

## **Nextseq Sequencing Submission Guidelines**

Nextseq sequencing is a next-generation sequencing instrument that is one branch of technologies available within the NEB DNA Sequencing Core. All sequencing submissions are to be made after approval from Rich Roberts.

Nextseq runs are available in Mid output coverage of **130 million reads** and High output coverage of **400 million reads**. Lengths vary from 75-cycle to 300-cycle kits

The order in which your samples will be sequenced depends on a variety of factors including: When your samples were first submitted and your place in the queue. If you are submitting multiple samples, please reflect the priority of your samples in the order you place them in your submission box. If applicable, list the individual completion date under the sample name on the bioanalyzer trace. We will do our best to accommodate your deadlines and ask for your patience in return. If you have any questions please contact members of the sequencing core.

### **Template Preparation**

- Please run an aliquot of your completed library on the Agilent Bioanalyzer to make sure your sample is free of excess primers, primer dimer, and that the reactions worked. Staple a copy of the bioanalyzer traces to the submission form along with the calculations you made for the dilutions to of your sample(s).
- Samples must be submitted at a concentration of **4nM** in sterile Low TE in 1.5mL LoBind tubes. We may be able to work with lower concentrations if you discuss in advance.

### **Template Information**

Sender name: **Sean Maguire**

Lab Group: **Guan Lab**

Extension number: **x7934**

Email: **smaguire@neb.com**

Date Submitted: **9-23-21**

Requested Date of Completion: **Next available time**

Project Name: **R-loop Mapping**

Sample Name: **HEK293-rloop**

Requested read lengths: Mid Output or **High Output** | **75** or 150 | **Paired-End** or Single-Read

Is your sample Low Diversity? Y/**N** If so, what % PhiX would you like:

Low Diversity means that the ratio of bases G, C, T, and A is not balanced equally.

Is your sample barcoded? **Y**/N

Please indicate which indexes were used: **NEBNext UMI-UDI barcodes see excel sheet**