

Sample Submission Ticket **Illumina/Solexa Deep Sequencing**
Deep Sequencing Core

Investigator Information:

Your Name: _____ Today's Date: _____
PI/Lab: _____ 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**(SR36 only)                      **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** \*Library **MUST** be built with PE Primer set

**Single Read 36 bases**

**LONG Single Read 76 bases**

**Paired-end\* Read 36+36 bases**

**LONG Paired-end\* Read 76+76 bases**

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. Who will be receiving the data from this analysis? Please list their name and email here: _____

If you need other arrangements (e.g. external hard drive) please indicate this in the notes section.

ANALYSIS: with each sample you may choose to have one alignment to a reference genome using ELAND. 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 quality information

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

alignment You will receive everything in "sequence" as well as a preliminary alignment to a reference genome. You must specify the reference genome 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.

ELK 11/2009

NOTES: