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.)

a) Sample Name: ______________________________ Median Insert Size: __________
Approximate Library Concentration: ___________ Volume Submitted: ___________

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

c) 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 to 25 microliters of a 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 Kits or Select Components</th>
</tr>
</thead>
<tbody>
<tr>
<td>______ (old) IlluminaGDE*</td>
<td>______ TruSeq DNA/RNA/Exome/PE</td>
<td>Name/ Part number: ______</td>
</tr>
<tr>
<td>______ (old) IlluminaPE</td>
<td>______ TruSeq Small RNA</td>
<td>Name/ Part number: ______</td>
</tr>
<tr>
<td>______ (old) Illumina small RNA*</td>
<td>______ TruSeq Stranded RNA</td>
<td>Description:</td>
</tr>
<tr>
<td>______ (old) Nextera</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

4. Multiplex Run: Index read analysis (required for Illumina-type indexes). You need this step even if you intend to perform the sorting as part of your own analysis. Note: There is an additional charge for the index read.

_____ MULTIPLEX, Single End (available on HiSeq or MiSeq)
_____ MULTIPLEX, Both Ends (available on HiSeq or MiSeq)

Request for Library Construction Information: To facilitate sample processing and run workflow, please submits a library design schematic, and results from topo cloning/sequencing (when available) and/or other QC analysis performed prior to library submission. 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.

Does your sample have any linkers, barcodes or other internal non-random sequences in the insert? YES or NO

If yes, list the sequences and the position(s) within the insert read on the back of this form or attach a separate sheet with the information. 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 of the construction. If using a custom primer for side 1, you must submit the schematic and the sequencing results from your topo clones. Please note that the use of a custom primer on side 2 is only feasible on the MiSeq instrument.

08/15
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).

HiSeq 2000
- Single Read 50 bases
- Single Read 100 bases
- Paired End Read 50 bases
- Paired End Read 100 bases

MiSeq
- Single Read 50 bases
- Paired End Read 25 bases
- Paired End Read 100 bases
- Paired End Read 150 bases
- Paired End Read 250 bases

GAIx Instrument
- For running 7 samples, pre-arrange

FIRST AVAILABLE
If pressed for time, check all run types that would be appropriate. Your libraries will assigned to the first run available. The cost of the type of run used will be charged accordingly.

Do you want the Phi X DNA control added to your sample? ______. If yes, circle one: 5%, 10%, 15%, and 20%. This addition is required for libraries with low sequence diversity/complexity to ensure base balance required for optimal imaging.

Please Note: Based on the information you provide, should we deem it necessary, we will automatically add the appropriate % of Phi X 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 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.

_____ Request for Archived Data  Sample ID Number: ___________  Sample Analysis Run Date: ___________

7. Who should the DSCL contact to arrange the transfer of data?
Name: ___________________________  Email Address: __________________________________________

8. Whom should we notify when the data is ready? (For all clients)
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 $75.00 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)