

### INTRO

---

NYGC offers sequencing of prepared libraries for paired-end and single-end sequencing on the HiSeq2500 (Rapid Run and High Output modes), HiSeqX and NovaSeq for delivery of fastq files.

### SUBMISSION REQUIREMENTS

---

- **HiSeq2500:** For submission of libraries for sequencing on the Rapid Run flowcell, NYGC requests full flowcell submissions (in units of two lanes). For submission of libraries for sequencing on the High Output flowcell, NYGC requests submission of at least 4 lanes for the paired-end 125 cycle (PE125) run types, and full flowcell submissions (in units of eight lanes) for all other run types.
- **HiSeqX:** Libraries can also be run on HiSeqX using the 2x150bp read length for a minimum submission of one lane
- **NovaSeq:** Libraries can be submitted for sequencing on Novaseq for the S2 or S4 flowcell using the 2x50bp, 2x100bp and 2x150bp read length. NYGC requests full flowcell submissions for a quicker turnaround time.

### LIBRARY REQUIREMENTS

---

Upon receipt of libraries, QC will be performed using three independent methods, first by measuring quantification by fluorescence using PicoGreen, second by measuring the integrity on the Fragment Analyzer and third by quantifying adapter-ligated libraries using qPCR. Investigators will be notified of libraries that fall below the required mass for sequencing, have inconsistent concentration measurements across the three QC methods, contain adapter dimer contamination, or show size distribution outside of the optimal range for sequencing. Libraries that do not meet the requirements may still be processed for sequencing based on customer decision. In that case NYGC takes no responsibility for failures or sub-optimal results.

The sample submission requirements are as follows:

#### **LIBRARY REQUIREMENTS for Hiseq2500 and HiSeqX**

- NYGC requests that the investigator verifies the concentration and quality of the libraries using PicoGreen (or equivalent), and BioAnalyzer Analyzer traces. This data should be provided to NYGC
- Please submit libraries at 10nM in a minimum volume of 20µl

#### **LIBRARY REQUIREMENTS for Novaseq**

- NYGC requests that the investigator verifies the concentration and quality of the libraries using PicoGreen (or equivalent), and Fragment Analyzer traces. This data should be provided to NYGC
- Please submit libraries at 3nM in a minimum volume of 300µl

### SEQUENCING

---

Sequencing can be performed on the HiSeq2500, HiSeqX or Novaseq instruments. The HiSeq 2500 generates roughly 200-250 million passed filter single end sequencing reads per flow cell lane for the High Output mode and roughly 150 million single end reads per flow cell lane for the Rapid Run mode. HiSeqX generates roughly 400 million passed filter single end sequencing reads per flow cell lane and Novaseq S2 generates roughly 1.4-1.6 billion single end passed filter sequencing reads per flow cell lane.

### QUALITY CONTROL METRICS

---



## LANE SEQUENCING

For library sequencing, expected read number and sequence quality is application dependent, and will be discussed prior to project initiation.

### DELIVERABLES

---

The files delivered at the completion of a project include;

- FASTQ files containing all pass filter reads and quality scores
- 3 months of data storage, unless otherwise specified

### TURNAROUND TIME

---

NYGC estimates turnaround time from the date libraries pass QC in the NYGC laboratory. Typical turnaround time is about 2 weeks for full flowcell submissions and 4 weeks for partial flowcell submissions, but can vary based on queue when libraries arrive. Please discuss any expedited turnaround needs with your Project Manager.