Deep Sequencing Core Facility @ UMass Medical School

Sample Submission Ticket (for UMass Investigators)

Lab Use Only: v.2.13

Sample ID# _____
BA File # _____
RunID # _____

Investigator Information

Your Name: _____ Date: _____

PI/Lab: _____ Phone Number: _____

Email Contact: _____@umassmed.edu

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

Please note, sample preparation is key to optimal performance. The addition of carrier, partial PCR products, modified bases, etc. can negatively affect performance. Please contact us if you have questions.

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
_____ IlluminaPE
_____ Illumina small RNA
_____ Illumina mRNA
_____ TruSeq DNA/RNA/Exome
_____ Other(describe): _____
_____ TruSeq small RNA

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

**Please note: if you turn in less than 10µl, your sample may only get one chance at sequencing due to insufficient volume!!!*

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

If so, list sequences and position within the reads on the back or attach. (If you did ANY modification to the construction scheme, added linkers, cloned out of a vector, etc. PLEASE include a schematic of your construction). If you are using a custom primer for side 1 you must submit the diagram and the results of your topo cloning. Custom primer on side 2 is only available on the MiSeq.**Please submit the results of your Topo Cloning and any other QC if available, it will help us set up your samples! Diagrams of custom designs are also requested. NOTE: That if you did not do any pre-run sequencing or TopoClones, Strataclones, or MiSeq tests, you may not be eligible for a rerun if there are problems due to sample issues.**

Chose the type of DeepSeq Analysis:

(Paired Reads are sequenced from both ends, a paired 50 is 50 bases side 1 + 50 bases side 2)

GAIIx Instrument	**HiSeq 2000**	**MiSeq**
____ Single Read 36 bases	____ Single Read 50 bases	____ Single Read 50 bases
____ Paired Read 36 bases	____ Single Read 100 bases	____ Paired Read 25 bases
	____ Paired Read 50 bases	____ Paired Read 100 bases
	____ Paired Read 100 bases	____ Paired Read 150 bases
		____ Paired Read 250 bases
		____ Paired Read 300 bases

MultiPlex, or barcode read (required to read *Illumina* bar codes, additional charge). Even if you are planning to sort the indexes yourself later, to get the sequences read you need to do this step.

____ MULTIPLEX 1 End (available on HiSeq or MiSeq)
____ MULTIPLEX BOTH ENDS (only available on MiSeq)

Do you want PhiX DNA control mixed into your sample? __ If yes, circle one: 5% 10% 15% 20%

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 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 be 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). v. DEC 2013