Illumina Next–Gen Sequencing Request Form

Genomics Core Facility

Institute for Genomics and Multiscale Biology

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http://www.mssm.edu/research/institutes/genomics-institute/genomics-core-facility

MOUNT SINAI SCHOOL OF MEDICINE

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 <u>one</u> box only)
- ☐ mRNA-SEQ/poly-A selection
- ☐ RNA-SEQ/RiboZero
- ☐ Small RNA (microRNA)
- ☐ Exome-SEQ
- ☐ gDNA-Whole Genome
- ☐ User prepared library*
- ☐ Other†

Run Type HiSeq (check <u>one</u> box only)
- ☐ 50nt Single Read
- ☐ 100nt Single Read
- ☐ 50nt Paired-End Read
- ☐ 100nt Paired-End Read

Run Type MiSeq
- ☐ 50 Single Read
- ☐ 150 Paired-End

Multiplex Instructions (check <u>one</u> box only)
- ☐ No multiplex -1 sample/lane
- ☐ 2 samples per lane
- ☐ 3 samples per lane
- ☐ 4 samples per lane
- ☐ Other:

Submission Instructions
- Use one submission sheet per sample type (do NOT combine sample types)!
- Please submit all DNA/RNA samples on dry ice
- DNA-Seq, please provide **1–5 µg** of genomic DNA
- RNA-Seq, please provide **1–3 µg** of total RNA
- Small RNA: **2–5 µg** of total RNA

- User prepared libraries, please provide at least 20µl of a 10nM stock.
- **Note:** User prepared libraries ≤2ng/µl produce unpredictable cluster densities; user assumes responsibility for re-sequencing costs.
- If you are multiplexing, please provide details on how to mix the samples.
- User prepared libraries - provide a photocopy of Bioanalyzer trace and email xad file to next-gen-gcf@mssm.edu

Sample Name	Organism	Concentration (ng/µl)	Volume (µl)	Mixing Instructions or User Prepared Barcode

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 requested, please describe.

Sample accepted by:

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