Illumina Sequencing Sample Submission Form

Customer Name:	
Organization:	
PI Name:	
Contact Phone:	
Contact Email:	
Fund Number (MGH):	
Billing Contact (non-MGH):	
Billing Address (non-MGH):	
Date:	

Massachusetts General Hospital
Sequencing Core Facility
185 Cambridge St.
Boston, MA 02114
Core Director: Mark Borowsky
Email: sequencing@molbio.mgh.harvard.edu

DEFINE LIBRARY

Type of library:
If other:

Adapters:
If custom, enter sequence(s):

Reference Genome:

QC Methods:
(select all that apply)

Note: Nanodrop is not acceptable library validation

- ☐ Gel for Size Verification
- ☐ qPCR
- ☐ PicoGreen
- ☐ Bioanalyzer
- ☐ Other:

Multiplexing Information (if applicable)

Details:

- ☐ Custom Barcoding
- ☐ Illumina Indexing

Custom Barcoding: refers to a sample which has a sequence at either the 3' or 5' end which is read *contiguously* with the sequence of interest and helps in the identification of different samples that are run in the same lane during a multiplexing run. It does NOT require an additional primer. In the details field, please enter the number of bases and in which position it is located (3' or 5'), and provide the barcode sequences in the table below.

Illumina Indexing: refers to use of an Illumina library prep kit in which a finished sample has a sequence within the length of the library that is read by an *additional sequencing primer* and helps in the identification of different samples that are run in the same lane during a multiplexing run. In the details field, please provide details about any pertinent deviations from the Illumina protocol and provide the Illumina Index # assigned to each sample in the table below.

Constant Region (if applicable)

Details:

- ☐ Constant Region

Constant Region: a constant or nearly-constant sequence present within the reads (can be a product of library construction or present naturally). Ex: 5' end always starts with GGGG.

Sample prep method:
(Description of the method used to obtain and purify the DNA or RNA sample.)

Library construction method:
(Description of the method used to generate the sample library. If applicable, name any specific protocols used; ex: Illumina PE protocol, target enrichment, etc.)

DEFINE SERVICES

Run type:

- ○ Single End Read
- ○ Paired End Read
- ☐ Multiplexing

Number of Cycles:

- ○ 36
- ○ 76

Sequencing Primer:

We provide sequencing primers for all Illumina adapters or their equivalents. If using a custom adapter (indicated above), please click the box below, provide the sequence, and include the primer in the shipment of your sample.

☐ Custom sequencing primer

Analysis: Standard

Analysis type defaults to standard. Standard analysis guarantees the delivery of sequence files along with high level summary and data quality information. Please contact us with custom analysis inquiries.

DEFINE SAMPLES

Sample #	Sample ID	Sample Description	Project	Volume (µl)	Concentration	Precious	Library Size (bp)	Barcode/Index Tag
1						☐		
2						☐		
3						☐		
4						☐		
5						☐		
6						☐		
7						☐		
8						☐		
9						☐		
10						☐		
Please fill out another form if you have >10 samples.	How the sample is clearly labeled on the tube. A new sample ID number will be assigned upon submission.	Your own description of the sample.	List new project or choose project that already exists in our system from previous submissions.	We request a minimum of 10 µl.	Indicate units. Should be be between 10-100nM. If <10nM, check precious box. If >100nM, dilute accordingly.	Click box if you can only submit <10µl and/or the concentration is below 10nM.	Size of your ***library*** , a total of the insert length PLUS the adapaters. Please give precise number or narrow range.	Indicate sequence of barcode tag or Illumina index # if requesting a multiplex run.

Other Comments: