

Single Cell RNASeq

Submission No. _____

DATE: _____

SUBMISSION FORM

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

PI: _____

Institution/Company Name: _____

Bill To/Accounts Payable: _____

Sample submitted by: _____

Telephone: _____

Email Address: _____

Account/P.O. No.: _____

PI Email Address: _____

Signature: _____

UW Affiliation: UWCCC Waisman Ctr. UW System ExternalFunding Source: NIH NSF GLBRC USDA OtherUW Institution: SMPH CALS L&S SOP COE Other _____

1) **Genome:** Human (hg19) Mouse (mm10) Custom (transgene, viral genome, alternative genome build, etc.)

a. If custom, please indicate what is needed: _____

2) **Submission type:** Cell Suspension Nuclei Suspension

3) **Cell type:** _____ Cell Culture Tissue Prep

4) **Cell suspension buffer:** _____

5) **Starting cell/nuclei concentration and viability range (if known):** _____

6) **Targeted cell/nuclei recovery:** _____

7) **Cells/nuclei fixed:** Yes No

8) **Number of samples:** _____

9) **Library type:**

 Single Cell-Gene Expression *de novo* assemble Single Cell-V(D)J Immune Profiling Genome Sequencing Single Cell-CNV Exome Sequencing Single Cell ATAC-Seq

10) **Date of experiment:** _____ **Estimated time of arrival:** _____

11) **Is this a joint submission with another group:** Yes No

- If Yes, list other group's PI: _____

*If submitting a joint submission please submit a separate submission form with the other group's information.

Bioinformatics options

12) Analysis

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): _____

Please e-mail the GEC at gecinfo@biotech.wisc.edu to coordinate a time between 12-2pm to submit samples and approve sample input for single cell capture. Samples should be submitted on ice to the Gene Expression Center (Rm. 3240 Biotech) in the Biotechnology Center at 425 Henry Mall.

For Internal Use

MiSeq QC Run:

- Micro
- Nano

MiSeq QC data analysis needed prior to sequencing

Sequencing Options:

- HiSeq Rapid Run, 2 lanes (2x50bp) (Avg: 150M reads/lane)
- HiSeq HighOutput, 8 lanes (2x50bp) (Avg: 200M reads/lane)
- NovaSeq S1, ____ lanes (2x50bp) (Avg: 720M reads/lane)
- NovaSeq S2, ____ lanes (2x50bp) (Avg: 1845M reads/lane)