Instructions for submitting samples for Illumina MiSeq sequencing

Samples need to be submitted along with

1. Download the *Illumina MiSeq Sequencing Submission Form*, and follow the instruction to fill it in completely. Sample names must be simple, short and should not contain period (.), coma (,), star signs (*) or spaces ( ).
2. Agilent Bioanalyzer or GX traces of the libraries to be sequenced need to be submitted along with the filled in Form. If you want the MCIC to run your libraries on the Bioanalyzer, please indicate this on your submission form. We do not sequence libraries without seeing the traces.
3. Submit the filled in form and the traces on line at
   http://mcic.osu.edu/genomics/illumina-sequencing/submit-samples
4. Bring or ship samples, on dry ice in carefully sealed tubes or plates, to:
   MCIC genomic core
   Selby Hall, room 009
   1680 Madison Avenue
   Wooster, OH
5. To coordinate sample transport from Columbus to Wooster contact:
   Stephen Opiyo, opiyo.1@osu.edu, tel.: 614-292-7717
   or
   Maria Elena Hernandez Gonzalez, hernandez-gonzal.2@osu.edu, tel.: 330-263-3828

Your samples will be put into our queue as soon as we receive them and the submission form and traces. No projects will be scheduled until samples and completely filled sample submission forms and have been dropped off to DNA Sequencing personnel.

Sample concentration (for a single library or a pool) should be at least 10nM or higher (measured by QuBit). If you have samples at a lower concentration, please check with the MCIC staff.

Libraries to be sequenced together in one MiSeq run have to be submitted as a single pool with a concentration of at least 10nM or higher (measured by QuBit).

If your pool has to be demultiplexed, or if you are using custom barcodes, you must also create and submit the Illumina Plate Sample Sheet using the Illumina Experiment Manager (IEM) software. Information about the IEM is found at http://support.illumina.com/sequencing/sequencing_software/experiment_manager.il mn, and the software can be downloaded from http://support.illumina.com/sequencing/sequencing_software/experiment_manager/d ownloads.ilmn.

We use the Illumina BaseSpace to deliver the data. You will need to create an Illumina account using your e-mail address. After the sequencing run is completed, we will give you the ownership of the run and projects. You will receive two e-mails from Illumina prompting you to take ownership of the run and project. The owner of the data is the only person who can subsequently share the data with other, therefore consult with your PI and colleagues who should be the owner.