



Illumina Next-Gen Sequencing Request Form

Genomics Core Facility (GCF)
Institute for Genomics and Multiscale Biology
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 genomics_core@mssm.edu
<http://icahn.mssm.edu/research/genomics/core-facility>

Date of Submission: _____ Principal Investigator: _____ [Required]
 Submitter Name: _____ Fund Acct #: _____ [Required]
 Submitter Email: _____ P.I. Signature: _____ [Required]

Signature indicates agreement to pay for services.

Sample Preparation Requested:
(Check Only One)
 mRNA-SEQ/poly-A selection
 RNA-SEQ/RiboZero
 RNA-SEQ/GlobinZero
 Small (micro) RNA-SEQ
 Exome-Seq
 gDNA-Whole Genome
 ChIP-Seq
 Amplicon-Seq
 User prepared library*
 Other†

Run Type- HiSeq:
 50nt Single Read (full 8-lane flowcell)
 50nt Paired-End Read (full 8-lane flowcell)
 100nt Single Read
 100nt Paired-End Read
 100nt Single Read_Rapid Run (full 2-lane flowcell)
 100nt Paired-End Read_Rapid Run (full 2-lane flowcell)

Run Type- MiSeq:
 50nt Single Read
 150nt Paired-End
 250nt Paired-End
 75nt Paired-End
 300nt_Paired-End
 Other†

Multiplex Instructions:
 No multiplex – 1 sample per lane
 2 samples per lane
 3 samples per lane
 4 samples per lane
 Other:

Note: If you are multiplexing, please provide details on how to mix the samples

Submission Instructions:

- Use one submission sheet per sample type
- Please submit all DNA/RNA samples on dry ice
- A minimum of 15uL total volume is required per sample
- DNA-Seq: Please provide **1-5 µg** of genomic DNA
- RNA-Seq: Please provide **1-3 µg** of total RNA
- Small RNA: Please provide **2-5 µg** of total RNA
- Prepared libraries: Please provide at least 20µl of a 10nM stock and email Bioanalyzer trace xad file to genomics_core@mssm.edu
Note: User prepared libraries ≤2ng/µl or 10nM produce unpredictable cluster densities; user assumes responsibility for re-sequencing costs.
- Submissions greater than 16 samples must be submitted in a 96-well plate

Sample Information: Please enter all pertinent sample information in the table below. If the table sample rows are insufficient, please create an Excel document containing a complete sample list and use the same column headers as shown below. Save the Excel document as a Microsoft Windows .csv file and email it to genomics_core@mssm.edu.

Sample ID	Index Barcode	Concentration	Volume	Plate ID	Well ID

Provide a brief description of your experimental design and number of reads desired per sample in the space below.

** For user prepared libraries, describe the sample prep method † Other sample prep/MiSeq parameters requested, please describe*

Samples accepted by: _____