

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 4000

- ___ Single Read 50 bases
- ___ Single Read 100 bases
- ___ Paired End Read 50 bases
- ___ Paired End 50 x 100 bases
(Trim for Chromium 10X pipeline to
 ___ 26 x 98 bases
 ___ 28 x 98 bases
 ___ x bases)
- ___ Paired End Read 100 bases
- ___ Paired End Read 150 bases* (*4 lane min.)

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___

FIRST AVAILABLE

If pressed for time, check all run types that would be appropriate. Your libraries will be assigned to the first run available. The cost of the type of run used will be charged accordingly. You can number them in order of preference in case more than one option is available.

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

Do you want the *PhiX* DNA control added to your sample? _____. If yes, circle one: 5%, 10%, 15%, or 20%. **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).

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)