Deep Sequencing Core Labs @ UMass Medical School
Sample Submission Ticket

1. **Investigator / Client Information**

Name: _____________________ Date: ___________________

PI/Lab: _____________________ Phone Number: ____________

Mailing address: ______________________________________________________

Email address: _____________________ @ ____________________________

Account to charge: ____________ PI Signature: _____________________ (required)

2. **Sample Information:** Complete one ticket per sample OR one ticket per sample set to be multiplexed and run in one lane. Sample name(s) on the ticket should match name(s) on sample tube(s). When multiplexing a sample set with Illumina or your own-designed barcodes, each sample should be submitted in a separate tube. Please indicate the desired mixing ratio of the samples in the sample set. For example: 1:1, 2:1, etc.:_____________________. (Note: Default mixing is equimolar.)

   **Lane/Mix Name:** ___________________  **Median Insert Size:** ____________ 

   **Sample Set Names:** Please attach an Excel sheet with each sample name, its index, its median insert size, the approximate library concentration, and the volume submitted.

   **Sample Classification:** Is the sample(s) infectious or pathogenic to humans? **YES** or **NO**. If yes, please describe the material(s) and any potential biohazards. ________________________________

   *Recommended Library Concentration and Volume for Submission: 20 microliters of a 10-20nM solution.
   Please note: if you submit less than 10 microliters of your sample, there may be insufficient volume for subsequent analysis runs! 

3. **Library Adaptors Used:**

   Please indicate the linker/adapter set used for library construction:

<table>
<thead>
<tr>
<th>No Index in Adapters</th>
<th>Illumina Index in Adapters</th>
<th>Other Vendor Kit/Index Set</th>
</tr>
</thead>
<tbody>
<tr>
<td>(<strong>old</strong>) Illumina PE</td>
<td>____TruSeq DNA/RNA/Exome/PE</td>
<td>____Chromium 10X Genomics* Version ____________</td>
</tr>
<tr>
<td>____TruSeq Small RNA</td>
<td>____TruSeq Small RNA</td>
<td><strong><strong>Takara/Clontech (Name, P/N:</strong></strong>_________)</td>
</tr>
<tr>
<td>____TruSeq Stranded RNA</td>
<td>____TruSeq Stranded RNA</td>
<td><strong><strong>NEB (Name, P/N:</strong></strong>_________)</td>
</tr>
<tr>
<td>____TruSeq Targeted Capture</td>
<td>____TruSeq Targeted Capture</td>
<td><strong><strong>Other (Name, P/N:</strong></strong>_________)</td>
</tr>
<tr>
<td>____Nextera</td>
<td>____Nextera</td>
<td><strong><strong>Custom (Describe:</strong></strong>_____________________)</td>
</tr>
</tbody>
</table>

\* 10X Genomics samples contain 4 indices per P7 adapter/plate well. Please do not mix 10X Gen. samples unless all four index sequences are different between samples. If you do not know which indices are in the mix, please list the ID#/adapter wells with your index information.

4. **Multiplexed/Indexed/Barcoded Run:** (Please answer all that apply.) Index read analysis is required for Illumina-type indexing, even if you intend to perform sorting as part of your own analysis. You will only be delivered index sequencing reads for the indexing that was requested here. Note: There is an additional charge for the index read.

   Please see the Example Ticket if you need an explanation of the different types.

   ____MULTIPLEX, i7 End - Does your sample have an Illumina-style index at the i7 (downstream) position? **Length:** _______bp

   ____MULTIPLEX, i5 End - Does your sample have an Illumina-style index at the i5 (upstream) position? **Length:** _______bp

   **In order to sort your indices, we need sample names and corresponding index sequences. Please list on the back, attach, or email.**

   ____UNSORTED - Do you want your results to **NOT** be demultiplexed, even though they contain Illumina-style indices?

   ____MERGED - Results will be sorted (unless you checked 'unsorted' above), and then merged back into a single fastq file.

   ____RANDOM - There are random bases in your index (as in GuideSeq). The Core's pipeline can read these but not sort them.

   ____INLINE BARCODES - Does your sample have in-line (part of the insert) barcodes or indices? (We cannot sort these for you.)

   *If yes, are they base-balanced? **YES** or **NO** Please give location and length or attach the information: ________________________________

   ____INLINE LINKERS - Does your sample have linkers, primers, or any other non-random sequences in the insert?

   *If yes, please give location and length or attach a sheet with the information: ________________________________

   **Request for Library Construction Information:** To facilitate processing and workflow, please submit a library design schematic, reference, results from topo cloning/sequencing (when available), and/or other QC analysis performed prior to library submission. If you made any modification to the library construction design (e.g. added linkers, cloned out of a vector, etc.) you must submit a schematic. If using a custom primer for side 1, you must submit a schematic and topo cloning results. Please note that the use of a custom primer on side 2 is only feasible on the MiSeq instrument. If you did not perform any pre-run QC analysis such as sequencing topo clones, MiSeq pre-check, or library profiling, you will be ineligible for a re-run should your library(s) fail during cluster formation or the actual sequence analysis run.

Sample preparation is key to optimal performance. The presence of carrier, partial PCR products, modified bases, etc. will adversely affects run performance. Please contact us if you have related questions.
5. Selection of Sequence Analysis Run Type:
Single Read (SR) is sequencing from one end of the library insert (e.g. a SR100 is 100 bases read on side 1). Paired End (PE) Reads are sequenced from both ends of the library fragment (e.g. a PE50 is 50 bases read on side 1 + 50 bases read on side 2).

<table>
<thead>
<tr>
<th>HiSeq 4000</th>
<th>MiSeq</th>
<th>FIRST AVAILABLE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Single Read 50 bases</td>
<td>Single Read 50 bases</td>
<td></td>
</tr>
<tr>
<td>Single Read 100 bases</td>
<td>Single Read 100 bases</td>
<td></td>
</tr>
<tr>
<td>Paired End Read 50 bases</td>
<td>Paired End Read 100 bases</td>
<td></td>
</tr>
<tr>
<td>Paired End 50 x 100 bases</td>
<td>Paired End 50 x 100 bases</td>
<td></td>
</tr>
<tr>
<td><em>(Trim for Chromium 10X pipeline to)</em>&lt;br&gt;26 x 98 bases</td>
<td><em>(Trim for Chromium 10X pipeline to)</em>&lt;br&gt;28 x 98 bases</td>
<td></td>
</tr>
<tr>
<td><em>(Trim for Chromium 10X pipeline to)</em>&lt;br&gt;x bases</td>
<td><em>(Trim for Chromium 10X pipeline to)</em>&lt;br&gt;x bases</td>
<td></td>
</tr>
<tr>
<td>Paired End Read 100 bases</td>
<td>Paired End Read 100 bases</td>
<td></td>
</tr>
<tr>
<td>Paired End Read 150 bases</td>
<td>Paired End Read 150 bases</td>
<td></td>
</tr>
<tr>
<td>Paired End Read 100 x bases</td>
<td>Paired End Read 150 x bases</td>
<td></td>
</tr>
<tr>
<td>Paired End Read 250 bases</td>
<td>Paired End Read 300 bases</td>
<td></td>
</tr>
<tr>
<td>Paired End Read 300 bases</td>
<td>Paired End Read 300 bases</td>
<td></td>
</tr>
<tr>
<td>Paired End Read 150 bases* (*4 lane min.)</td>
<td>Paired End Read 150 bases* (*4 lane min.)</td>
<td></td>
</tr>
</tbody>
</table>

Do you want the PhiX DNA control added to your sample? Yes or No? If yes, circle one: 5%, 10%, 15%, or 20%. This addition is required for libraries with low sequence diversity/completeness (such as Chromium 10X) to ensure the base balance needed for optimal imaging.

Please Note: Based on the information you provide, should we deem it necessary, we will automatically add the appropriate % of PhiX DNA to your sample(s).

6. Data Delivery Information
The resulting data files can be quite large in size; the DSCL delivers the entire data set generated. Please make arrangements for the mode of data transfer before sample submission. Data should be retrieved within five business days of notification, unless other arrangements are made in advance. We do not routinely archive analysis run data. However, we offer a data archive option and data recovery service at an hourly fee. If data archiving is required, you must notify the DSCL within the same five business days of notification. For UMass investigators, the default mode for data delivery is to the pick-up area on the Green High Performance Cluster. For all non-UMass clients, your data can be uploaded to an outside server (using an SFTP) or transferred to an external drive and shipped overnight.

Please contact DeepSequencingCoreLabs@umassmed.edu to arrange for archiving or retrieval.

7. Whom should the DSCL contact to arrange the transfer of data?

Name: ______________________ Email Address: ______________________

8. Whom should we notify when the data is ready?

Name: ______________________ Email Address: ______________________

Name: ______________________ Email Address: ______________________

9. Payment Policy
Sample processing requires time and reagents. Clients withdrawing samples that fail the QC process or prior to the analysis run will be charged a fee to recover the assay costs. For the return of samples post-run analysis, the client will be charged a fee per sample. In the event of a reagent or equipment failure, samples will be re-run at no additional charge. Payment for services rendered should occur in a timely fashion.

Questions? Contact us at DeepSequencingCoreLabs@umassmed.edu

DSCL Notes:

Samples should be shipped overnight for delivery on Monday through Thursday.

Ship to:

Drs. E. Kittler / M. L. Zapp
UMass Medical School, DSCL
222 Maple Avenue
Reed Rose Gordon Building, Room 141
Shrewsbury MA 01545 (508-856-4787)