Plate-Based Sample Submission

JGI JOINT GENOME INSTITUTE
UNITED STATES DEPARTMENT OF ENERGY

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.

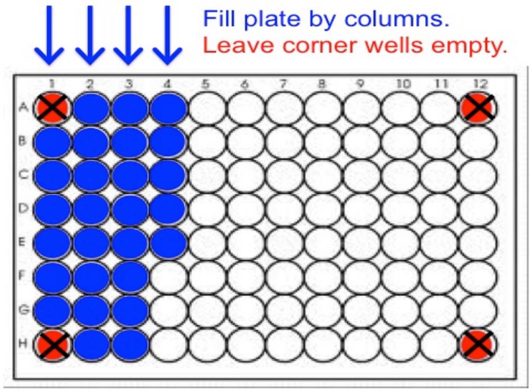
Sample Preparation

- 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 DNase treated and 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 prelableled, 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**	**Prokaryotic RNA (riboZero depletion)**	**Eukaryotic RNA (polyA selection)**
Volume per well	25 uL	50-100 uL	25-30 uL	25-50 uL
Concentration	4-6 ng/uL	5-10 ng/ul	10-12 ng/uL	60-120 ng/uL
Mass	100-150 ng/well	>500 ng/well	300 ng total mass/well	3 ug total mass/well
DNase Treatment Required?	No	No	Yes	Yes



Fill plate by columns.
Leave corner wells empty.

Last updated 8/25/2014

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 8/25/2014