

# RNASeq-ILLUMINA SUBMISSION FORM

DATE: \_\_\_\_\_

(Office use) Submission #: \_\_\_\_\_

(Office use) Case #: \_\_\_\_\_

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

1 PI: \_\_\_\_\_

PI E-mail Address: \_\_\_\_\_

Signature: \_\_\_\_\_

Sample Submitted By: \_\_\_\_\_

Submitter E-mail Address: \_\_\_\_\_

Telephone No.: \_\_\_\_\_

Institution/Company Name: \_\_\_\_\_

Bill To/Accounts Payable: \_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

Grant/P.O. no: \_\_\_\_\_

Funding Source:  NIH  NSF  GLBRC  
 USDA  Other

2 Number of Samples: \_\_\_\_\_

Replacement samples (please note this on the spreadsheet)

- ≤ 24 samples must be submitted in 1.5mL single tubes. All sample tubes must be labeled with the sample name (≤ 8 characters with no special characters) on the top of the tube and PI last name/submission date on the side of the tube.
- > 24 samples must be submitted in a **clear, semi-skirted, conical** 96-well PCR plate with a -80 °C-stable adhesive seal. Label plates with the PI last name and submission date.

3 Name of Organism: \_\_\_\_\_

4 RNA source:      Tissue              Cells              Blood

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

Other (provide explanation of content) \_\_\_\_\_

6 RNA Extraction Method: \_\_\_\_\_

Sample Buffer: \_\_\_\_\_ (if not using water, please provide an aliquot)

DNase Treated:      Yes              No

7 Library Type:

- TruSeq Stranded mRNA (polyA enrichment)
- TruSeq Stranded Total RNA Gold (Human/Mouse/Rat mitochondrial + cytoplasmic rRNA reduction)
- TruSeq Stranded Total RNA (Plant; rRNA reduction)
- Ribo-Zero Plus rRNA Depletion w/ Stranded Total RNA (H/M/R + *B. subtilis*/*E. coli* rRNA; Globin reduction)  
Optional: Additional custom rRNA depletion probes supplied
- Takara SMART-Seq® v4 Ultra® Low Input RNA/NexteraXT (polyA enrichment)
- Takara SMARTer® Stranded Total RNA-Seq Kit v2 - Pico Input Mammalian (rRNA reduction)
- QIAseq miRNA Library

8 Submission Requirements:

- You must submit an electronic copy of this Submission Form and the [Sample Submission Spreadsheet](#). E-mail all electronic sample information to [gecinfo@biotech.wisc.edu](mailto:gecinfo@biotech.wisc.edu).

FOR OFFICE USE ONLY:

Run # \_\_\_\_\_ Run Date \_\_\_\_\_ Bill Date \_\_\_\_\_ Order # \_\_\_\_\_

## 9 Sequencing Options

### MiSeq

# of samples \_\_\_\_\_

# of flowcells \_\_\_\_\_

### NovaSeq6000\*

# of samples \_\_\_\_\_

# of lanes \_\_\_\_\_

\*MiSeq nano required for all full flow cells and lanes.

### NovaSeq6000 (2x150 shared ONLY)

# of samples \_\_\_\_\_

# of reads per sample (in millions)\*\* \_\_\_\_\_

\*\*  $\pm 20\%$  of stated value above

Use sample list to denote variable read requests.

### Custom Sequencing Run

(scRNA, assymetric read lengths, etc)

Must be approved by DNA Sequencing Facility.

Must be purchased as a full flow cell.

Sequencer: \_\_\_\_\_

Parameters: \_\_\_\_\_

## BIOINFORMATICS OPTIONS (OPTIONAL)

Analysis to be done by (please choose one):

- UWBC Bioinformatics Resource Center (Please email [brc@biotech.wisc.edu](mailto:brc@biotech.wisc.edu) to inform them of your project.)
- Collaborator - Name \_\_\_\_\_ Email \_\_\_\_\_ UWNnetID \_\_\_\_\_

## 10 Sample Disposal

### Please select one option for each category:

**RNA stocks:** Hold to return to client

Discard after completion of service

**cDNA libraries:** Hold to return to client

Discard after completion of service

You MUST contact [gecinfo@biotech.wisc.edu](mailto:gecinfo@biotech.wisc.edu) to arrange a time to pick up your samples. All samples will be discarded six months after completion of service.

I have read and understand the Illumina Sequencing Policy found on the [UWBC website](#) (please initial): \_\_\_\_\_