _____

_____ Illumina small RNA _____ TruSeq small RNA (100 base only)

_____ Illumina mRNA

Approximate Concentration: _____ Volume Submitted: _____ (not sure? Email us)

Do you want a Multiplex Read (additional cost) for Illumina BarCode Indexes? _____

Does your sample have any linkers, indexes or internal barcodes in the insert? _____

If so, list sequences and position within the reads:

Chose the type of DeepSeq Analysis:

- _____ Single Read, 36 bases
- _____ Single Read, 75 bases
- _____ Paired Read, 36 x 36 bases
- _____ Single Read, 50 bases
- _____ Single Read, 100 bases
- _____ Paired Read, 100 x 100 bases
- _____ MultiPlex, barcode read (required to read *Illumina* bar codes, additional charge)

Do you want an alignment to a reference genome? _____ If Yes, which one? _____

Data Delivery Information

The resulting data files can be quite large. We deliver your entire data set (it's yours). We do NOT archive data, that is the responsibility of each investigator. The default delivery is to a pickup area on the High Performance Cluster nearline storage. If you need your data copied to a portable hard drive you must provide a 1TB drive when you drop off your sample(s). We can also upload your data to an outside server but you must provide access and are responsible for the security of the data. If you select the "alignment" option above, one preliminary alignment to a reference genome will be included during the analysis pipeline. Additional alignments and other analyses may incur additional fees.

Who should be notified and sent data pick up info?

Name: _____ Email Address: _____

Name: _____ Email Address: _____

Payment Policy

Processing a sample requires time and reagents. Payment for services is the responsibility of the user submitting the sample. In the event of a reagent or equipment failure, the samples will be rerun at the next opportunity at no additional charge (no refunds).

If you have questions, please contact us at Nemo@umassmed.edu