Instructions for submitting samples for Illumina Library preparation

Samples need to be submitted along with

1. Download the *Illumina Library Sample Submission Form*, and fill it in completely. Sample names must be simple, short and should not contain period (.), coma (,), star signs (*) or spaces ( ). E-mail the form to mcic_seq.osu.edu and also include a copy with your samples.
2. Samples gel image or Agilent Bioanalyzer or GX traces of the DNA/RNA sample(s) when requested needs to be e-mailed along with the form to mcic_seq.osu.edu.
3. Sample tubes need to be carefully labeled. More than 16 samples have to be submitted in a microtiter plate in the order indicated in the submission form.
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

Amounts of DNA or RNA sample and quality required:

Library type	Quality and amounts needed
Genomic DNA-Seq	4-5ug of RNAase treated genomic DNA in 50uL (OD260/280=1.8; OD260/230=2) and gel image
RNA-Seq	4-5ug of total RNA in 50ul and Agilent Bioanalyzers traces of the sample
GBS, ddRAD, RAD libraries	3ug of RNAase treated genomic DNA 50uL, (OD260/280=1.8; OD260/230=2) and gel image
Ribosomal 16S/ITS or custom amplicons	25ul of 5 ng/ul RNAase treated genomic DNA (OD260/280=1.8; OD260/230=2), as starting concentration

- For other types of library preparation, please contact the MCIC staff.
- Samples need to be submitted in equimolar amounts, if not, we charge $50.00 per plate or samples set to dilute them to the working concentration.

Ribosomal (or other) custom amplicons: samples need to be submitted in microtiter plates (no empty wells between samples; we will charge for these 'empty' sample wells, as we are using a liquid handler to prepare the libraries) and all samples need to be at the same concentration. If they are not, we can make the dilutions for a fee. For 16S and ITS amplicons the sequence primers available at http://mcic.osu.edu/genomics/documents/AmpliconPrimers.pdf. Let us know if your samples have been already tested with the amplicon primers, or if we need to optimize the condition.

Low input DNA or RNA library preparation. The amounts of sample needed for the library preparation listed in the table above are for standard library preparation protocols. If you do not have the required amounts of sample, contact the MCIC staff. We have protocols for preparing libraries with very low amounts of input DNA or RNA.