Deep Sequencing Core Facility @ UMass Medical School
Sample Submission Ticket (for UMass Investigators)

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

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!!!

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

Does your sample have any linkers, indexes or internal barcodes in the <u>insert</u>? _____ If so, list sequences and position within the reads (If you did ANY modification to the construction scheme, added linkers, cloned out of a vector, etc. PLEASE include a schematic of your construction):

Chose the type of DeepSeq Analysis:

_____	Single Read, 36 bases	_____	If more than one run type is acceptable, and you would prefer whichever is fastest, please check here as well as each of the run types.
_____	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 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. FEB 2013

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