# Genomics Resources Core Facility at Weill Cornell Medicine

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## Sample Submission Guidelines

1. iLab registration and submission: Please register and "request access" to GRCF page through iLab (wcmc.corefacilities.org) to initiate the service request. Once access request has been approved on our end, you can select the service of your choice to submit a service request to our core. It is your responsibility to keep track of the identification of your samples and be precise on the method of sample library preparation and the sequencing type, etc. When filling out submission forms in iLab, use the sample ID and description that matches your records.

2. Nucleic Acid Extraction: We accept samples from any extraction method, but TRIzol extractions are not recommended as they can carry over phenol and salt that affect some downstream applications. If you have to use TRIzol, we recommend column cleanups. Total RNA sample must be free of DNA.

3. Sample Volume and Concentration Guidelines

(1) Quality-Control Volume Requirements

All extracted DNA or RNA samples will be evaluated for quantity with NanoDrop Spectrophotometer or Qubit Fluorometer, and quality with Agilent 2100 Bioanalzyer or 4200 TapeStation. The QC results or the issues with sample quality and quantity will be reported to the users via email, and uploaded to iLab system before sample library construction.

For quality control, please provide at least 3-5 µL of sample volume plus 1 µL or more to allow for pipetting errors:

- TapeStation: 1-2 µL
- Bioanalyzer: 1-2 µL

- NanoDrop: ~1 μL
- Qubit: 1 μL

(2) Submit your samples in 1.5 ml microcentrifuge tubes. The tubes must be clearly labeled on the lid. We suggest using low-retention tubes (e.g. Eppendorf LoBind).

Note: Please don't dilute your nucleic acid sample after the concentration is measured.

4. Sample shipment:

- For genomic DNA and other dsDNA shipments in tubes, cold packs (e.g. "blue ice") are usually sufficient.
- RNA samples should be shipped on dry ice. Please only ship with courier services (FedEx, UPS, DHL).

5. RNA-Seq and miRNA-Seq sample submission:

(1) For RNA sample library preparation, please provide the following (with NanoDrop measurement):

- Stranded PolyA selection: 100 to 500 ng of DNase-digested total RNA in 10 - 30 μL water, RNA integrity number (RIN) > 8
- Stranded rRNA depletion: 100 to 500 ng of DNase-digested total RNA in 10 μL water, RNA integrity number (RIN) 2 – 8.

- Low-input RNA-seq: 5-10 ng using Illumina TruSeq or NEBNext Ultra kits, the data is not guaranteed.

(2) For miRNA sample library preparation, please provide the following:

1 μg of total RNA in 5 μl water (200ng/ μl).

6. DNA sample for Whole Exome Sequencing (WES) and Whole Genome Sequencing (WGS) sample submission:

Please provide 10 ng – 2 μg of gDNA (with Qubit measurement) depending on the sample construction method. We recommend DNA purity with an OD260/280=1.8-2.0 with high molecular weight and without RNA contamination. Please contact our staff for detail information.

7. ChIP-Seq sample submission:

Please submit 10-50ng of ChIP DNA in nuclease-free water. We will check the fragment size and the quality / quantity of the sample before library construction. We strongly recommend ChIP DNA be fragmented to 200-600bp in size for optimal library performance and reduced background noise levels.

8. Sequence-ready sample library submission:

If you prepare the sample library in your own lab and use our sequencing service only, please inform our staff and discuss about the selection of sample index for sample pooling before library preparation. After the completion of library prepped, you need to precisely check the concentration and quality of

each final sample library before pooling. Then you can submit 10 - 50 µl (depending on the sequencer type) of 10 nM pooled library sample using nuclease-free 1.5 ml low-bind microfuge tube together with sample index information.

9. Single-cell sequencing:

Droplet-based single-cell system like 10X Genomics Chromium platform has been installed in our core lab. We provide the services including RNA-Seq, ATAC-Seq and multiple single-cell solutions. Please contact us if you would like to initiate single-cell sequencing projects.

10. Next Generation Sequencing platforms:

Besides Illumina NovaSeq6000, NextSeq2000/500 and MiSeq.

The capacity and features of the NovaSeq6000, the highest throughput are listed below. Please contact us for any questions regarding the usage of the sequencing systems.

| **Flow cell type** | **S Prime Flow Cell** | **S1 Flow Cell** | **S2 Flow Cell** | **S4 Flow Cell** |
|---|---|---|---|---|
| **Lanes** | 2 | 2 | 2 | 4 |
| **Sequencing reagent type (cycles)** | 2x50/2x100/2x150/2x250 | 2x50/2x100/2x150 | 2x50/2x100/2x150 | 2x50/2x100/2x150 |
| **Output** | 80-250 Gb | 167-500 Gb | 417-1250 Gb | 2000-3000 Gb |
| **Single reads (PF reads)** | 0.65-0.8 B | 1.3-1.6 B | 3.3-4.1 B | 8-10 B |
| **Run Time** | 13 - 25 hours | 13 - 25 hours | 16 - 36 hours | 36 - 44 hours |
| **Sample Throughput** | | | | |
| Human Genome / run (30X coverage/sample) | 4 | 8 | 20 | 48 |
| Exomes / run (100X coverage/sample) | 40 | 80 | 200 | 400 |
| Transcriptomes / run (50 million reads/sample) | 32 | 64 | 164 | 500 |

For more information:

Please read about the NovaSeq 6000 specs at
https://www.illumina.com/systems/sequencing-platforms/novaseq/specifications.html