

# ILLUMINA SUBMISSION FORM

Submission No. \_\_\_\_\_

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

**\*PLEASE ENSURE BOTH SIDES OF FORM ARE FILLED OUT ENTIRELY\***

Sample submitted by: \_\_\_\_\_  
PI: \_\_\_\_\_

Institution/Company Name: \_\_\_\_\_  
Bill To/Accounts Payable: \_\_\_\_\_

Telephone: \_\_\_\_\_

\_\_\_\_\_

Email Address: \_\_\_\_\_

Account/P.O. No.: \_\_\_\_\_

PI Email Address: \_\_\_\_\_

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

Funding Source:  NIH  NSF  GLBRC

USDA  Other

UW Affiliation:  UWCCC  Waisman Ctr.

UW Institution:  SMPH  CALS  L&S  SOP

UW System  External

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  exome  16s

Genotyping by Sequencing (GBS)  stranded mRNA  mRNA  smallRNA  amplicon

Other (discuss with facility before submitting) \_\_\_\_\_

Sample Buffer: \_\_\_\_\_

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/μl)	A <sub>260</sub> /A <sub>280</sub>	Volume (μl)	Total (μg)	Index #
Sample 1						
Sample 2						
Sample 3						
Sample 4						
Sample 5						
Sample 6						
Sample 7						
Sample 8						

FOR OFFICE USE ONLY:

GS  Protocol  Run # \_\_\_\_\_  Run Date \_\_\_\_/\_\_\_\_/\_\_\_\_  Bill Date \_\_\_\_/\_\_\_\_/\_\_\_\_  ASANA

Attach gel image here, or send via email to [nextgen-seq@biotech.wisc.edu](mailto:nextgen-seq@biotech.wisc.edu):

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Sequencing options:

- |  |   |                                |
|--|---|--------------------------------|
| <input type="checkbox"/> HiSeq 2000    | <input type="checkbox"/> HS2500 (Rapid Run) | <input type="checkbox"/> MiSeq |
| <input type="checkbox"/> 1x50          | <input type="checkbox"/> 1x50               | <input type="checkbox"/> 1x50  |
| <input type="checkbox"/> 2x50          | <input type="checkbox"/> 2x50               | <input type="checkbox"/> 2x75  |
| <input type="checkbox"/> 1x100         | <input type="checkbox"/> 1x100              | <input type="checkbox"/> 2x150 |
| <input type="checkbox"/> 2x100         | <input type="checkbox"/> 2x100              | <input type="checkbox"/> 2x250 |
| <input type="checkbox"/> Full Flowcell | <input type="checkbox"/> 1x150              | <input type="checkbox"/> 2x300 |
|  | <input type="checkbox"/> 2x150              | <input type="checkbox"/> Nano  |
|  | <input type="checkbox"/> Full Flowcell      |                                |

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