

ILLUMINA SUBMISSION FORM

Submission No. _____

DATE: _____

PLEASE ENSURE BOTH SIDES OF FORM ARE FILLED OUT ENTIRELY

Sample submitted by: _____

PI: _____

Telephone: _____

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 ☐ GLBRC

☐ USDA ☐ Other

UW Institution: ☐ SMPH ☐ CALS ☐ L&S ☐ SOP

☐ COE ☐ Other _____

Library Preparation:

Name of Organism: _____

Input Nucleic Acid: ☐ gDNA ☐ cDNA ☐ ChIP (shearing size _____)

☐ total RNA ☐ mRNA ☐ ribo-Reduced RNA ☐ smallRNA

☐ Other (provide explanation of content) _____

☐ Library prepared by lab (QC only) _____

Library Type: ☐ gDNA no-PCR ☐ gDNA low input ☐ Nextera gDNA ☐ ChIP ☐ mate pair

☐ Genotyping by Sequencing (GBS) ☐ stranded mRNA ☐ mRNA ☐ smallRNA

☐ Other (discuss with facility before submitting) _____

Sample Requirements: 1-2ug of high quality input DNA at ≥ 50 ng/ul with an A_{260}/A_{280} of ~ 1.8 is requested.

For RNA-based projects, 1-2ug of high quality total RNA, or 100 ng of mRNA is requested.

Sample Buffer: _____

Have samples been purified?

☐ Yes

☐ No

Method used: _____

Indexing: ☐ Yes ☐ No

samples per lane: _____

Sample Information: Please fill out the following table with appropriate information. Attach a second sheet if necessary.

	Sample Name	Conc. (ng/ μ l)	A_{260}/A_{280}	Volume (μ l)	Total (μ g)
Sample 1					
Sample 2					
Sample 3					
Sample 4					
Sample 5					
Sample 6					
Sample 7					
Sample 8					

Attach gel image here, or send via email to nextgen-seq@biotech.wisc.edu:

Sequencing options:

☐ HiSeq 2000

☐ 1x50

☐ 2x50

☐ 1x100

☐ 2x100

☐ HS2500 (Rapid Run)

☐ 1x50

☐ 2x50

☐ 1x100

☐ 2x100

☐ 1x150

☐ 2x150

☐ MiSeq

☐ 1x50

☐ 2x150

☐ 2x250

Data Format:

☐ FASTQ

☐ ELAND (Organism and Alignment Genome Name): _____

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