**MiSeq Sequencing Submission Guidelines**

MiSeq 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.

Miseq runs average around **25 million** reads per run and lengths vary from 50-cycles to 600 cycles.

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: **Erbay Yigit**

Lab Group: **Yigit Group**

Extension number: 7913

Email: **yigit@neb.com**

Date Submitted: **June 24, 2021.**

Requested Date of Completion: **June 25, 2021.**

Project Name: **ADA-Seq Project**

Sample Name: **B42p134 @ 4nM.**

Requested read lengths: 50 or 75 or 150 or 300 | Paired-End or Single Read

**60 cycles | Paired End (2 x 60 cycle)**

Is this a Small RNA library? Y/N. **Long RNA insert but contains Small RNA adapters (same as NEBNext small RNA kit adapter sequences)**

Is your sample Low Diversity? **No.** If so, what % PhiX would you like: **~5% will be helpful for diagnostics.**

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

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

Please indicate which indexes were used:

**This is a single library made using small RNA index-6 primer. Doing index reading is not necessary, but it would be nice if it can be read.**