

Sample Submission Ticket

Illumina/Solexa Deep Sequencing

Deep Sequencing Core

Investigator Information:

Your Name: _____ Today's Date: _____

PI/Lab: 1 _____ Phone Number: _____

Email Contact: _____@umassmed.edu

Speed Type: _____ PI Signature*: _____
(original signature required)

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

Sample Name: \_\_\_\_\_

Linker Set (which primer set was used to make this library?) VERY IMPORTANT !!

**Circle one:** **DNA** (genomic and Chip) **RNA** **Paired-End (PE)**

Median library Size (bp): \_\_\_\_\_ Concentration: \_\_\_\_\_ (10nM in water or EB best)

Volume Submitted: \_\_\_\_\_ (at least 25ul please)

Are there BAR CODES or INDEXES ? (any non-random bases in your sequence need to be reported as well as their positions in the sequence) eg "first 6 bases are bar code", or "only positions 9 through 27 should be aligned, first 8 and last 9 are linkers" TELL US here : \_\_\_\_\_

Which type of Analysis do you want? **Circle one please**

**Standard** 36 base read, strands are separated and each forms a cluster for sequencing

**Paired-End** 36 bases are read from each end of each strand, requires PE linkers

**LONG-75** (available in March '09) 75 base read of each strand (longer version of Standard)

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](mailto:nemo@umassmed.edu)

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Data Information: The results from Deep Sequencing analysis are routinely deposited in a pick up directory on one of the high performance clusters. You (or someone in your group) must have an account on one of these machines. Which machine do you use ? _____ Who is the account holder (their name please): _____ their account ID: _____. If you need other arrangements (e.g. external hard drive) please let us know right here _____

Analysis of Data: with each sample you may choose to have one alignment to a reference genome, along with your sequences and quality files. Your other choices are NO analysis, just sequences and sequences with quality files and a fastq file. Please choose below: (circle)

none You will receive raw sequences and the .sig2 and .prb files

sequence You will receive sequences, quality files, and a fastq file of all sequences

alignment You will receive everything in "sequence" as well as an alignment to a reference genome. You must specify the reference genome here: _____

We routinely deliver the ENTIRE data output, if you want only certain files or if you want it compressed, please tell us here: _____

Images are only held for 2 weeks from the completion of the pipeline analysis. Please contact us immediately if you need the raw images or if there is any required re-analysis. If you request special analysis or extra genomes, there may be a fee.