Core Lab Use Only v01.23

Sample ID# _____

FA File1 # _____

FA File2 # _____

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 be charged: _____ PI Signature: _____(required)*

*Signature of PI / client indicates consent to process samples as described in DSCL Policies & Procedures, available online.

2.Sample Information: Complete one ticket AND one Sample Information List *per sample set or flowcell* and send the electronic version to the Core in addition to your paper submission.

Sample name(s) on the list should match the name(s) on sample tube(s). When multiplexing a sample set with Illumina or your self-designed barcodes, each sample should be submitted in a separate tube.

Sample preparation is key to optimal performance. The presence of carrier, partial PCR products, modified bases, *etc.* will adversely affect run performance. 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. To facilitate processing and workflow, if not using a commercial kit 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, you must submit a schematic and topo cloning results. Please contact us if you have related questions.

Sample Classification: Is the sample(s) infectious or pathogenic to humans? If yes, please describe the material(s) and any potential biohazards. _____

Recommended Library Concentration and Volume for Submission: 20ul of a 10 - 20nM solution. Please note: If you submit less than the recommended amount, there may be insufficient volume for subsequent runs!

3.Library Adaptors Used:

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

No Index in Adapters

- ☐ old Illumina PE - Do not submit without prior approval.

Illumina Kit with Index in Adapters

- ☐ Illumina or TruSeq DNA/ChIP/etc.
- ☐ TruSeq small RNA
- ☐ Illumina or TruSeq RNA
- ☐ Illumina or TruSeq Stranded RNA
- ☐ Nextera v._____
- ☐ Targeted Capture assay

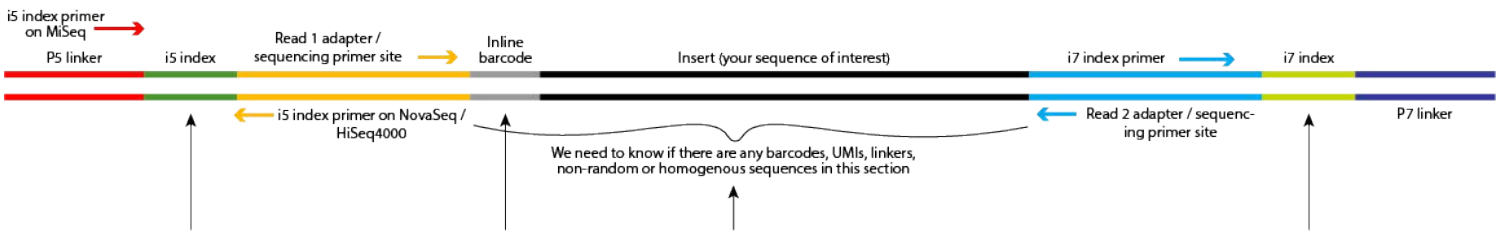
Other Vendor Kit/Index Set

- ☐ Chromium 10X Genomics‡ Version _____
- ☐ Takara/Clontech (Name, P/N:_____)
- ☐ NEB (Name, P/N:_____)
- ☐ NanoString (Name, P/N:_____)
- ☐ Other (Name, P/N:_____)
- ☐ Custom* (Describe:_____)

‡ 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.
*Adapters requiring custom primers must be pre-approved by the Core.

4.Multiplexed/Indexed/Barcoded Run: (Please indicate 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.



Length:_____bp **Length:_____bp** **Length & description:_____** **Length:_____bp**

(We cannot sort these)

Do you want PhiX DNA control added to your sample? If yes, choose one: 1% (NovaSeq std), 5%, 10%, 15%, 20%, other 0%.

This addition is required for libraries with low sequence diversity/complexity (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).**

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).
**Sample insert sizes >800bp are not guaranteed!*

NovaSeq 6000 - choose both read length and # of reads per sample

- ☐ Single Read 100 bases
- ☐ Paired End Read 50 bases
- ☐ Paired End for Chromium 10X pipeline

  _____ x _____ *bases (must be <=138 bases total including indexes)*
- ☐ Paired End Read 100 bases
- ☐ Paired End Read 150 bases* (*full flowcell only)

- ☐ 50M
- ☐ 100M
- ☐ 200M
- ☐ 400M
- ☐ 500M
- ☐ 1000M

MiSeq

- ☐ Single Read 50 bases
- ☐ Paired End Read 25 bases
- ☐ Single Read 100 bases
- ☐ Paired End Read 100 bases
- ☐ Single Read 150 bases
- ☐ Paired End Read 150 bases
- ☐ Paired End Read 250 bases
- ☐ Paired End Read 300 bases
- ☐ Asymmetric Read _____x_____

6a. Data Demultiplexing Options

Please choose how you would like multiplexed sample data delivered.

- ☐ STANDARD DEMULTIPLEX - Results will be demultiplexed, and there will be a separate fastq for each index and read group.
- ☐ UNSORTED - Do you want your results to NOT be demultiplexed, even though they contain Illumina-style indices which are read?
- ☐ MERGED - Results will be demultiplexed, and then concatenated back into a single fastq file (as for Chromium).
- ☐ RANDOM - There are random bases in your index (as in GuideSeq). The Core's pipeline can read these but not sort them.

6b. 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. The default mode for data delivery is by Globus. You do not need a full Globus subscription to receive data, however you do need a registered email account. Information about Globus subscription and personal use is available at https://app.globus.org.

If you have a Globus account, what is the email address assigned to it? _____

Do you want md5sum values? _____

We do not archive primary or analyzed run data. Please make your own arrangements.

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)