



Next-Generation Sequencing Services Request Form

NIPM NGS and Genotyping Services (NNGS)
Harry Reid Center, 4th Floor, UNLV
nipm-ngs@unlv.edu

<http://www.unlv.edu/nipm>

Date of Submission: _____

Principal Investigator: _____ [Required]

Submitter Name: _____

Fund Acct #: _____ [Required]

Email Address: _____

P.I.
Signature:
[Print]

*Signature
indicates
agreement to
pay for
services.*

**** Desired Run Date:** _____ (allow 2 weeks from today)
 Please check 'Run Calendar' to ensure availability of run date

<p>Sample Preparation Requested: (Circle Only One)</p> <p>mRNA-SEQ/poly-A selection</p> <p>RNA-SEQ</p> <p>Small (micro) RNA-SEQ</p> <p>User prepared library*</p> <p>Other†</p> <p>Contact NNGS with specifics</p>	<p>Run Type- NextSeq (circle only one):</p> <p>75nt Paired-End (preferred)</p> <p>150nt Paired-End</p> <p>250nt Paired-End</p> <p>300nt_Paired-End</p> <p>Other†</p> <p>Contact NNGS with specifics</p>	<p>Multiplex Instructions:</p> <p>No multiplex – 1 sample/run</p> <p>Up to 3 samples per run</p> <p>Up to 12 samples per run</p> <p>Other:</p> <p>Note: If you are multiplexing, please provide details on how to mix the sample</p>
---	--	---

Submission Instructions:

- Use one submission sheet per sample type
- Please submit all DNA/RNA samples on minimum 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 to Shirley Shen shirley.shen@unlv.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

* For user prepared libraries, describe the sample prep method

† Other sample prep/NextSeq parameters requested, please describe

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 shirley.shen@unlv.edu

Sample ID	Index Barcode	Concentration	Volume	Plate ID	Well ID

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

Notes: