

## Guidelines for Submission of Materials in 96-well Plate Format

For submission of materials in 96-well plate format, the JGI requires that investigators adhere to the guidelines outlined below in addition to the program- and product-specific sample submission requirements described on our website.

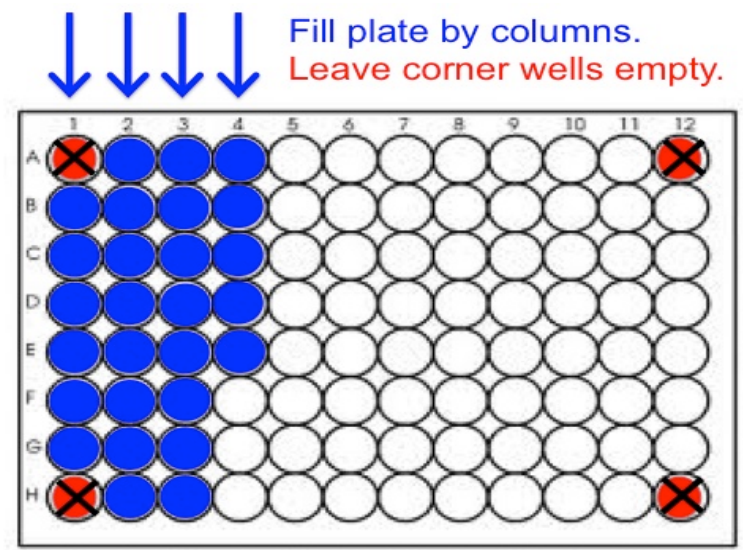
### Sample Preparation

- If you are shipping **22 or more** samples at one time, you must submit in 96-well plate format.
- DNA samples must be in TE buffer. RNA samples must be in nuclease-free water.
- You must assess the quality of at least 10% of samples prior to submission.
  - Guidelines for quality assessment (“Genomic DNA QC protocol”) can be found here: <http://my.jgi.doe.gov/general/protocols.html>

### Plate Preparation

- **We require the use of the pre-labeled, barcoded plates provided by the JGI.**
- Leave the corner wells (A1, A12, H1 and H12) **EMPTY**.
- Fill the plate by column, placing the first sample in well B1 (Column 1 B-G, then Column 2 A-H, Column 3 A-H, etc.).
- The mass should be consistent across all samples in the plate and within the ranges below
- Leave unused wells empty.
- After placing samples in the plate, seal with the **new** sealer contained within the shipment.

General Guidelines:	iTag Sequencing (16s and ITS)	DNA	Total RNA
Volume per well	20 uL	50-100 uL	50-100 uL
Concentration	10 ng/uL	5-10 ng/ul	50-100 ng/uL
Mass	200 ng/well	>500 ng/well	>5 ug/well
DNase Treatment Required?	No	No	Yes



Last updated 12/6/2013

### **Plate Naming**

- Plate name must be unique and descriptive
- "Plate Label" is the field in the metadata submission tool in which you will enter this information.
- Prior to shipment, confirm that the plate label information submitted with the metadata matches the physical label on the plate.
- For 16s or ITS tag sequencing, please include "itags" in the plate name.
- **Mismatched or improperly labeled materials will be returned to the shipper.**

Please name your plate using the following convention:

- Up to 10 characters of the last name of the Principal Investigator or Organization Name
- Designation of library type (max 6 characters):
  - DNA270 = Illumina DNA fragment library, 270 bp insert
  - DNA500 = Illumina DNA fragment library, 500 bp insert
  - RNA-P = RNA polyA selection
  - RNA-D = RNA with rRNA depletion
  - ExCap = Exome capture
  - iTag = 16S or ITS on MiSeq
- Counter (if multiple plates are sent)
- Entire plate name cannot be more than 20 characters in length

#### Examples:

Jones\_iTag\_21  
Smith\_RNA-P\_2  
DSMZ\_DNA270\_5

If you are having trouble determining a unique name for your plate, please consult your Project Manager.

*Last updated 12/6/2013*