

RNASeq- ILLUMINA SUBMISSION FORM

Submission No. _____

DATE: _____

Please ensure all ALL 9 sections on the front and back of this form are filled out completely.

1 PI: _____

Sample submitted by: _____

Telephone: _____

Email Address: _____

PI Email Address: _____

Signature: _____

UW Affiliation: UWCCC Waisman Ctr.UW System External

Institution/Company Name: _____

Bill To/Accounts Payable: _____

Account/P.O. No.: _____

Funding Source: NIH NSF GLBRCUSDA OtherUW Institution: SMPH CALs L&S SOPCOE Other _____

2 Number of samples: _____

Sample Information:

- Please provide an electronic and paper copy of this submission form and your sample spreadsheet with the following information - sample ID, concentration (ng/ul) and sample volume. Email all electronic sample information to gecinfo@biotech.wisc.edu and nextgen-seq@biotech.wisc.edu
- < 24 samples maybe submitted in 1.5mL single tubes, > 24 samples must be submitted in a skirted 96-well PCR plate with a temperature-stable adhesive seal capable of withstanding -80° C. Samples submitted in plates must be filled by column A1-H1, A2-H2, etc.

- **All sample tube/plates must be labeled with the sample name (6-8 characters with no special characters), PI last name and submission date.**

3 Name of Organism: _____

4 Input Nucleic Acid: total RNA mRNA Ribo-Reduced RNA Small RNA

Other (provide explanation of content) _____

5 RNA Extraction Method: _____

Sample Buffer: _____

DNase Treated: Yes No (Select One)

6 Library Type:

 Stranded mRNA (poly-A enrichment) Stranded Total RNA (Mouse/Rat/ Human rRNA reduction) Stranded RiboZero RNA (Bacteria, Yeast, etc.) Ultra Low input _____ Small RNA

FOR OFFICE USE ONLY:

Submission # _____ Run # _____ Run Date _____ Bill Date _____ Order # _____

7 Sequencing Options:

samples total: _____ # lanes: _____ # samples per lane: _____

HiSeq HighOutput

Full Flowcell

HiSeq Rapid Run

Full Flowcell*

*HiSeq Rapid flowcells must have the same library (or pool) loaded into both lanes. If 2 lanes and not same library, you will be charged on a per lane basis.)

samples total: _____ # flowcells: _____

MiSeq

samples total: _____

NovaSeq

NovaSeq (Shared*)

OR

lanes: _____

reads per sample (M): _____

* Shared 2x150 runs only. If varied reads/sample required, note in Excel file.

8 Bioinformatics Options- Analysis of my data will be done by:

UWBC Bioinformatics Resource Center (I acknowledge that I am responsible for communicating all necessary project information to the BRC <brc@biotech.wisc.edu>)

Collaborator: Name _____ Email _____

By Submitting Lab

I have read and understand the Illumina Sequencing Policy found on the UWBC website (please initial): _____

1) Please bring a copy and e-mail (nextgen-seq@biotech.wisc.edu) an electronic copy of this form and a sample spreadsheet with sample name, concentration and volume when samples are submitted.

2) All RNA samples may be submitted to the Gene Expression Center, lab3240, in the Biotechnology Center at 425 Henry Mall.

Sample location (internal use only)